

1/498

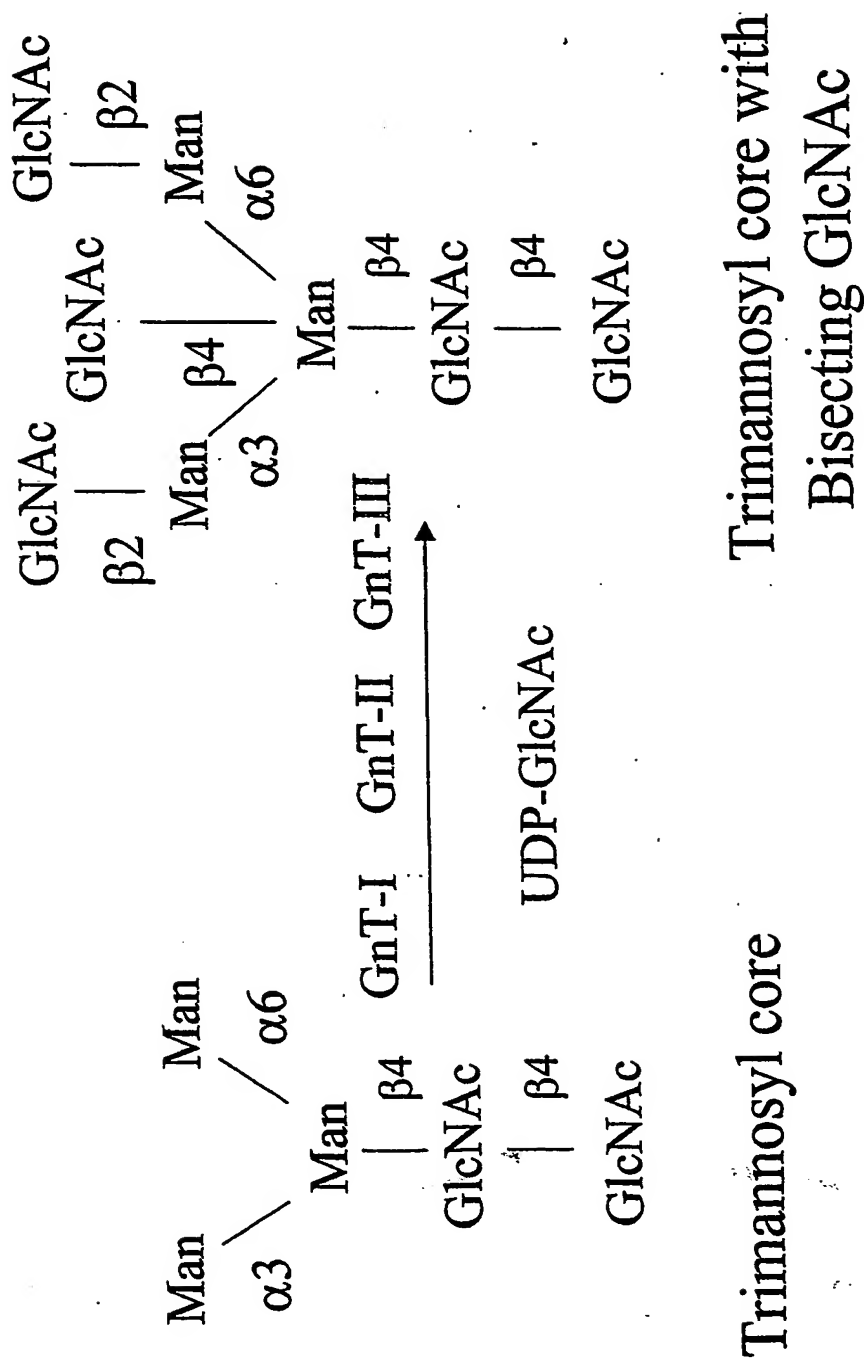


FIG. 1

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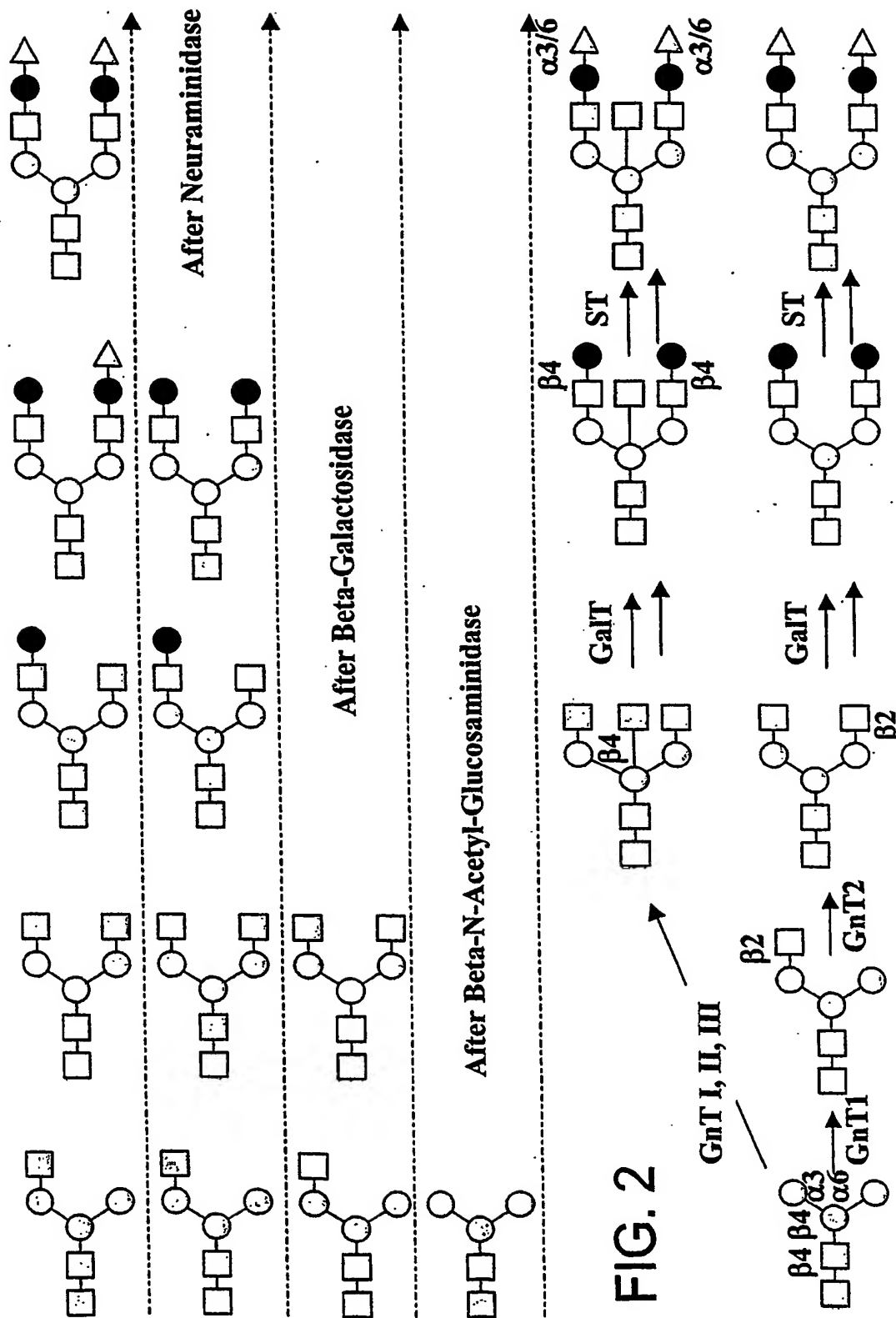


FIG. 2



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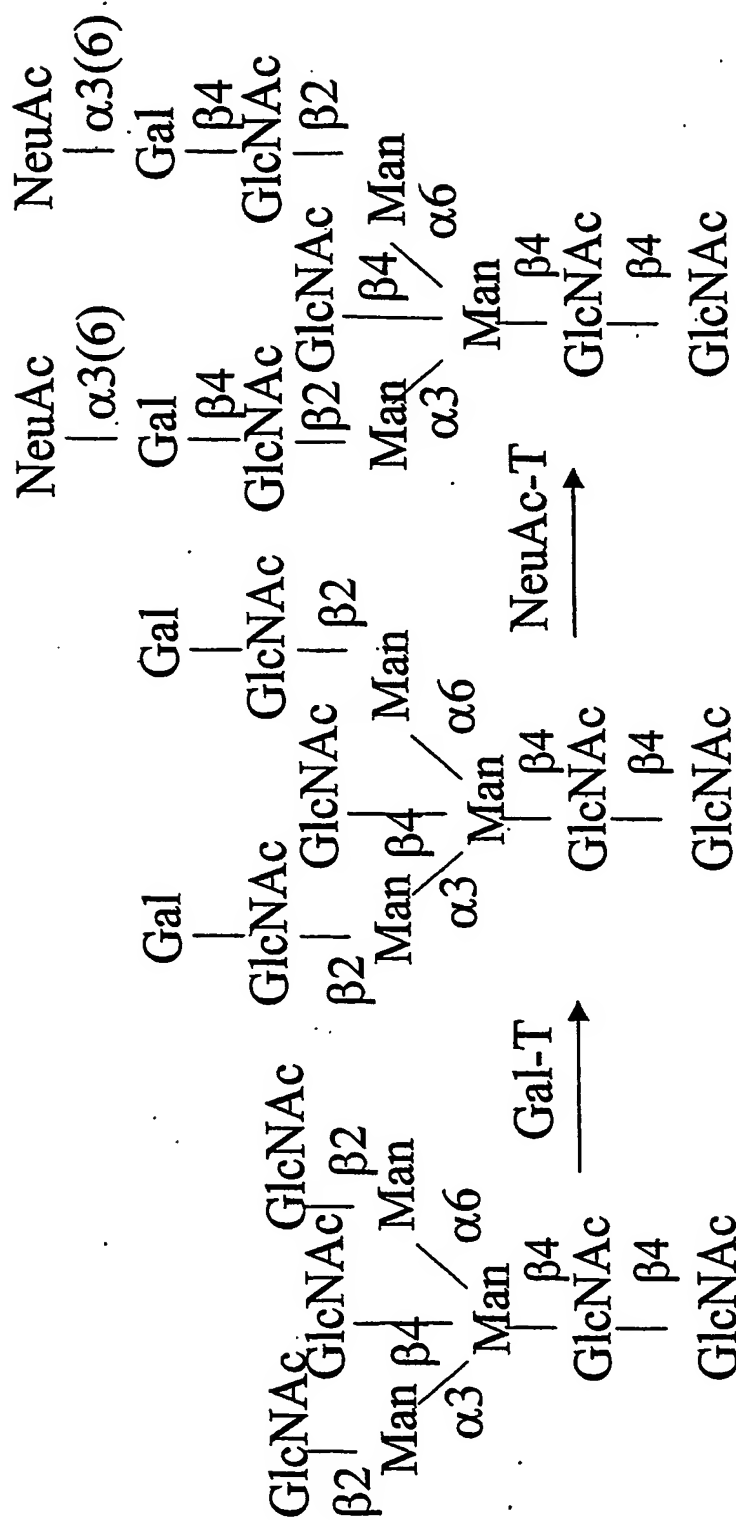


FIG. 3

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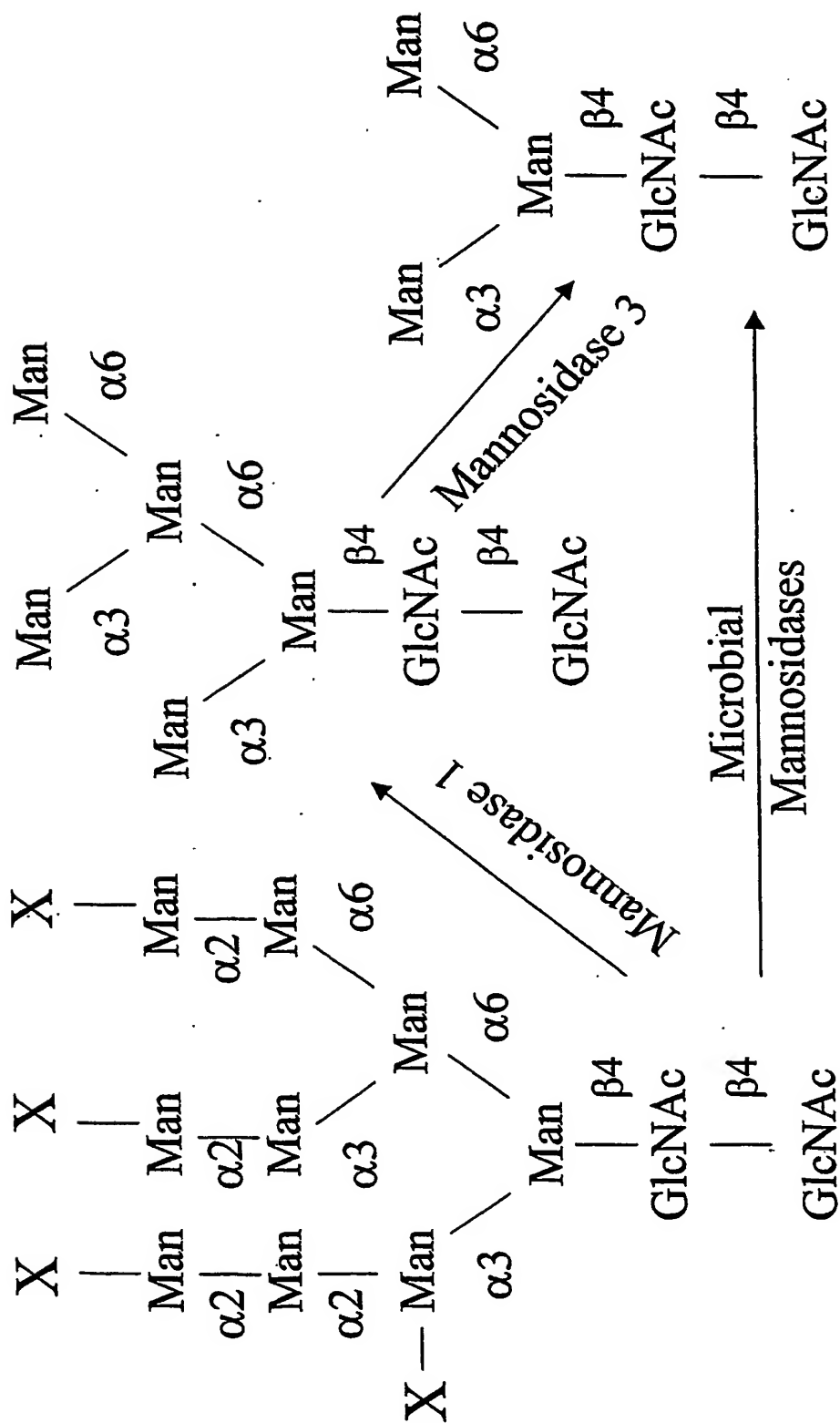


FIG. 4

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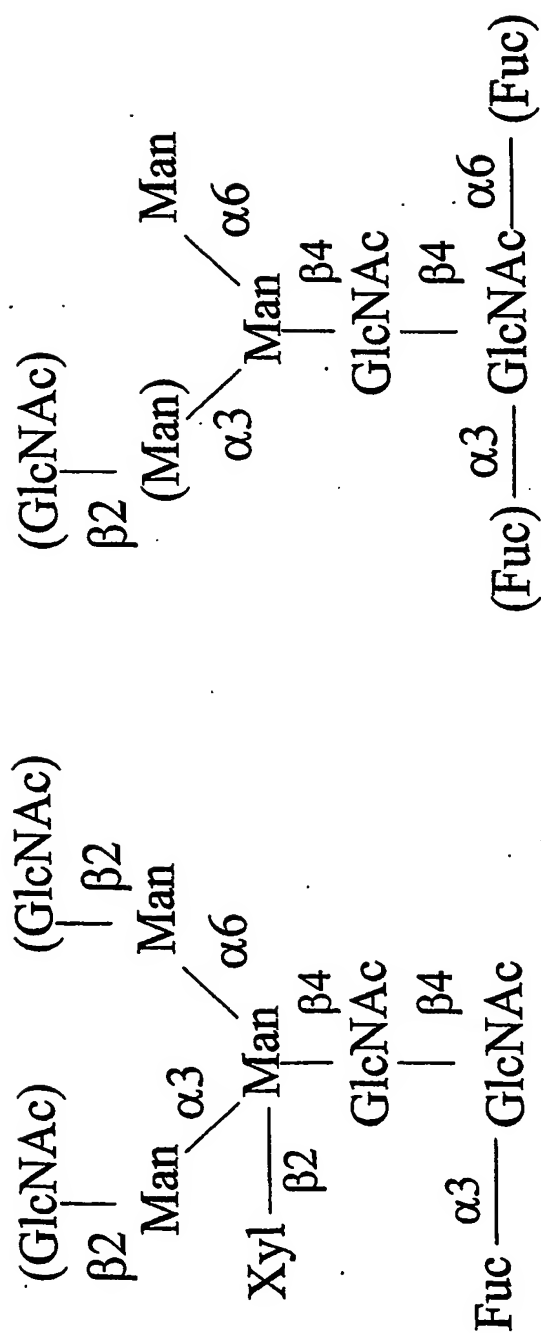


FIG. 6

FIG. 5

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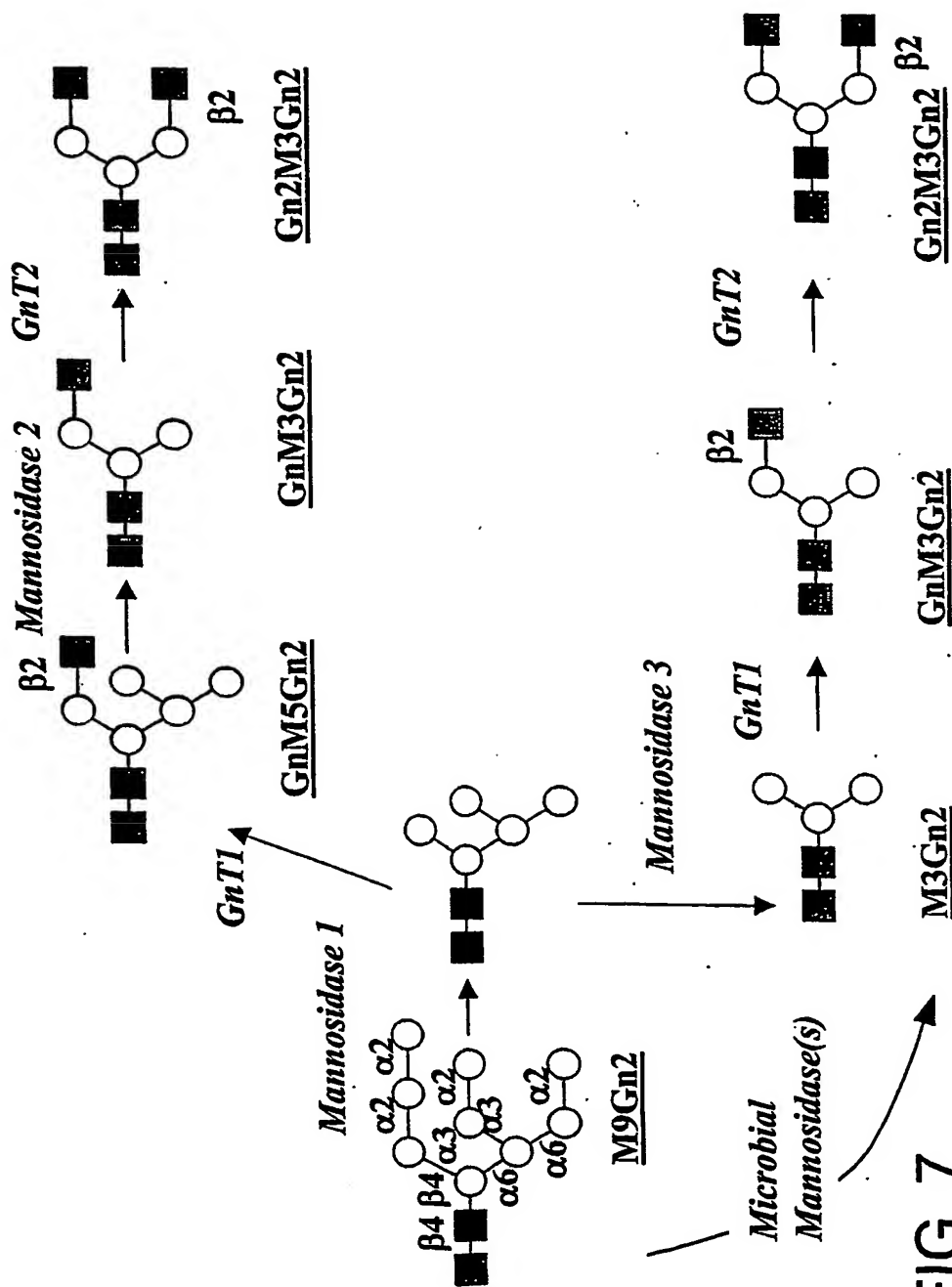


FIG. 7

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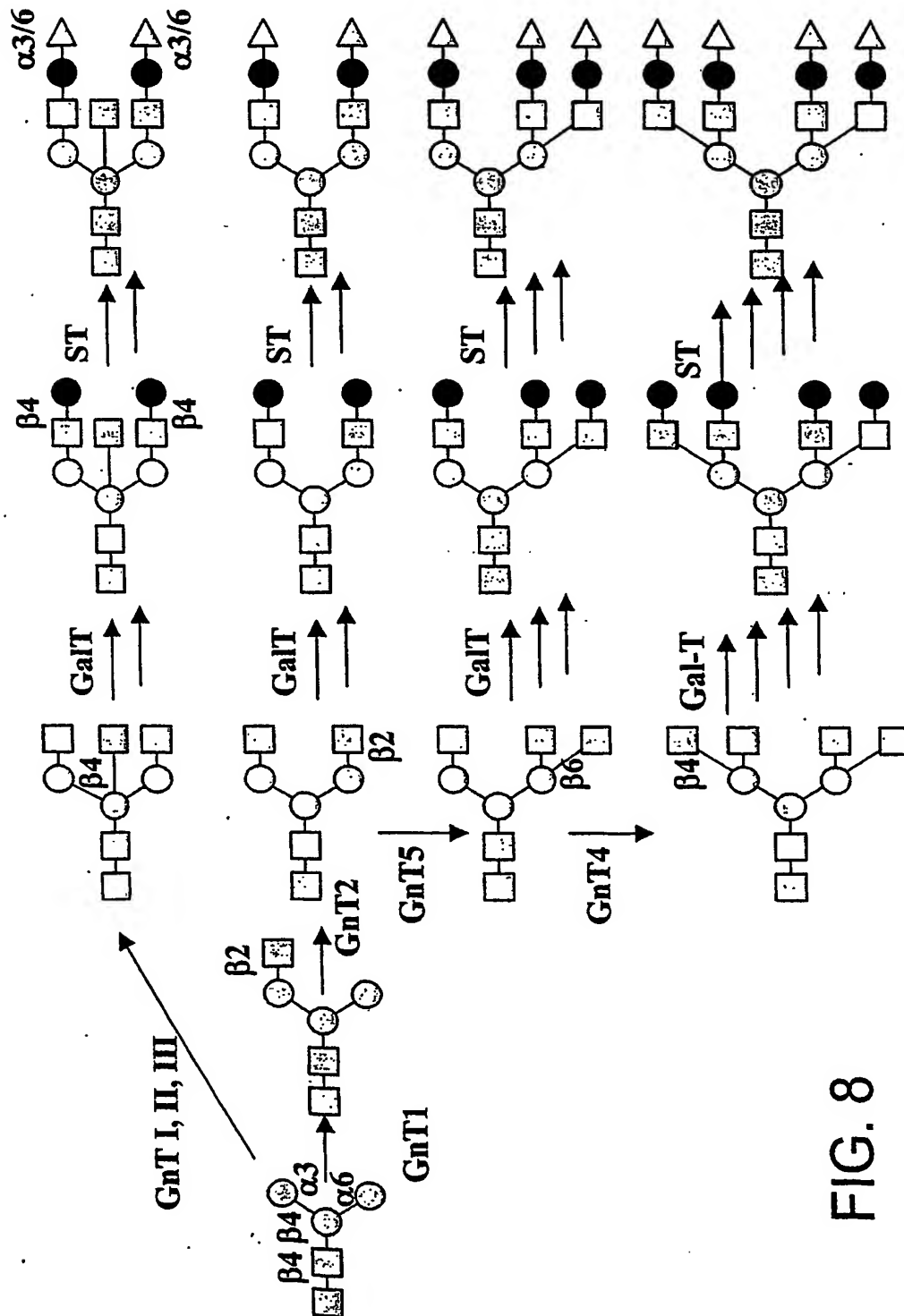


FIG. 8

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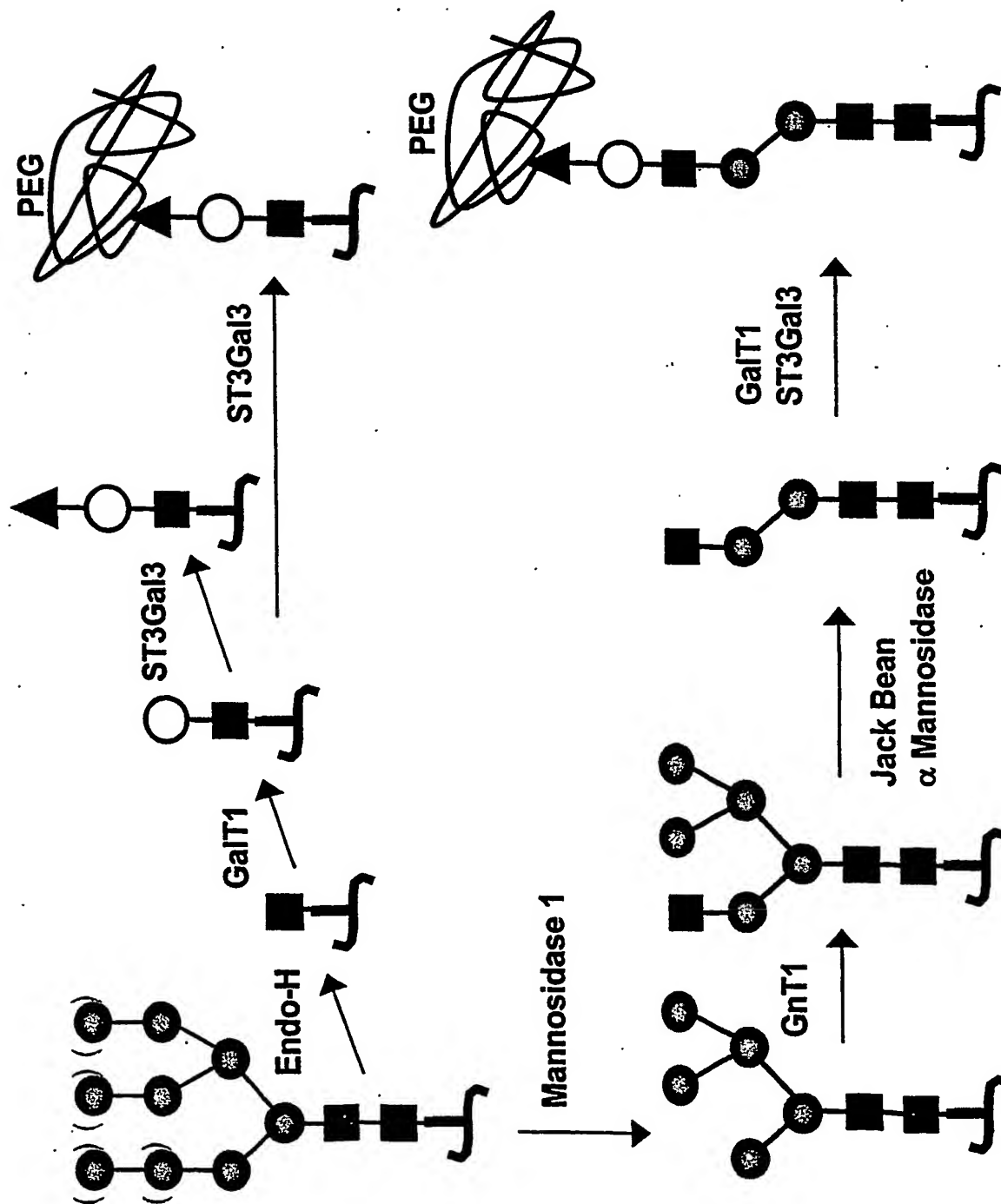


FIG. 9

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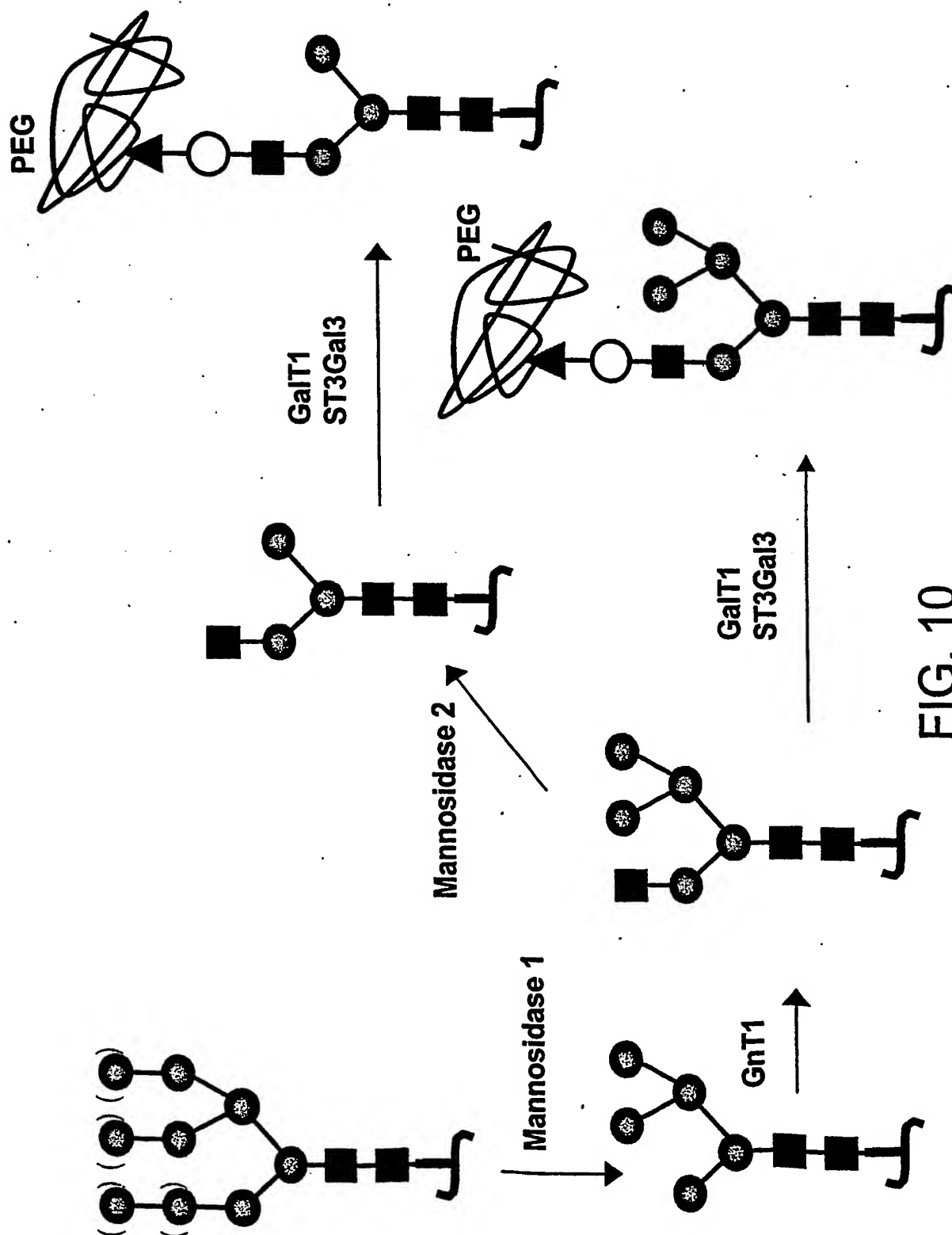
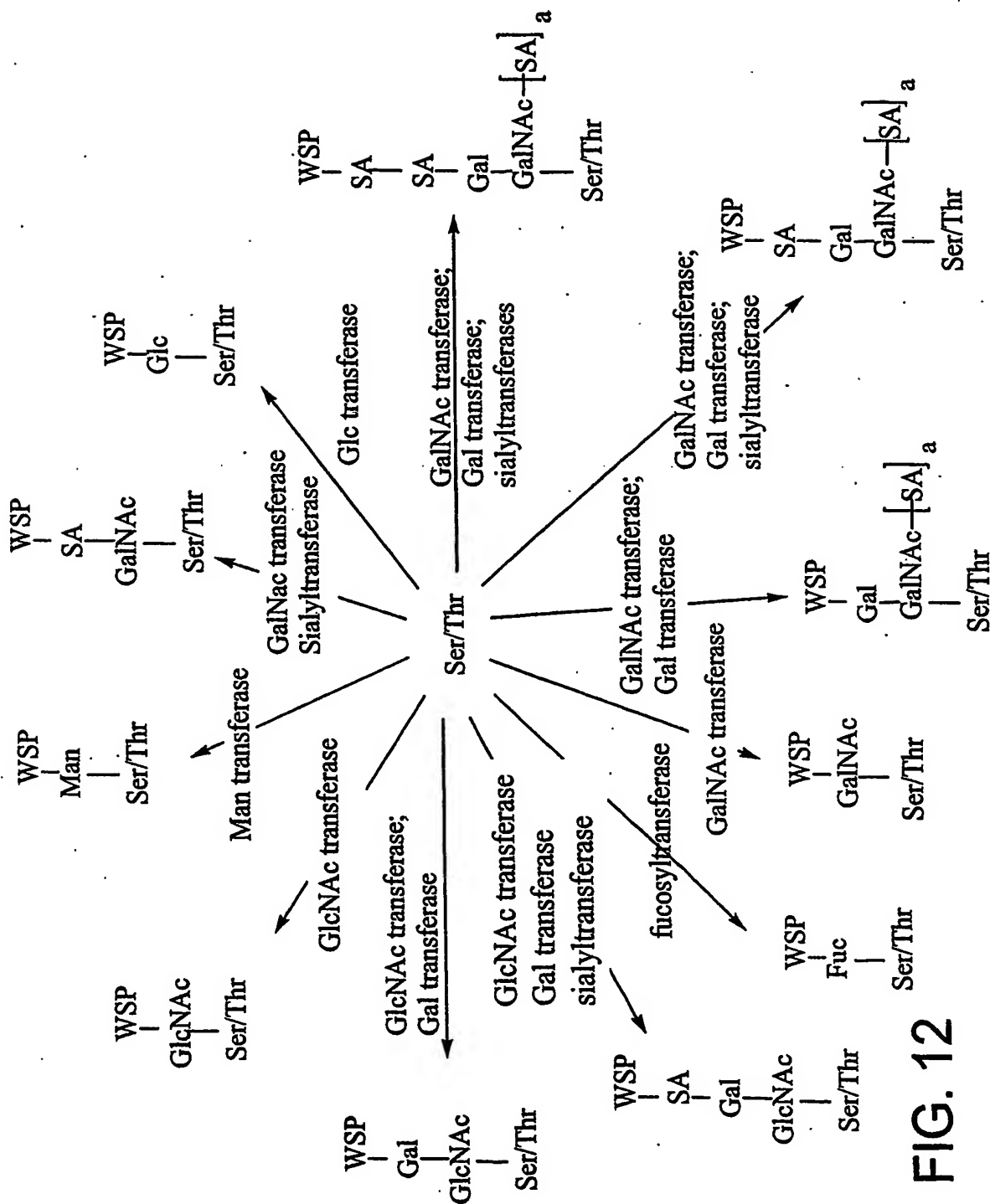


FIG. 10







**FIG. 12**

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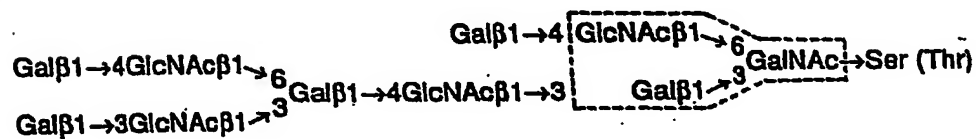
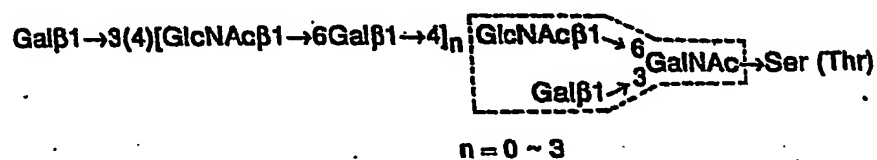
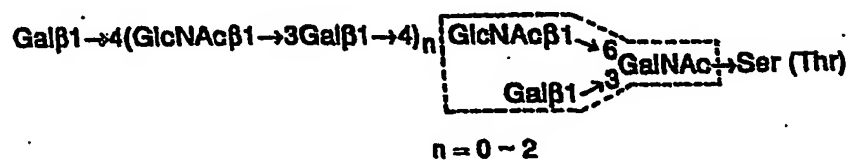
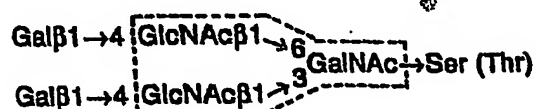
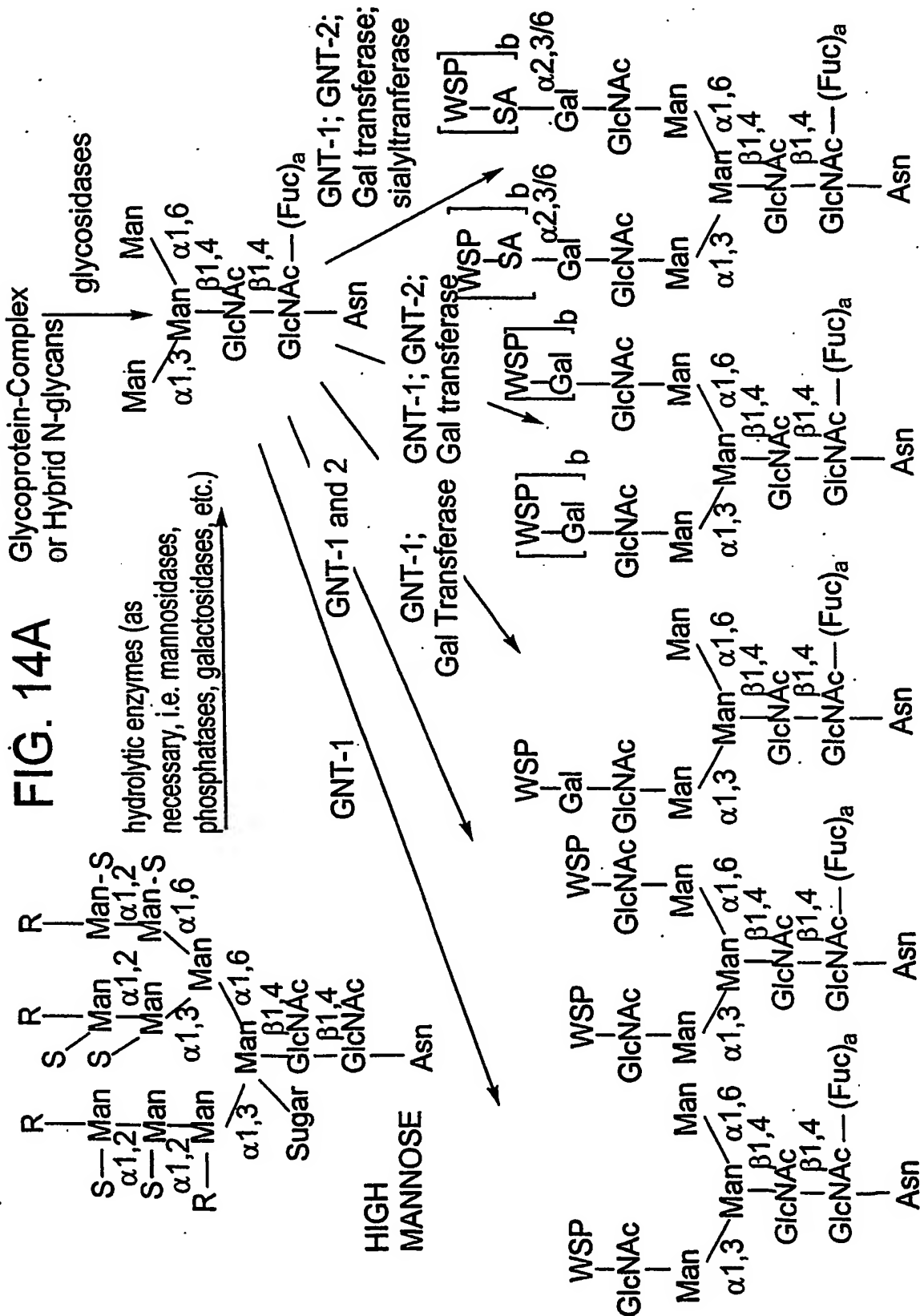
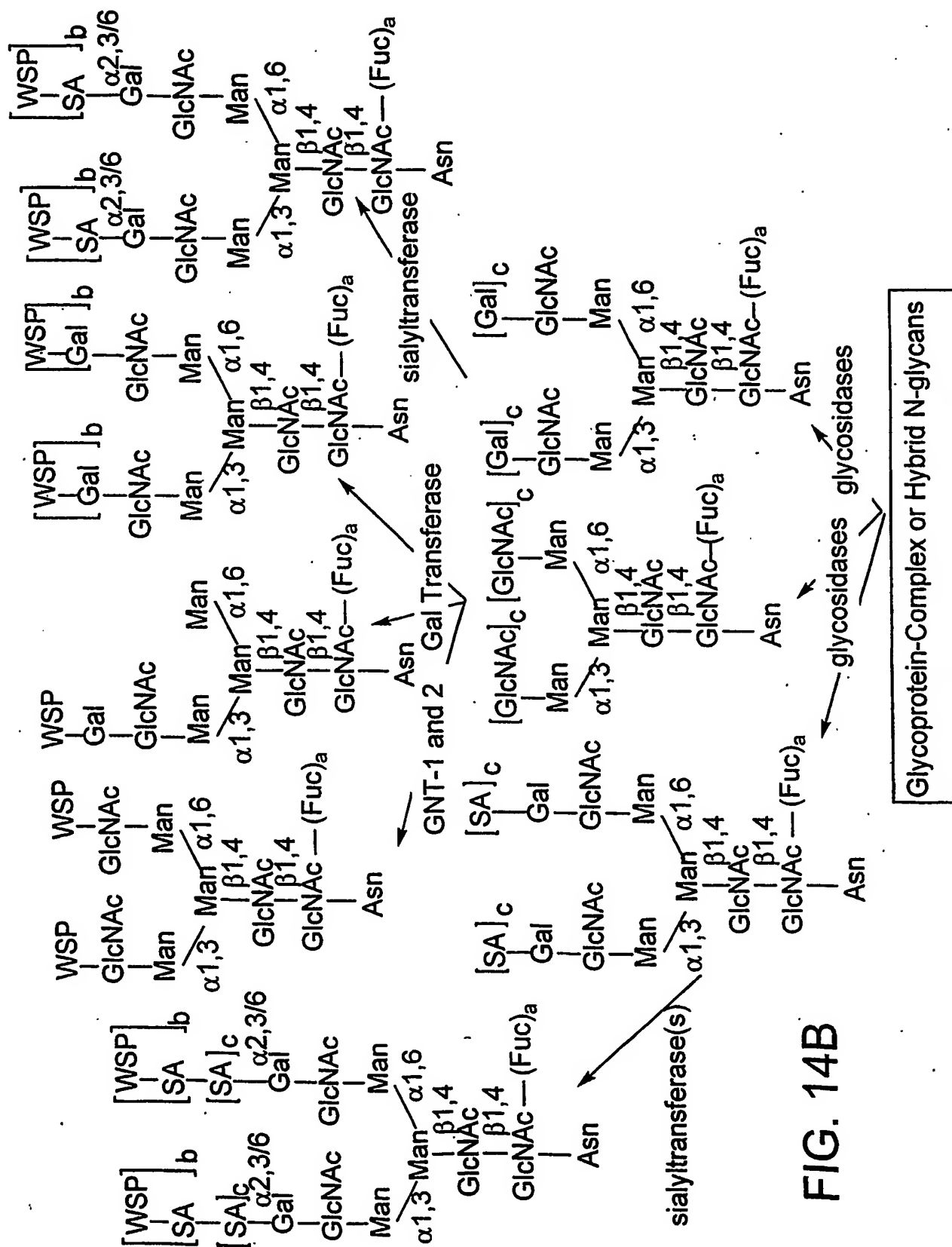
**Core 1****Core 2****Core 3****Core 4**

FIG. 13

## Glycoprotein-Complex or Hybrid N-glycans



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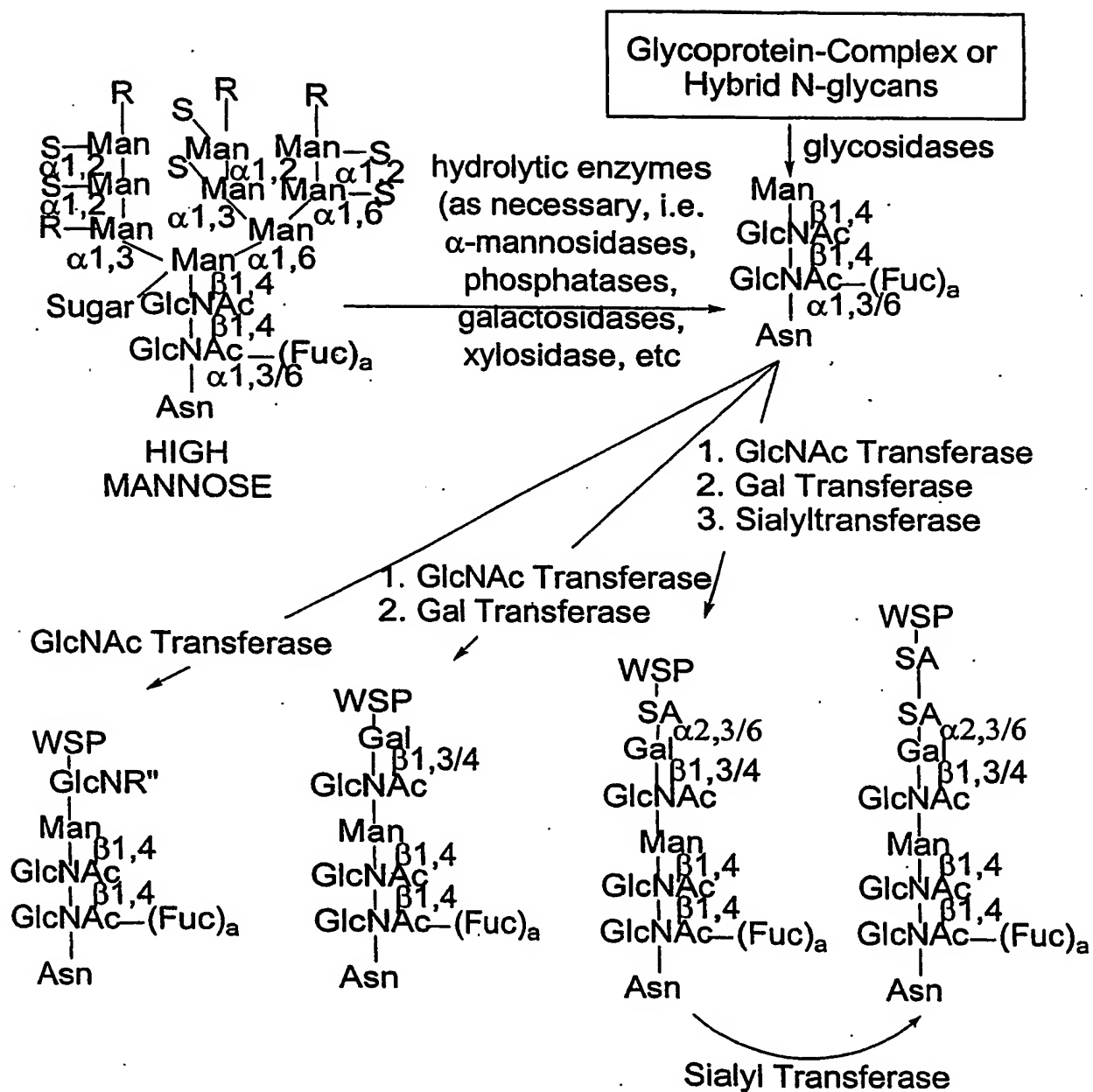


FIG. 15

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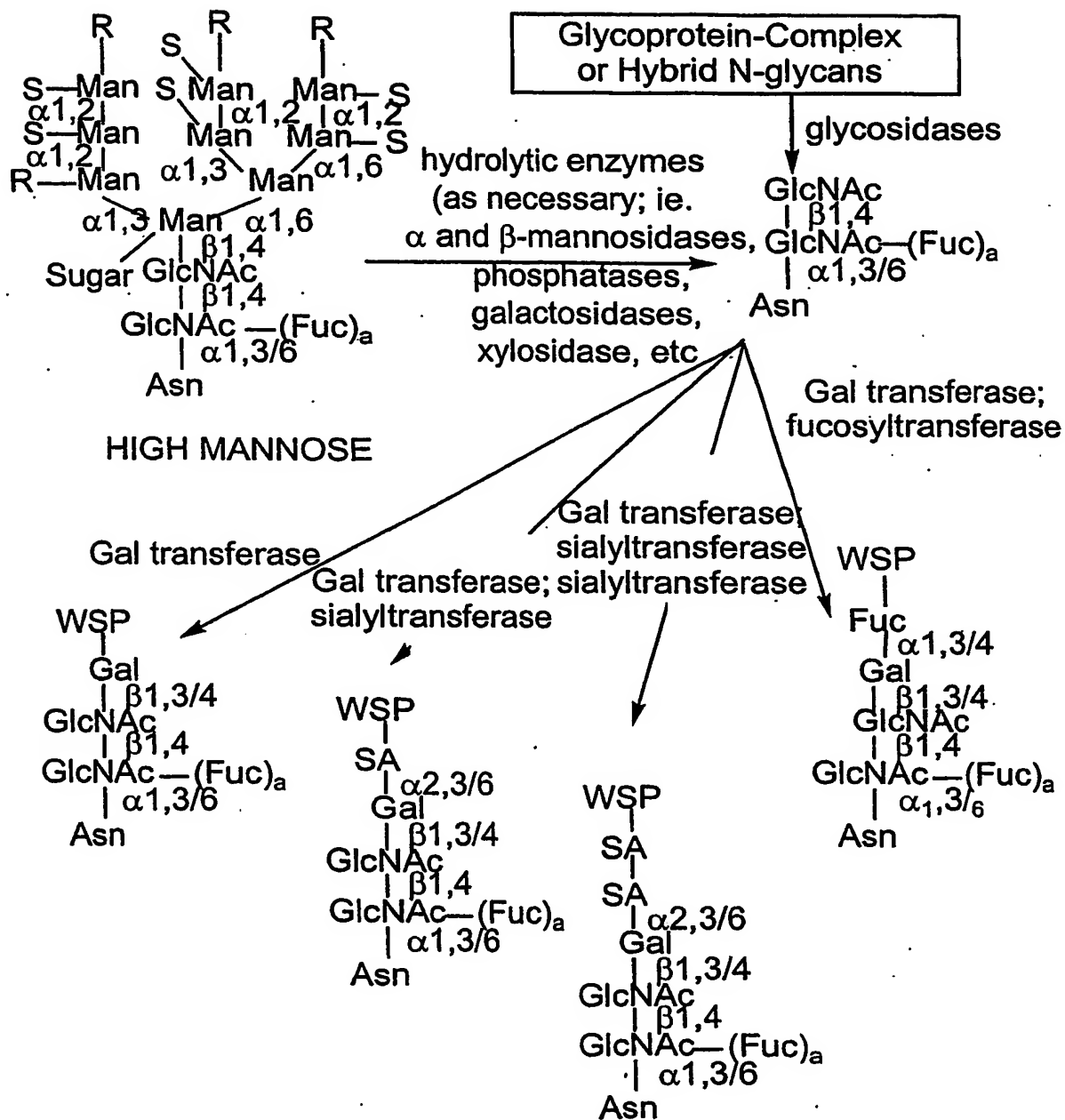


FIG. 16

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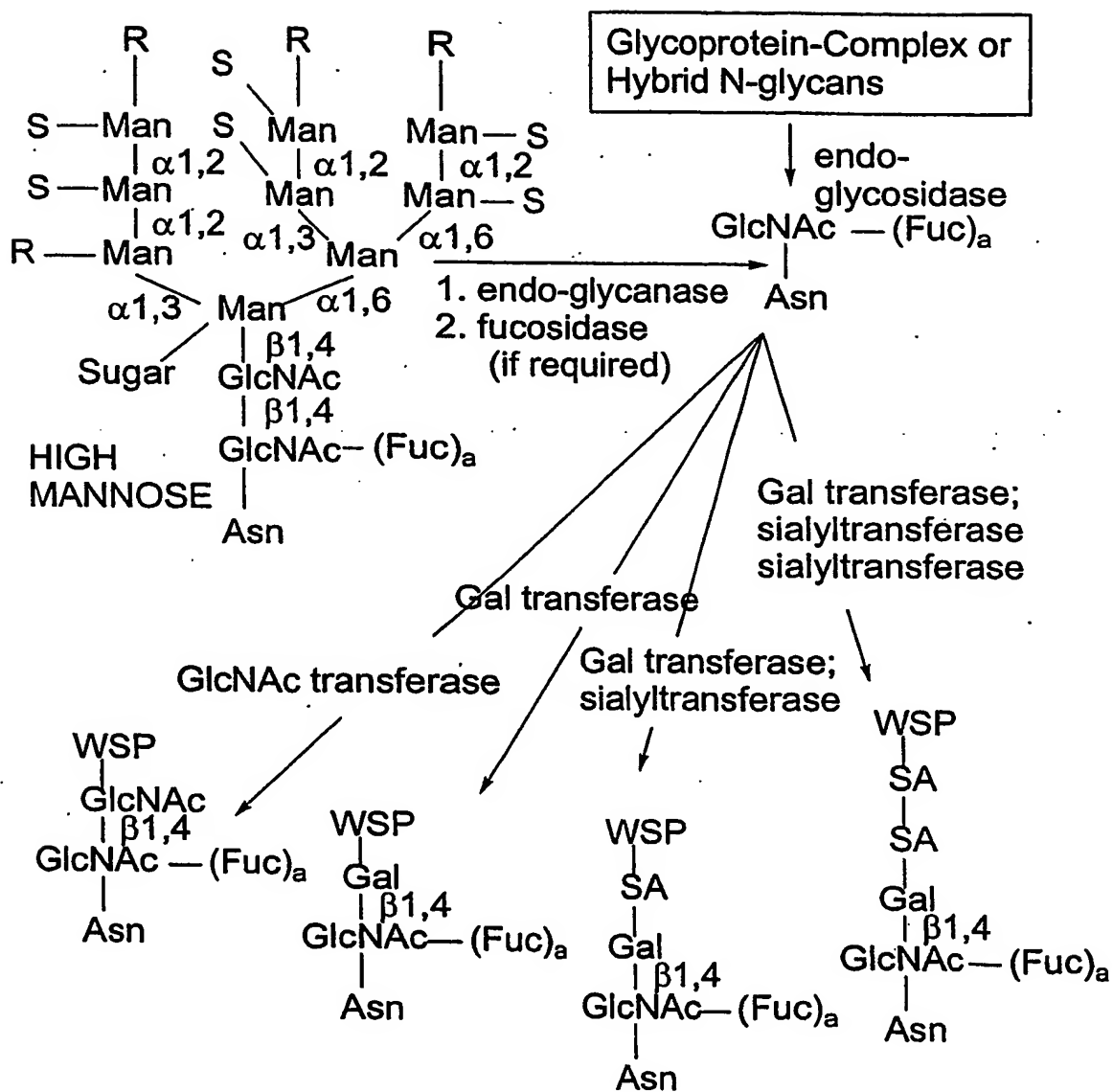
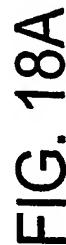


FIG. 17







[illegible]

**FIG. 19A**

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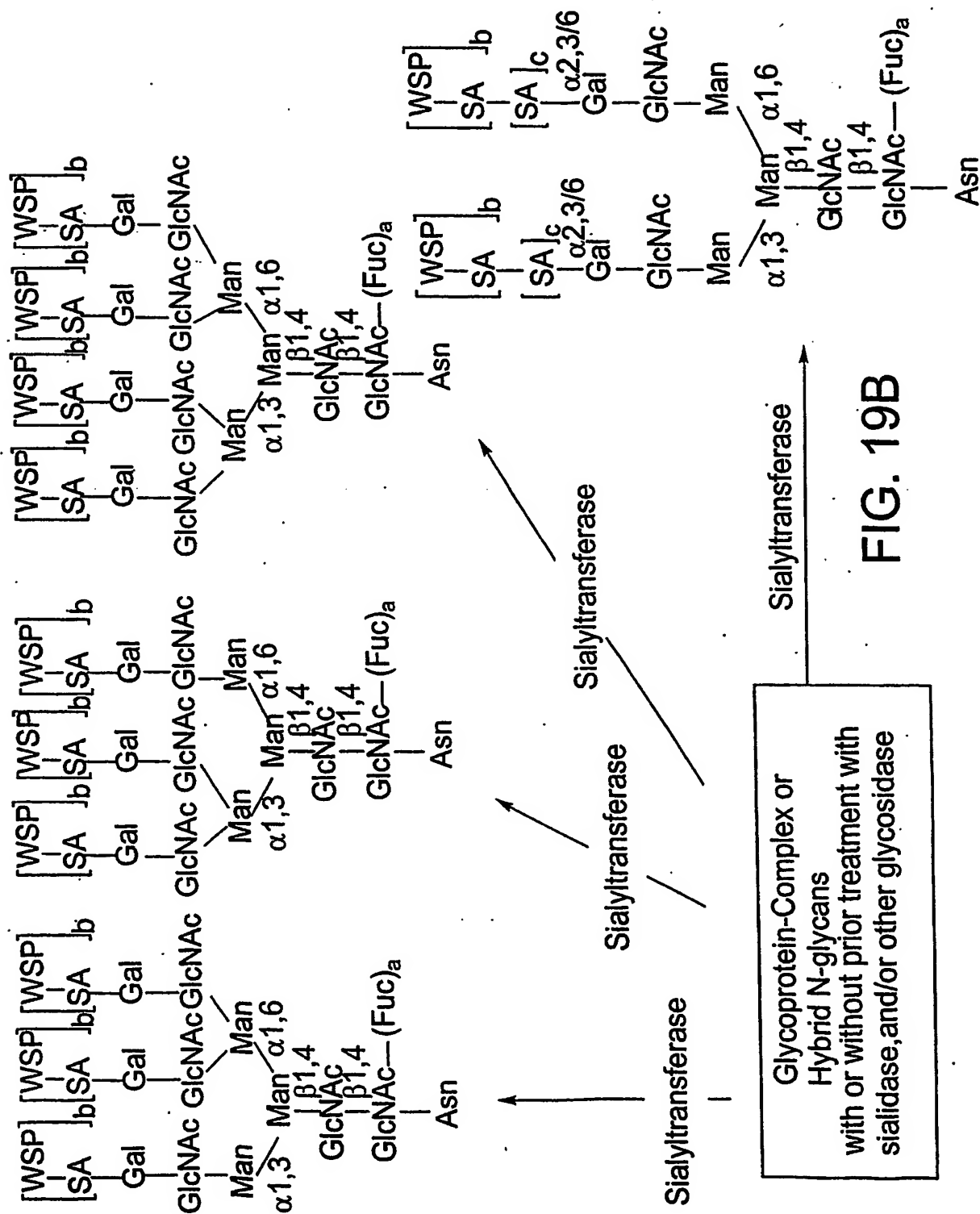


FIG. 19B

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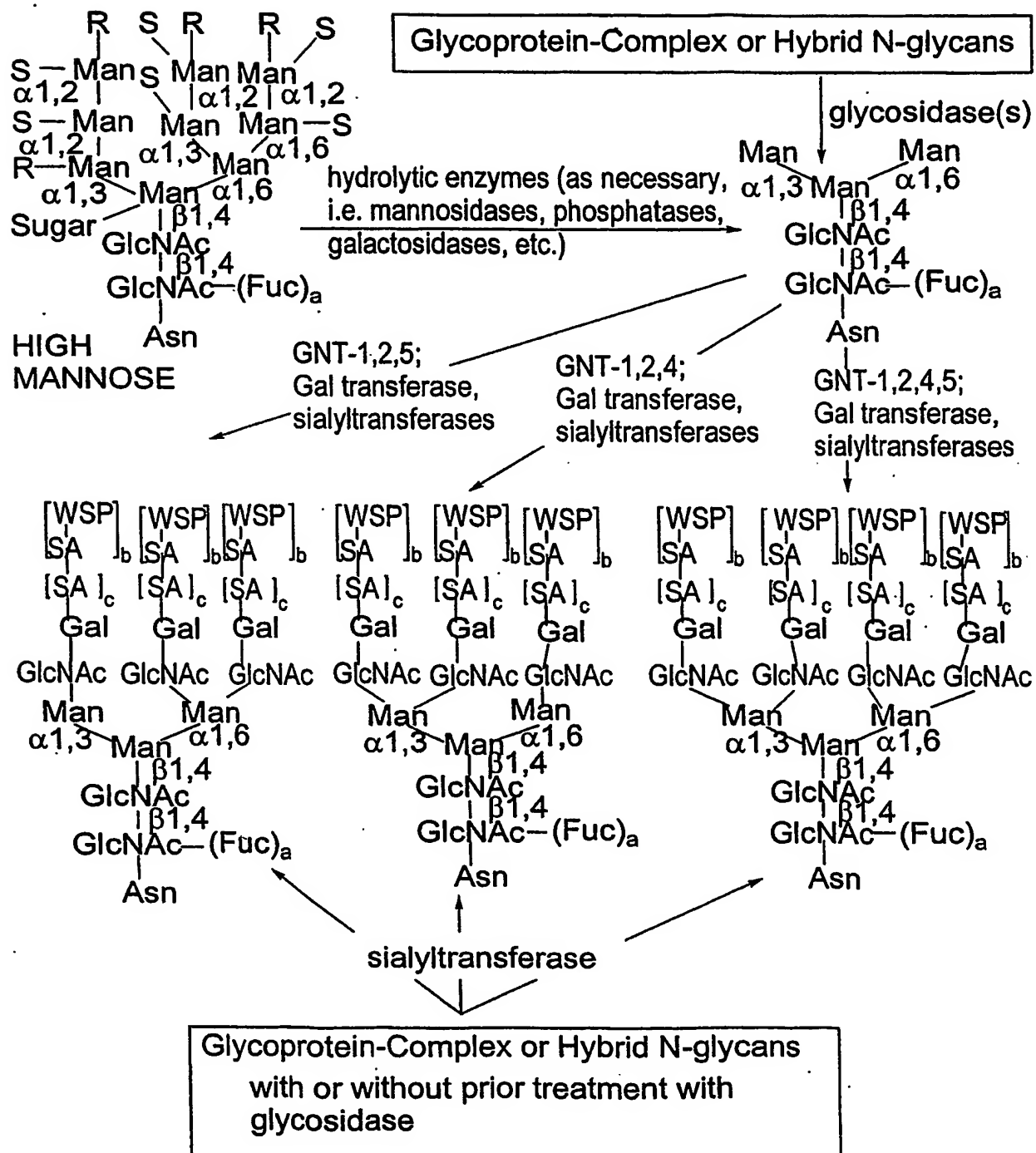
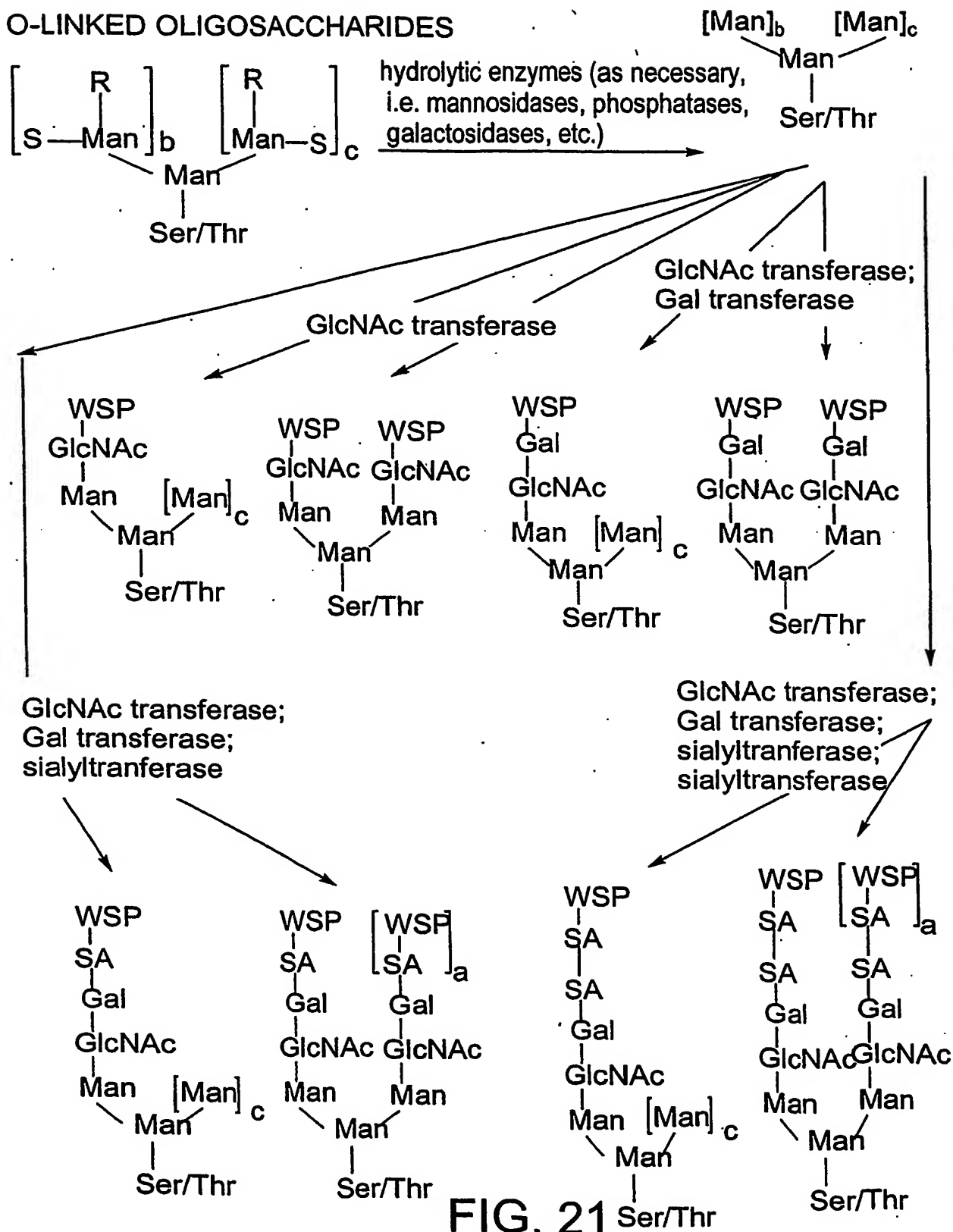


FIG. 20

## O-LINKED OLIGOSACCHARIDES



**FIG. 21** Ser/Thr

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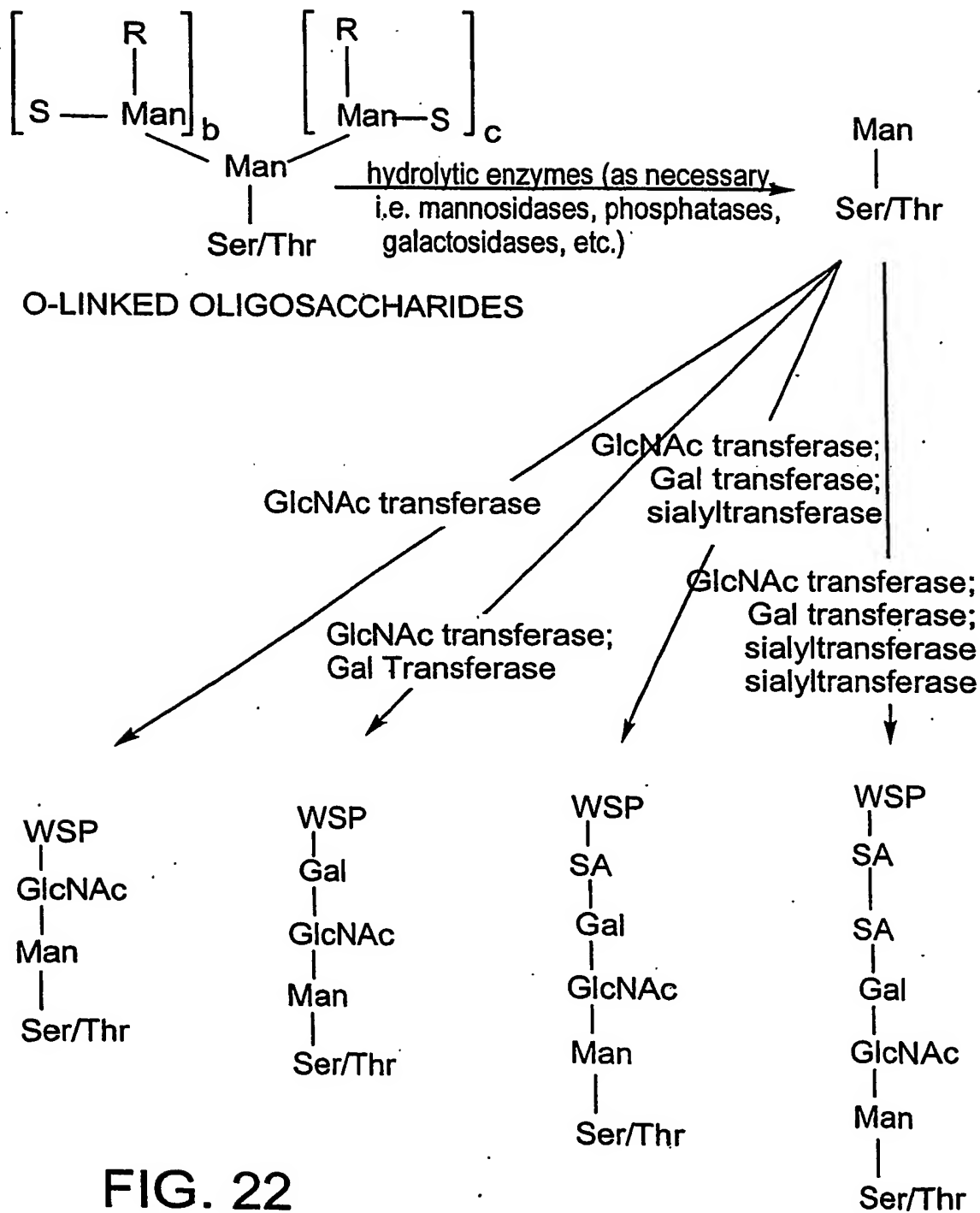


FIG. 22

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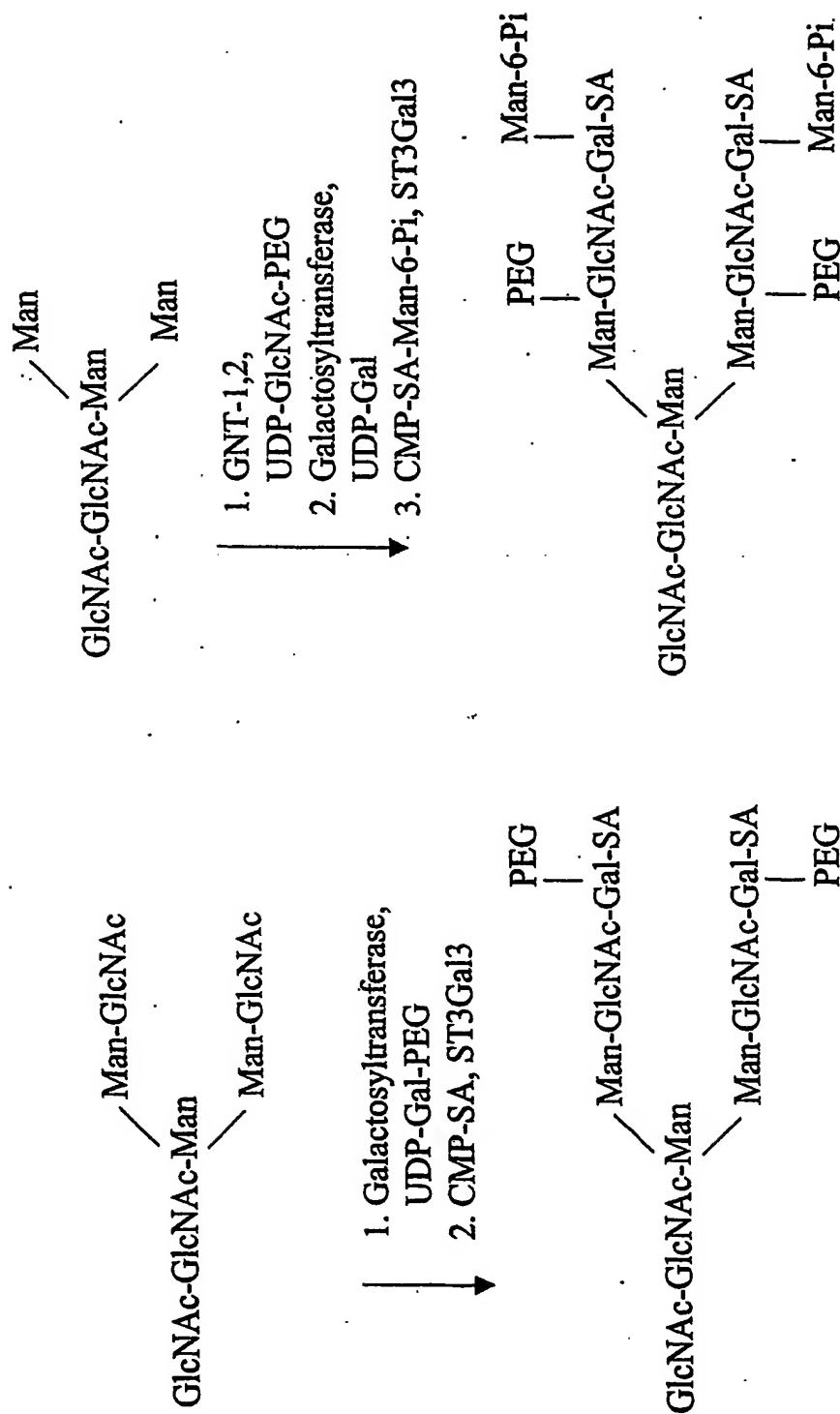


FIG. 23B

FIG. 23A

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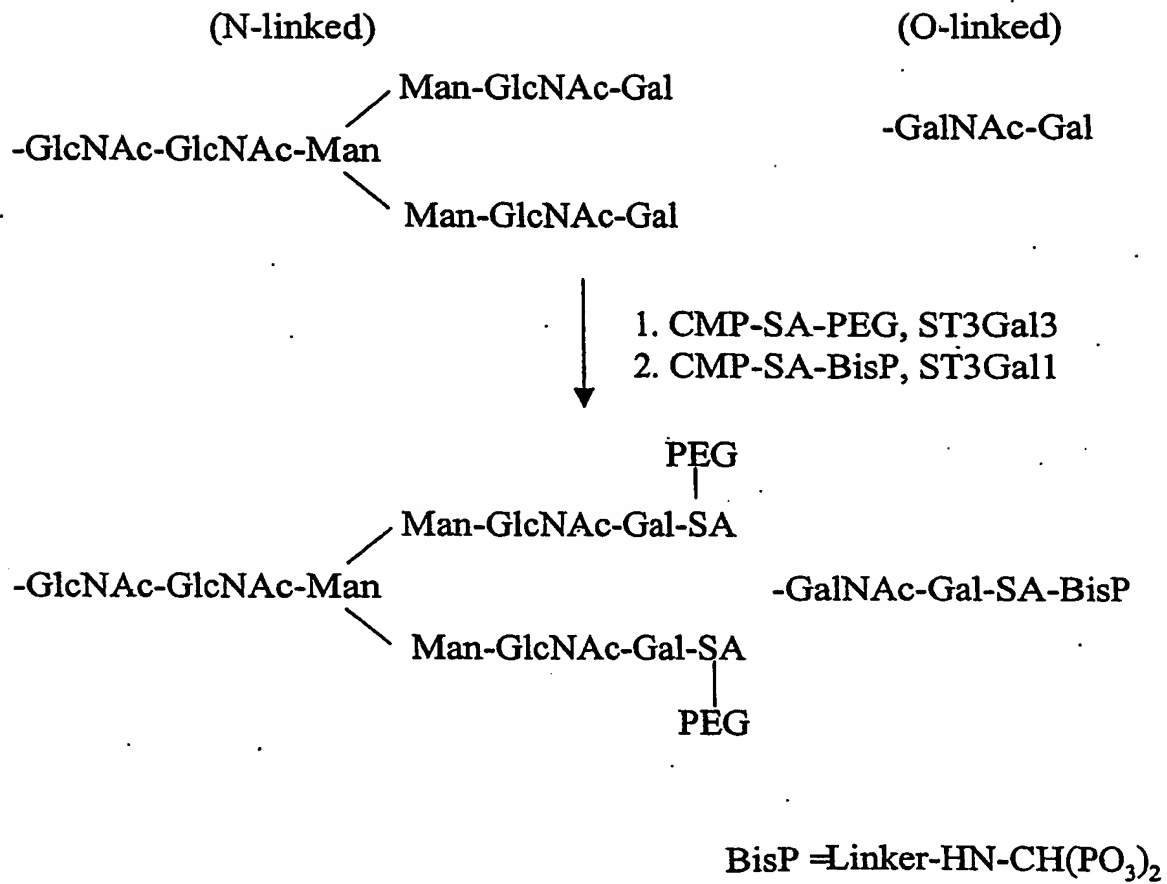


FIG. 23C



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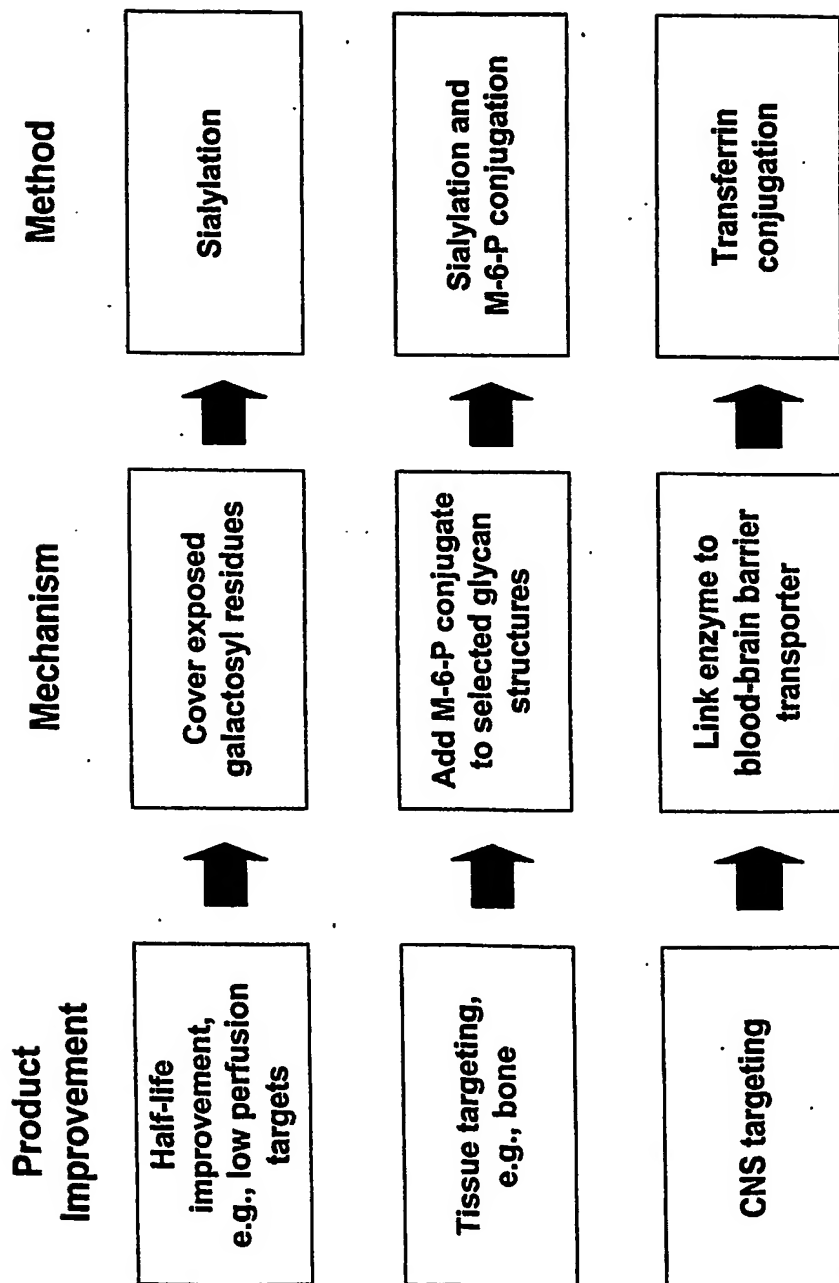


FIG. 24

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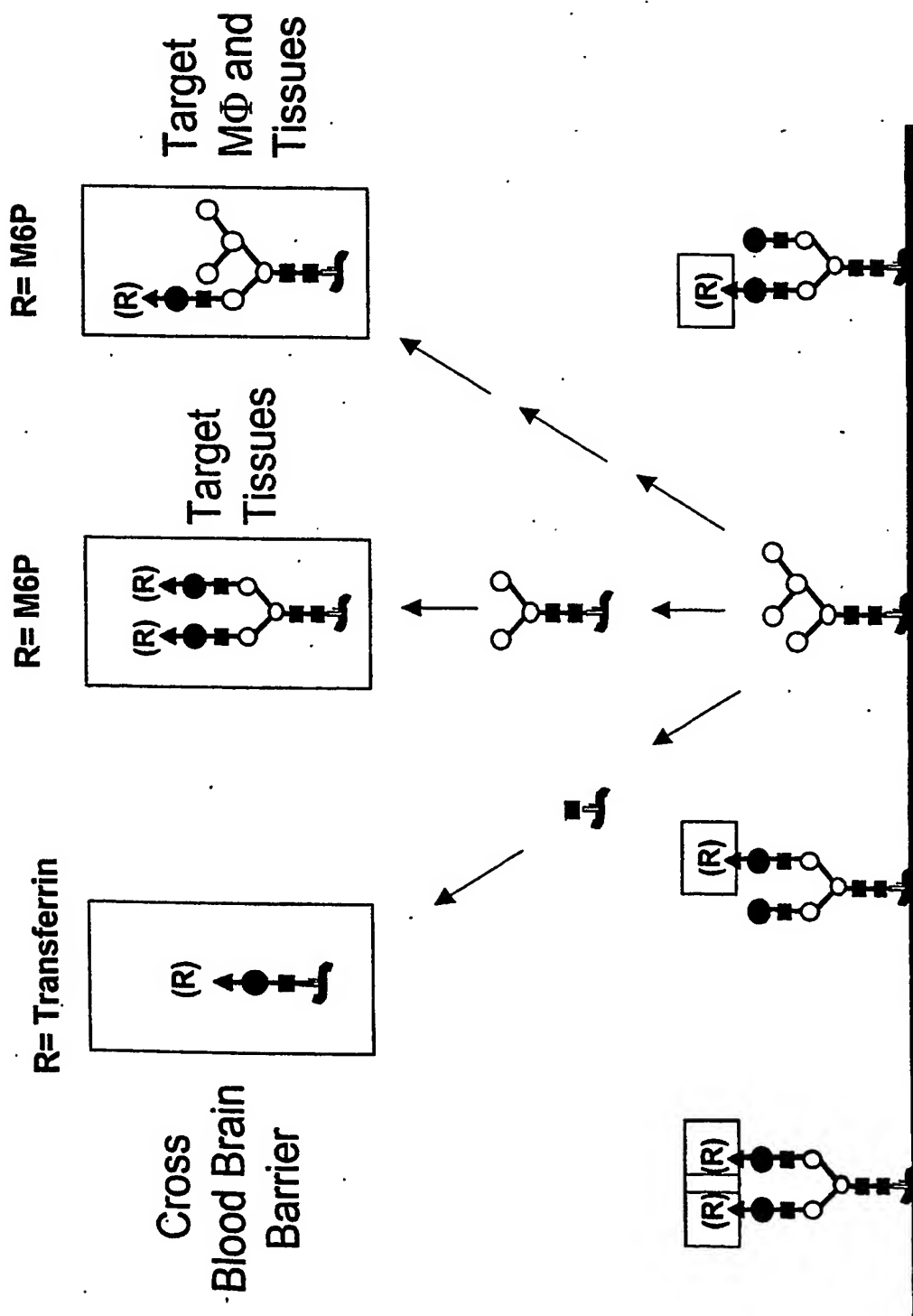


FIG. 25

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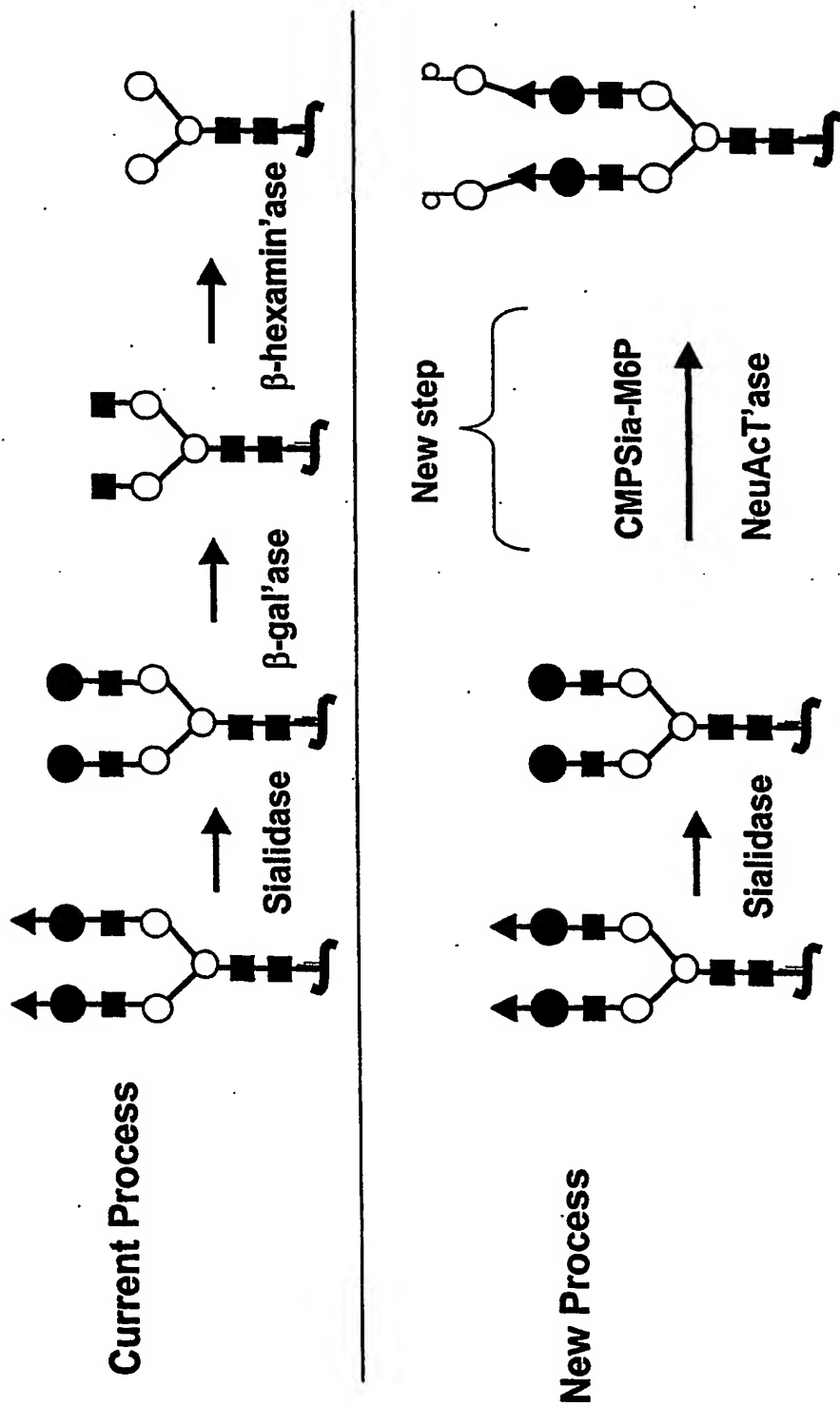


FIG. 26

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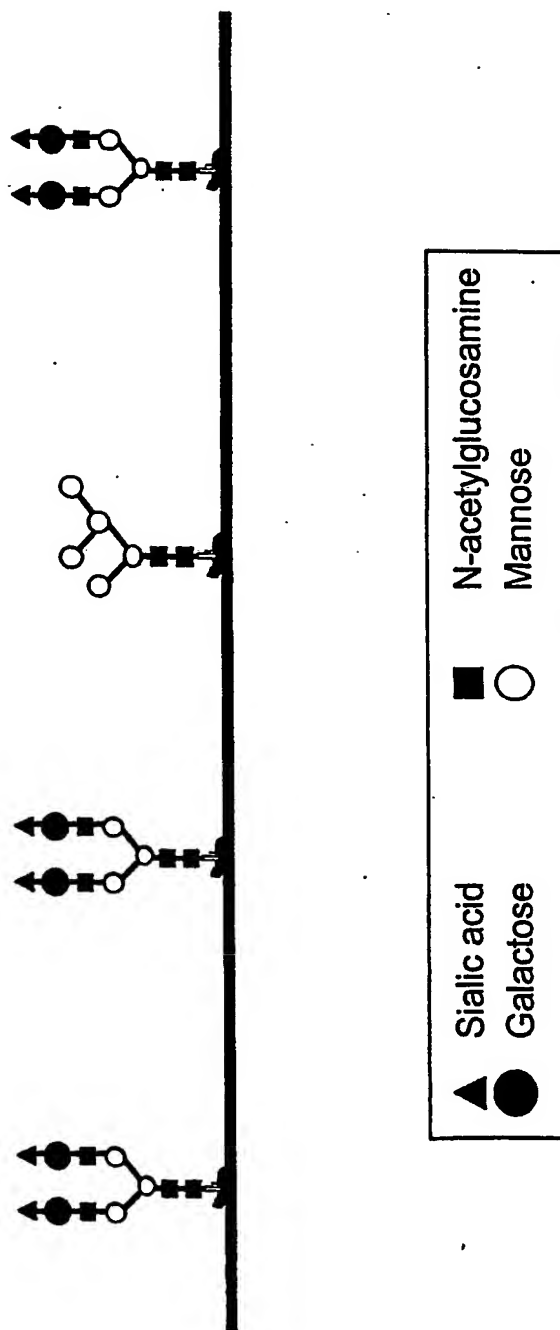


FIG. 27

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12AP1/E5 -- Viventia Biotech	AI-201 -- AutoImmune
1964 -- Aventis	AI-301 -- AutoImmune
20K growth hormone -- AMUR	AIDS vaccine -- ANRS, CIBG, Hesed
28P6/E6 -- Viventia Biotech	Biomed, Hollis-Eden, Rome, United
3-Hydroxyphthaloyl-beta-lactoglobulin --	Biomedical, American Home Products,
4-IBB ligand gene therapy --	Maxygen
64-Cu MAb conjugate TETA-1A3 --	airway receptor ligand -- IC Innovations
Mallinckrodt Institute of Radiology	AJvW 2 -- Ajinomoto
64-Cu MAb conjugate TETA-cT84.66	AK 30 NGF -- Alkermes
64-Cu Trastuzumab TETA conjugate --	Albuferon -- Human Genome Sciences
Genentech	albumin -- Biogen, DSM Anti-Infectives,
A 200 -- Amgen	Genzyme Transgenics, PPL Therapeutics,
A10255 -- Eli Lilly	TranXenoGen, Welfide Corp.
A1PDX -- Hedral Therapeutics	aldesleukin -- Chiron
A6 -- Angstrom	alefacept -- Biogen
aaAT-III -- Genzyme	Alemtuzumab
Abciximab -- Centocor	Allergy therapy -- ALK-Abello/Maxygen,
ABI.001 -- Atlantic BioPharmaceuticals	ALK-Abello/RP Scherer
ABT-828 -- Abbott	allergy vaccines -- Allergy Therapeutics
Accutin	Alnidofibatide -- Aventis Pasteur
Actinohivin	Alnorine -- SRC VB VECTOR
activin -- Biotech Australia, Human	ALP 242 -- Gruenenthal
Therapeutics, Curis	Alpha antitrypsin -- Arriva/Hyland
AD 439 -- Tanox	Immuno/ProMetic/Protease Sciences
AD 519 -- Tanox	Alpha-1 antitrypsin -- Cutter, Bayer, PPL
Adalimumab -- Cambridge Antibody Tech.	Therapeutics, Profile, ZymoGenetics,
Adenocarcinoma vaccine -- Biomira -- NIS	Arriva
Adenosine deaminase -- Enzond	Alpha-1 protease inhibitor -- Genzyme
Adenosine A2B receptor antagonists --	Transgenics, Welfide Corp.
Adenosine Therapeutics	Alpha-galactose fusion protein --
ADP-001 -- Axis Genetics	Immunomedics
AF 13948 -- Affymax	Alpha-galactosidase A -- Research
Afelimomab -- Knoll	Corporation Technologies, Genzyme
AFP-SCAN -- Immunomedics	Alpha-glucosidase -- Genzyme, Novazyme
AG 2195 -- Corixa	Alpha-lactalbumin
agalsidase alfa -- Transkaryotic Therapies	Alpha-L-iduronidase -- Transkaryotic
agalsidase beta -- Genzyme	Therapies, BioMarin
AGENT-- Antisoma	alteplase -- Genentech
AI 300 -- AutoImmune	alvircept sudotox -- NIH
AI-101 -- Teva	ALX-0600, a GLP-2 agonist -- NPS Allelix
AI-102 -- Teva	Corp.

**FIG. 28A**

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ALX1-11 –sNPS Pharmaceuticals	Anti-alphav $\beta$ 3 integrin MAb – Applied
Alzheimer's disease gene therapy	Molecular Evolution
AM-133 -- AMRAD	Anti-angiogenesis monoclonal antibodies --
Amb a 1 immunostim conj. -- Dynavax	KS Biomedix/Schering AG
AMD 3100 – AnorMED -- NIS	Anti-B4 MAb-DC1 conjugate -- ImmunoGen
AMD 3465 – AnorMED -- NIS	Anti-B7 antibody PRIMATIZED -- IDEC
AMD 3465 – AnorMED -- NIS	Anti-B7-1 MAb 16-10A1
AMD Fab -- Genentech	Anti-B7-1 MAb 1G10
Amediplase – Menarini, Novartis	Anti-B7-2 MAb GL-1
AM-F9	Anti-B7-2-gelonin immunotoxin –
Amoebiasis vaccine	Antibacterials/antifungals --
Amphiregulin -- Octagene	Diversa/IntraBiotics
anakinra -- Amgen	Anti-beta-amyloid monoclonal antibodies --
analgesic -- Nobex	Cambridge Antibody Tech., Wyeth-Ayerst
ancestim -- Amgen	Anti-BLyS antibodies -- Cambridge
AnergiX.RA – Corixa, Organon	Antibody Tech. /Human Genome Sciences
Angiocidin -- InKine	Antibody-drug conjugates -- Seattle
angiogenesis inhibitors -- ILEX	Genetics/Eos
AngioMab – Antisoma	Anti-C5 MAb BB5-1 -- Alexion
Angiopoietins -- Regeneron/Procter &	Anti-C5 MAb N19-8 -- Alexion
Gamble	Anti-C8 MAb
angiostatin -- EntreMed	anticancer cytokines -- BioPulse
Angiostatin/endostatin gene therapy --	anticancer matrix – Telios Integra
Genetix Pharmaceuticals	Anticancer monoclonal antibodies – ARIUS,
angiotensin-II, topical -- Maret	Immunex
Anthrax -- EluSys Therapeutics/US Army	anticancer peptides – Maxygen, Micrologix
Medical Research Institute	Anticancer prodrug Tech. -- Alexion
Anthrax vaccine	Antibody Technologies
Anti platelet-derived growth factor D human	anticancer Troy-Bodies -- Affite -- Affitech
monoclonal antibodies -- CuraGen	anticancer vaccine – NIH
Anti-17-1A MAb 3622W94 --	anticancers -- Epimmune
GlaxoSmithKline	Anti-CCR5/CXCR4 sheep MAb -- KS
Anti-2C4 MAb -- Genentech	Biomedix Holdings
anti-4-1BB monoclonal antibodies -- Bristol-	Anti-CD11a MAb KBA –
Myers Squibb	Anti-CD11a MAb M17
Anti-Adhesion Platform Tech. -- Cytovax	Anti-CD11a MAb TA-3 –
Anti-adipocyte MAb -- Cambridge Antibody	Anti-CD11a MAb WT.1 –
Tech./ObeSys	Anti-CD11b MAb -- Pharmacia
antiallergics -- Maxygen	Anti-CD11b MAb LM2
antiallergy vaccine -- Acambis	Anti-CD154 MAb -- Biogen
Anti-alpha-4-integrin MAb	Anti-CD16-anti-CD30 MAb -- Biotest

FIG. 28B

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Anti-CD18 MAb -- Pharmacia	Anti-CD4 MAb -- Centocor, IDEC
Anti-CD19 MAb B43 --	Pharmaceuticals, Xenova Group
Anti-CD19 MAb -liposomal sodium butyrate conjugate --	Anti-CD4 MAb 16H5
Anti-CD147	Anti-CD4 MAb 4162W94 -- GlaxoSmithKline
Anti-CD19 MAb-saporin conjugate --	Anti-CD4 MAb B-F5 -- Diaclone
Anti-CD19-dsFv-PE38-immunotoxin --	Anti-CD4 MAb GK1-5
Anti-CD2 MAb 12-15 --	Anti-CD4 MAb KT6
Anti-CD2 MAb B-E2 -- Diaclone	Anti-CD4 MAb OX38
Anti-CD2 MAb OX34 --	Anti-CD4 MAb PAP conjugate -- Bristol-Myers Squibb
Anti-CD2 MAb OX54 --	Anti-CD4 MAb RIB 5-2
Anti-CD2 MAb OX55 --	Anti-CD4 MAb W3/25
Anti-CD2 MAb RM2-1	Anti-CD4 MAb YTA 3.1.2
Anti-CD2 MAb RM2-2	Anti-CD4 MAb YTS 177-9
Anti-CD2 MAb RM2-4	Anti-CD40 ligand MAb 5c8 -- Biogen
Anti-CD20 MAb BCA B20	Anti-CD40 MAb
Anti-CD20-anti-Fc alpha RI bispecific MAb -- Medarex, Tenovus	Anti-CD40 MAb 5D12 -- Tanox
Anti-CD22 MAb-saporin-6 complex --	Anti-CD44 MAb A3D8
Anti-CD3 immunotoxin --	Anti-CD44 MAb GKWA3
Anti-CD3 MAb 145-2C11 -- Pharming	Anti-CD44 MAb IM7
Anti-CD3 MAb CD4IgG conjugate -- Genentech	Anti-CD44 MAb KM81
Anti-CD3 MAb humanised -- Protein Design, RW Johnson	Anti-CD44 variant monoclonal antibodies -- Corixa/Hebrew University
Anti-CD3 MAb WT32	Anti-CD45 MAb BC8-I-131
Anti-CD3 MAb-ricin-chain-A conjugate --	Anti-CD45RB MAb
Anti-CD3 MAb-xanthine-oxidase conjugate --	Anti-CD48 MAb HuLy-m3
Anti-CD30 MAb BerH2 -- Medac	Anti-CD48 MAb WM-63
Anti-CD30 MAb-saporin conjugate	Anti-CD5 MAb -- Becton Dickinson
Anti-CD30-scFv-ETA'-immunotoxin	Anti-CD5 MAb OX19
Anti-CD38 MAb AT13/5	Anti-CD6 MAb
Anti-CD38 MAb-saporin conjugate	Anti-CD7 MAb-PAP conjugate
Anti-CD3-anti-CD19 bispecific MAb	Anti-CD7 MAb-ricin-chain-A conjugate
Anti-CD3-anti-EGFR MAb	Anti-CD8 MAb -- Amerimmune, Cytodyn, Becton Dickinson
Anti-CD3-anti-interleukin-2-receptor MAb	Anti-CD8 MAb 2-43
Anti-CD3-anti-MOV18 MAb -- Centocor	Anti-CD8 MAb OX8
Anti-CD3-anti-SCLC bispecific MAb	Anti-CD80 MAb P16C10 -- IDEC
Anti-CD4 idiotype vaccine	Anti-CD80 MAb P7C10 -- ID Vaccine
	Anti-CD8-idarubicin conjugate
	Anti-CEA MAb CE-25
	Anti-CEA MAb MN 14 -- Immunomedics

FIG. 28C

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Anti-CEA MAb MN14-PE40 conjugate -- Immunomedics	Anti-heparanase human monoclonal antibodies -- Oxford Glycosciences/Medarex
Anti-CEA MAb T84.66-interleukin-2 conjugate	Anti-hepatitis C virus human monoclonal antibodies -- XTL Biopharmaceuticals
Anti-CEA sheep MAb -- KS Biomedix Holdings	Anti-HER-2 antibody gene therapy
Anti-cell surface monoclonal antibodies -- Cambridge Antibody Tech. /Pharmacia	Anti-herpes antibody -- Epicyte
Anti-c-erbB2-anti-CD3 bifunctional MAb -- Otsuka	Anti-HIV antibody -- Epicyte
Anti-CMV MAb -- Scotgen	anti-HIV catalytic antibody -- Hesed Biomed
Anti-complement	anti-HIV fusion protein -- Idun
Anti-CTLA-4 MAb	anti-HIV proteins -- Cangene
Anti-EGFR catalytic antibody -- Hesed Biomed	Anti-HM1-24 MAb -- Chugai
anti-EGFR immunotoxin -- IVAX	Anti-hR3 MAb
Anti-EGFR MAb -- Abgenix	Anti-Human-Carcinoma-Antigen MAb -- Epicyte
Anti-EGFR MAb 528	Anti-ICAM-1 MAb -- Boehringer Ingelheim
Anti-EGFR MAb KSB 107 -- KS Biomedix	Anti-ICAM-1 MAb 1A-29 -- Pharmacia
Anti-EGFR MAb-DM1 conjugate -- ImmunoGen	Anti-ICAM-1 MAb HA58
Anti-EGFR MAb-LA1 --	Anti-ICAM-1 MAb YN1/1.7.4
Anti-EGFR sheep MAb -- KS Biomedix	Anti-ICAM-3 MAb ICM3 -- ICOS
Anti-FAP MAb F19-I-131	Anti-idiotypic breast cancer vaccine 11D10
Anti-Fas IgM MAb CH11	Anti-idiotypic breast cancer vaccine ACA14C5 --
Anti-Fas MAb Jo2	Anti-idiotypic cancer vaccine -- ImClone Systems/Merck KGaA ImClone, Viventia Biotech
Anti-Fas MAb RK-8	Anti-idiotypic cancer vaccine 1A7 -- Titan
Anti-Flt-1 monoclonal antibodies -- ImClone	Anti-idiotypic cancer vaccine 3H1 -- Titan
Anti-fungal peptides -- State University of New York	Anti-idiotypic cancer vaccine TriAb -- Titan
antifungal tripeptides -- BTG	Anti-idiotypic Chlamydia trachomatis vaccine
Anti-ganglioside GD2 antibody-interleukin-2 fusion protein -- Lexigen	Anti-idiotypic colorectal cancer vaccine -- Novartis
Anti-GM2 MAb -- Kyowa	Anti-idiotypic colorectal cancer vaccine -- Onyvax
Anti-GM-CSF receptor monoclonal antibodies -- AMRAD	Anti-idiotypic melanoma vaccine -- IDEC Pharmaceuticals
Anti-gp130 MAb -- Tosoh	Anti-idiotypic ovarian cancer vaccine ACA 125
Anti-HCA monoclonal antibodies -- AltaRex/Epigen	Anti-idiotypic ovarian cancer vaccine AR54 - AltaRex
Anti-hCG antibodies -- Abgenix/AVI BioPharma	

FIG. 28D



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Anti-idiotypic ovarian cancer vaccine CA-125 -- AltaRex, Biomira	Anti-L-selectin monoclonal antibodies -- Protein Design Labs, Abgenix, Stanford University
Anti-IgE catalytic antibody -- Hersed Biomed	Anti-MBL monoclonal antibodies -- Alexion/Brigham and Women's Hospital
Anti-IgE MAb E26 -- Genentech	Anti-MHC monoclonal antibodies
Anti-IGF-1 MAb	Anti-MIF antibody humanised -- IDEC, Cytokine PharmaSciences
anti-inflammatory -- GeneMax	Anti-MRSA/VRSA sheep MAb -- KS Biomedix Holdings
anti-inflammatory peptide -- BTG	Anti-mu MAb -- Novartis
anti-integrin peptides -- Burnha	Anti-MUC-1 MAb
Anti-interferon-alpha-receptor MAb 64G12 -- Pharma Pacific Management	Anti-MUC 18
Anti-interferon-gamma MAb -- Protein Design Labs	Anti-Nogo-A MAb IN1
Anti-interferon-gamma polyclonal antibody - Advanced Biotherapy	Anti-nuclear autoantibodies -- Procyon
Anti-interleukin-10 MAb --	Anti-ovarian cancer monoclonal antibodies -
Anti-interleukin-12 MAb --	- Dompe
Anti-interleukin-1-beta polyclonal antibody -- R&D Systems	Anti-p185 monoclonal antibodies
Anti-interleukin-2 receptor MAb 2A3	Anti-p43 MAb
Anti-interleukin-2 receptor MAb 33B3-1 -- Immunotech	Antiparasitic vaccines
Anti-interleukin-2 receptor MAb ART-18	Anti-PDGF/bFGF sheep MAb -- KS Biomedix
Anti-interleukin-2 receptor MAb LO-Tact-1	Anti-properdin monoclonal antibodies -- Abgenix/Gliatech
Anti-interleukin-2 receptor MAb Mikbeta1	Anti-PSMA (prostrate specific membrane antigen)
Anti-interleukin-2 receptor MAb NDS61	Anti-PSMA MAb J591 -- BZL Biologics
Anti-interleukin-4 MAb 11B11	Anti-Rev MAb gene therapy --
Anti-interleukin-5 MAb -- Wallace Laboratories	Anti-RSV antibodies -- Epicyte, Intracell
Anti-interleukin-6 MAb -- Centocor, Diaclone, Pharmadigm	Anti-RSV monoclonal antibodies -- Medarex/MedImmune, Applied Molecular Evolution/MedImmune
Anti-interleukin-8 MAb -- Abgenix	Anti-RSV MAb, inhalation -- Alkermes/MedImmune
Anti-interleukin-8 MAb -- Xenotech	Anti-RT gene therapy
Anti-JL1 MAb	Antisense K-ras RNA gene therapy
Anti-Klebsiella sheep MAb -- KS Biomedix Holdings	Anti-SF-25 MAb
Anti-Laminin receptor MAb-liposomal doxorubicin conjugate	Anti-sperm antibody -- Epicyte
Anti-LCG MAb -- Cytoclonal	Anti-Tac(Fv)-PE38 conjugate
Anti-lipopolysaccharide MAb -- VitaResc	Anti-TAPA/CD81 MAb AMP1
	Anti-tat gene therapy

FIG. 28E

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Anti-TCR-alphabeta MAb H57-597	AOP-RANTES -- Senetek
Anti-TCR-alphabeta MAb R73	Apan-CH -- Praecis Pharmaceuticals
Anti-tenascin MAb BC-4-I-131	APC-8024 -- Demegen
Anti-TGF-beta human monoclonal antibodies -- Cambridge Antibody Tech., Genzyme	ApoA-1 -- Milano, Pharmacia
Anti-TGF-beta MAb 2G7 -- Genentech	Apogen -- Alexion
Antithrombin III -- Genzyme Transgenics, Aventis, Bayer, Behringwerke, CSL, Myriad	apolipoprotein A1 -- Avanir
Anti-Thy1 MAb	Apolipoprotein E -- Bio-Tech. General
Anti-Thy1.1 MAb	Applaggin -- Biogen
Anti-tissue factor/factor VIIA sheep MAb -- KS Biomedix	aprotinin -- ProdiGene
Anti-TNF monoclonal antibodies -- Centocor, Chiron, Peptech, Pharacia, Serono	APT-070C -- AdProTech
Anti-TNF sheep MAb -- KS Biomedix Holdings	AR 177 -- Aronex Pharmaceuticals
Anti-TNFalpha MAb -- Genzyme	AR 209 -- Aronex Pharmaceuticals, Antigenics
Anti-TNFalpha MAb B-C7 -- Diaclone	AR545C
Anti-tooth decay MAb -- Planet BioTech.	ARGENT gene delivery systems -- ARIAD
Anti-TRAIL receptor-1 MAb -- Takeda	Arresten
Antitumour RNases -- NIH	ART-123 -- Asahi Kasei
Anti-VCAM MAb 2A2 -- Alexion	arylsulfatase B -- BioMarin
Anti-VCAM MAb 3F4 -- Alexion	Arylsulfatase B, Recombinant human -- BioMarin
Anti-VCAM-1 MAb	AS 1051 -- Ajinomoto
Anti-VEC MAb -- ImClone	ASI-BCL -- Intracell
Anti-VEGF MAb -- Genentech	Asparaginase - Merck
Anti-VEGF MAb 2C3	ATL-101 -- Alizyme
Anti-VEGF sheep MAb -- KS Biomedix Holdings	Atrial natriuretic peptide -- Pharis
Anti-VLA-4 MAb HP1/2 -- Biogen	Aurintricarboxylic acid-high molecular weight
Anti-VLA-4 MAb PS/2	Autoimmune disorders -- GPC Biotech/MorphoSys
Anti-VLA-4 MAb R1-2	Autoimmune disorders and transplant rejection -- Bristol-Myers Squibb/Genzyme Tra
Anti-VLA-4 MAb TA-2	Autoimmune disorders/cancer -- Abgenix/Chiron, CuraGen
Anti-VAP-1 human MAb	Autotaxin
Anti-VRE sheep MAb -- KS Biomedix Holdings	Avicidin -- NeoRx
ANUP -- TranXenoGen	axogenesis factor-1 -- Boston Life Sciences
ANUP-1 -- Pharis	Axokine -- Regeneron
	B cell lymphoma vaccine -- Biomira
	B7-1 gene therapy --
	BABS proteins -- Chiron

FIG. 28F

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BAM-002 -- Novelos Therapeutics	BMP 2 -- Genetics Institute/Medtronic-
Basiliximab (anti CD25 MAb) -- Novartis	Sofamor Danek, Genetics Institute/
Bay-16-9996 -- Bayer	Collagenesis, Genetics
Bay-39-9437 -- Bayer	Institute/Yamanouch
Bay-50-4798 -- Bayer	BMP 2 gene therapy
BB-10153 -- British Biotech	BMP 52 -- Aventis Pasteur, Biopharm
BBT-001 -- Bolder BioTech.	BMP-2 -- Genetics Institute
BBT-002 -- Bolder BioTech.	BMS 182248 -- Bristol-Myers Squibb
BBT-003 -- Bolder BioTech.	BMS 202448 -- Bristol-Myers Squibb
BBT-004 -- Bolder BioTech.	bone growth factors -- IsoTis
BBT-005 -- Bolder BioTech.	BPC-15 -- Pfizer
BBT-006 -- Bolder BioTech.	brain natriuretic peptide --
BBT-007 -- Bolder BioTech.	Breast cancer -- Oxford
BCH-2763 -- Shire	GlycoSciences/Medarex
BCSF -- Millenium Biologix	Breast cancer vaccine -- Therion Biologics,
BDNF -- Regeneron -- Amgen	Oregon
Becaplermin -- Johnson & Johnson, Chiron	BSSL -- PPL Therapeutics
Bectumomab -- Immunomedics	BST-2001 -- BioStratum
Beriplast -- Aventis	BST-3002 -- BioStratum
Beta-adrenergic receptor gene therapy --	BTI 322 --
University of Arkansas	butyrylcholinesterase -- Shire
bFGF -- Scios	C 6822 -- COR Therapeutics
BI 51013 -- Behringwerke AG	C1 esterase inhibitor -- Pharming
BIBH 1 -- Boehringer Ingelheim	C3d adjuvant -- AdProTech
BIM-23190 -- Beaufour-Ipsen	CAB-2.1 -- Millennium
birch pollen immunotherapy -- Pharmacia	calcitonin -- Inhale Therapeutics Systems,
bispecific fusion proteins -- NIH	Aventis, Genetronics, TranXenoGen,
Bispecific MAb 2B1 -- Chiron	Unigene, Rhone Poulenc Rohrer
Bitistatin	calcitonin -- oral -- Nobex, Emisphere,
BIWA 4 -- Boehringer Ingelheim	Pharmaceutical Discovery
blood substitute -- Northfield, Baxter Intl.	Calcitonin gene-related peptide -- Asahi
BLP-25 -- Biomira	Kasei -- Unigene
BLS-0597 -- Boston Life Sciences	calcitonin, human -- Suntory
BLyS -- Human Genome Sciences	calcitonin, nasal -- Novartis, Unigene
BLyS radiolabelled -- Human Genome	calcitonin, Panoderm -- Elan
Sciences	calcitonin, Peptitrol -- Shire
BM 06021 -- Boehringer Mannheim	calcitonin, salmon -- Therapicon
BM-202 -- BioMarin	calin -- Biopharm
BM-301 -- BioMarin	Calphobindin I
BM-301 -- BioMarin	calphobindin I -- Kowa
BM-302 -- BioMarin	calreticulin -- NYU

FIG. 28G

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Campath-1G	CD4 fusion toxin -- Senetek
Campath-1M	CD4 IgG -- Genentech
cancer therapy -- Cangene	CD4 receptor antagonists --
cancer vaccine -- Aixlie, Aventis Pasteur,	Pharmacopeia/Progenics
Center of Molecular Immunology ,YM	CD4 soluble -- Progenics
BioSciences, Cytos, Genzyme,	CD4, soluble -- Genzyme Transgenics
Transgenics, GlobelImmune, Igeneon,	CD40 ligand -- Immunex
ImClone, Virogenetics, InterCell, Iomai,	CD4-ricin chain A -- Genentech
Jenner Biotherapies, Memorial Sloan-	CD59 gene therapy -- Alexion
Kettering Cancer Center, Sydney Kimmel	CD8 TIL cell therapy -- Aventis Pasteur
Cancer Center, Novavax, Protein	CD8, soluble -- Avidex
Sciences, Argonex, SIGA	CD95 ligand -- Roche
Cancer vaccine ALVAC-CEA B7.1 --	CDP 571 -- Celltech
Aventis Pasteur/Therion Biologics	CDP 850 -- Celltech
Cancer vaccine CEA-TRICOM -- Aventis	CDP-860 (PEG-PDGF MAb) -- Celltech
Pasteur/Therion Biologics	CDP 870 -- Celltech
Cancer vaccine gene therapy -- Cantab	CDS-1 -- Ernest Orlando
Pharmaceuticals	Cedelizumab -- Ortho-McNeil
Cancer vaccine HER-2/neu -- Corixa	Cetermin -- Insmad
Cancer vaccine THERATOPE -- Biomira	CETP vaccine -- Avant
cancer vaccine, PolyMASC -- Valentis	Cetorelix
Candida vaccine -- Corixa, Inhibitex	Cetuximab
Canstatin -- ILEX	CGH 400 -- Novartis
CAP-18 -- Panorama	CGP 42934 -- Novartis
Cardiovascular gene therapy -- Collateral	CGP 51901 -- Tanox
Therapeutics	CGRP -- Unigene
carperitide -- Suntory	CGS 27913 -- Novartis
Casocidin-1 -- Pharis	CGS 32359 -- Novartis
CAT 152 -- Cambridge Antibody Tech.	Chagas disease vaccine -- Corixa
CAT 192 -- Cambridge Antibody Tech.	chemokines -- Immune Response
CAT 213 -- Cambridge Antibody Tech.	CHH 380 -- Novartis
Catalase-- Enzon	chitinase -- Genzyme, ICOS
Cat-PAD -- Circassia	Chlamydia pneumoniae vaccine -- Antex
CB 0006 -- Celltech	Biologics
CCK(27-32)-- Akzo Nobel	Chlamydia trachomatis vaccine -- Antex
CCR2-64I -- NIH	Biologics
CD, Procept -- Paligent	Chlamydia vaccine -- GlaxoSmithKline
CD154 gene therapy	Cholera vaccine CVD 103-HgR -- Swiss
CD39 -- Immunex	Serum and Vaccine Institute Berne
CD39-L2 -- Hyseq	Cholera vaccine CVD 112 -- Swiss Serum
CD39-L4 -- Hyseq	and Vaccine Institute Berne

FIG. 28H

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Cholera vaccine inactivated oral -- SBL Vaccin	CRL 1605 -- CytRx
Chrysalin -- Chrysalis BioTech.	CS-560 -- Sankyo
CI-782 -- Hitachi Kase	CSF -- ZymoGenetics
Ciliary neurotrophic factor -- Fidia, Roche	CSF-G -- Hangzhou, Dong-A, Hanmi
CIM project -- Active Biotech	CSF-GM -- Cangene, Hunan, LG Chem
CL 329753 -- Wyeth-Ayerst	CSF-M -- Zarix
CL22, Cobra -- ML Laboratories	CT 1579 -- Merck Frosst
Clenoliximab -- IDEC	CT 1786 -- Merck Frosst
Clostridium difficile antibodies -- Epicyte	CT-112 <sup>^</sup> -- BTG
clotting factors -- Octagene	CTB-134L -- Xenova
CMB 401 -- Celltech	CTC-111 -- Kaketsuken
CNTF -- Sigma-Tau	CTGF -- FibroGen
Cocaine abuse vaccine -- Cantab, ImmuLogic, Scripps	CTLA4-Ig -- Bristol-Myers Squibb
coccidiomycosis vaccine -- Arizo	CTLA4-Ig gene therapy --
collagen -- Type I -- Pharming	CTP-37 -- AVI BioPharma
Collagen formation inhibitors -- FibroGen	C-type natriuretic peptide -- Suntory
Collagen/hydroxyapatite/bone growth factor -- Aventis Pasteur, Biopharm, Orquest	CVS 995 -- Corvas Intl.
collagenase -- BioSpecifics	CX 397 -- Nikko Kyodo
Colorectal cancer vaccine -- Wistar Institute	CY 1747 -- Epimmune
Component B, Recombinant -- Serono	CY 1748 -- Epimmune
Connective tissue growth factor inhibitors -- FibroGen/Taisho	Cyanovirin-N
Contortrostatin	Cystic fibrosis therapy -- CBR/IVAX
contraceptive vaccine -- Zonagen	CYT 351
Contraceptive vaccine hCG	cytokine Traps -- Regeneron
Contraceptive vaccine male reversible -- IMMUCON	cytokines -- Enzon, Cytoclonal
Contraceptive vaccine zona pellucida -- Zonagen	Cytomegalovirus glycoprotein vaccine -- Chiron, Aquila Biopharmaceuticals, Aventis Pasteur, Virogenetics
Copper-64 labelled MAb TETA-1A3 -- NCI	Cytomegalovirus vaccine live -- Aventis Pasteur
Coralyne	Cytosine deaminase gene therapy -- GlaxoSmithKline
Corsevin M	DA-3003 -- Dong-A
C-peptide analogues -- Schwarz	DAB389interleukin-6 -- Senetek
CPI-1500 -- Consensus	DAB389interleukin-7
CRF -- Neurobiological Tech.	DAC:GLP-2 -- ConjuChem, Inc.
cRGDfV pentapeptide --	Daclizumab (anti-IL2R MAb) -- Protein Design Labs
CRL 1095 -- CytRx	DAMP <sup>^</sup> -- Incyte Genomics
CRL 1336 -- CytRx	Daniplestim -- Pharmacia
	darbepoetin alfa -- Amgen

FIG. 28I

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DBI-3019 -- Diabetogen	dural graft matrix -- Integra
DCC -- Genzyme	Duteplase -- Baxter Intl.
DDF -- Hyseq	DWP-401 -- Daewoong
decorin -- Integra, Telios	DWP-404 -- Daewoong
defensins -- Large Scale Biology	DWP-408 -- Daewoong
DEGR-VIIa	Dx 88 (Epi-KAL2) -- Dyax
Delimmunised antibody 3B6/22 AGEN	Dx 890 (elastin inhibitors) -- Dyax
Deimmunised anti-cancer antibodies -- Biovation/Viragen	E coli O157 vaccine -- NIH
Dendroamide A	E21-R -- BresaGen
Dengue vaccine -- Bavarian Nordic, Merck	Eastern equine encephalitis virus vaccine --
denileukin diftitox -- Ligand	Echicetin --
DES-1101 -- Desmos	Echinhibin 1 --
desirudin -- Novartis	Echistatin -- Merck
desmopressin -- Unigene	Echitamine --
Desmoteplase -- Merck, Schering AG	Ecromeximab -- Kyowa Hakko
Destabilase	EC-SOD -- PPL Therapeutics
Diabetes gene therapy -- DeveloGen, Pfizer	Eculizumab (5G1.1) -- Alexion
Diabetes therapy -- Crucell	EDF -- Ajinomoto
Diabetes type 1 vaccine -- Diamyd Therapeutics	EDN derivative -- NIH
DiaCIM -- YM BioSciences	EDNA -- NIH
dialytic oligopeptides -- Research Corp	Edobacomab -- XOMA
Diamyd -- Diamyd Therapeutics	Edrecolomab -- Centocor
DiaPep227-- Pepgen	EF 5077
DiavaX -- Corixa	Efalizumab -- Genentech
Digoxin MAb -- Glaxo	EGF fusion toxin -- Seragen, Ligand
Diphtheria tetanus pertussis-hepatitis B vaccine -- GlaxoSmithKline	EGF-P64k vaccine -- Center of Molecular Immunology
DIR therapy -- Solis Therapeutics --	EL 246 -- LigoCyte
DNase -- Genentech	elastase inhibitor -- Synergen
Dornase alfa -- Genentech	elcatonin -- Therapicon
Dornase alfa, inhalation -- Genentech	EMD 72000 -- Merck KGaA
Doxorubicin-anti-CEA MAb conjugate -- Immunomedics	Emdogain -- BIORA
DP-107 -- Trimeris	emfilermin -- AMRAD
drotrecogin alfa -- Eli Lilly	Emoctakin -- Novartis
DTctGMCSF	enamel matrix protein -- BIORA
DTP-polio vaccine -- Aventis Pasteur	Endo III -- NYU
DU 257-KM231 antibody conjugate -- Kyowa	endostatin -- EntreMed, Pharis
	Enhancins -- Micrologix
	Enlimomab -- Isis Pharm.
	Enoxaparin sodium -- Pharmuka

FIG. 28J

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enzyme linked antibody nutrient depletion therapy -- KS Biomedix Holdings	Factor IX gene therapy -- Cell Genesys
Eosinophil-derived neutralizing agent -- EP-51216 -- Asta Medica	Factor VII -- Novo Nordisk, Bayer, Baxter Intl.
EP-51389 -- Asta Medica	Factor VIIa -- PPL Therapeutics, ZymoGenetics
EPH family ligands -- Regeneron	Factor VIII -- Bayer Genentech, Beaufour-Ipsen, CLB, Inex, Octagen, Pharmacia, Pharming
Epidermal growth factor -- Hitachi Kasei, Johnson & Johnson	Factor VIII -- PEGylated -- Bayer
Epidermal growth factor fusion toxin -- Senetek	Factor VIII fragments -- Pharmacia
Epidermal growth factor-genistein -- EPI-HNE-4 -- Dyax	Factor VIII gene therapy -- Targeted Genetics
EPI-KAL2 -- Dyax	Factor VIII sucrose formulation -- Bayer, Genentech
Epoetin-alfa -- Amgen, Dragon Pharmaceuticals, Nanjing Huaxin	Factor VIII-2 -- Bayer
Epratuzumab -- Immunomedics	Factor VIII-3 -- Bayer
Epstein-Barr virus vaccine -- Aviron/SmithKline Beecham, Bioresearch	Factor Xa inhibitors -- Merck, Novo Nordisk, Mochida
Eptacog alfa -- Novo Nordisk	Factor XIII -- ZymoGenetics
Eptifibatide -- COR Therapeutics	Factors VIII and IX gene therapy -- Genetics Institute/Targeted Genetics
erb-38 --	Famoxin -- Genset
Erlizumab -- Genentech	Fas (delta) TM protein -- LXR BioTech.
erythropoietin -- Alkermes, ProLease, Dong-A, Elanex, Genetics Institute, LG Chem, Protein Sciences, Serono, Snow Brand, SRC VB VECTOR, Transkaryotic Therapies	Fas TR -- Human Genome Sciences
Erythropoietin Beta -- Hoffman La Roche	Felvizumab -- Scotgen
Erythropoietin/Epoetin alfa -- Chugai	FFR-VIIa -- Novo Nordisk
Escherichia coli vaccine -- North American Vaccine, SBL Vaccin, Swiss Serum and Vaccine Institute Berne	FG-001 -- F-Gene
etanercept -- Immunex	FG-002 -- F-Gene
examorelin -- Mediolanum	FG-004 -- F-Gene
Exendin 4 -- Amylin	FG-005 -- F-Gene
exonuclease VII	FGF + fibrin -- Repair
F 105 -- Centocor	Fibrimage -- Bio-Tech. General
F-992 -- Fornix	fibrin-binding peptides -- ISIS Innovation
Factor IX -- Alpha Therapeutics, Welfide Corp., CSL, enetics Institute/AHP, Pharmacia, PPL Therapeutics	fibrinogen -- PPL Therapeutics, Pharming
	fibroblast growth factor -- Chiron, NYU, Ramot, ZymoGenetics
	fibrolase conjugate -- Schering AG
	Filgrastim -- Amgen
	filgrastim -- PDA modified -- Xencor
	FLT-3 ligand -- Immunex
	FN18 CRM9 --

FIG. 28K

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follistatin -- Biotech Australia, Human Therapeutics	Glucocerebrosidase -- Genzyme
follitropin alfa -- Alkermes, ProLease, PowderJect, Serono, Akzo Nobel	glutamate decarboxylase -- Genzyme Transgenics
Follitropin Beta -- Bayer, Organon FP 59	Glycoprotein S3 -- Kureha
FSH -- Ferring	GM-CSF -- Immunhex
FSH + LH -- Ferring	GM-CSF tumour vaccine -- PowderJect
F-spondin -- CeNeS	GnRH immunotherapeutic -- Protherics
fusion protein delivery system -- UAB Research Foundation	Goserelin (LhRH antagonist) -- AstraZeneca
fusion toxins -- Boston Life Sciences	gp75 antigen -- ImClone
G 5598 -- Genentech	gp96 -- Antigenics
GA-II -- Transkaryotic Therapies	GPI 0100 -- Galenica
Gamma-interferon analogues -- SRC VB VECTOR	GR 4991W93 -- GlaxoSmithKline
Ganirelix -- Roche	Granulocyte colony-stimulating factor -- Dong-A
gastric lipase -- Meristem	Granulocyte colony-stimulating factor conjugate
Gavilimomab --	grass allergy therapy -- Dynavax
G-CSF -- Amgen, SRC VB VECTOR	GRF1-44 -- ICN
GDF-1 -- CeNeS	Growth Factor -- Chiron, Atrigel, Atrix, Innogenetics, ZymoGenetics, Novo
GDF-5 -- Biopharm	growth factor peptides -- Biotherapeutics
GDNF (glial derived neurotrophic factor) -- Amgen	growth hormone -- LG Chem
gelsolin -- Biogen	growth hormone, Recombinant human -- Serono
Gemtuzumab ozogamicin -- Celltech	GT 4086 -- Gllatech
Gene-activated epoetin-alfa -- Aventis Pharma -- Transkaryotic Therapies	GW 353430 -- GlaxoSmithKline
Glanzmann thrombasthenia gene therapy --	GW-278884 -- GlaxoSmithKline
Glatiramer acetate -- Yeda	H 11 -- Viventia Biotech
glial growth factor 2 -- CeNeS	H5N1 influenza A virus vaccine -- Protein Sciences
GLP-1 -- Amylin, Suntory, TheraTech, Watson	haemoglobin -- Biopure
GLP-1 peptide analogues -- Zealand Pharmaceuticals	haemoglobin 3011, Recombinant -- Baxter Healthcare
GLP-2 -- Novo Nordisk, Ontario, Inc., Suntory Limited	haemoglobin crosfumaril -- Baxter Intl.
glucagon -- Eli Lilly, ZymoGenetics	haemoglobin stabilized -- Ajinomoto
Glucagon-like peptide-1 7-36 amide -- Suntory	haemoglobin, recombinant -- Apex
Glucogen-like peptide -- Amylin	HAF -- Immune Response
	Hantavirus vaccine
	HB 19
	HBNF -- Regeneron
	HCC-1 -- Pharis

FIG. 28L



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hCG -- Milkhaus	Herpes simplex glycoprotein DNA vaccine --
hCG vaccine -- Zonagen	Merck, Wyeth-Lederle Vaccines-Malvern,
HE-317 -- Hollis-Eden Pharmaceuticals	Genentech, GlaxoSmithKline, Chiron,
Heat shock protein cancer and influenza	Takeda
vaccines -- StressGen	Herpes simplex vaccine -- Cantab
Helicobacter pylori vaccine -- Acambis,	Pharmaceuticals, CEL-SCI, Henderson
AstraZeneca/CSL, Chiron, Provalis	Morley
Helistat-G -- GalaGen	Herpes simplex vaccine live -- ImClone
Hemolink -- Hemosol	Systems/Wyeth-Lederle, Aventis Pasteur
hepapoietin -- Snow Brand	HGF derivatives -- Dompe
heparanase -- InSight	hIAPP vaccine -- Crucell
heparinase I -- Ibex	Hib-hepatitis B vaccine -- Aventis Pasteur
heparinase III -- Ibex	HIC 1
Hepatitis A vaccine -- American Biogenetic	HIP-- Altachem
Sciences	Hirudins -- Biopharma, Cangene, Dongkook,
Hepatitis A vaccine inactivated	Japan Energy Corporation, Pharmacia
Hepatitis A vaccine Nothav -- Chiron	Corporation, SIR International, Sanofi-
Hepatitis A-hepatitis B vaccine --	Synthelabo, Sotragene, Rhein Biotech
GlaxoSmithKline	HIV edible vaccine -- ProdiGene
hepatitis B therapy -- Tripep	HIV gp120 vaccine -- Chiron, Ajinomoto,
Hepatitis B vaccine -- Amgen, Chiron SpA,	GlaxoSmithKline, ID Vaccine, Progenics,
Meiji Milk, NIS, Prodeva, PowderJect,	VaxGen
Rhein Biotech	HIV gp120 vaccine gene therapy --
Hepatitis B vaccine recombinant -- Evans	HIV gp160 DNA vaccine -- PowderJect,
Vaccines, Epitex Combiotech, Genentech,	Aventis Pasteur, Oncogen, Hyland
MedImmune, Merck Sharp & Dohme,	Immuno, Protein Sciences
Rhein Biotech, Shantha Biotechnics,	HIV gp41 vaccine -- Panacos
Vector, Yeda	HIV HGP-30W vaccine -- CEL-SCI
Hepatitis B vaccine recombinant TGP 943 --	HIV immune globulin -- Abbott, Chiron
Takeda	HIV peptides -- American Home Products
Hepatitis C vaccine -- Bavarian Nordic,	HIV vaccine -- Applied bioTech., Axis
Chiron, Innogenetics Acambis,	Genetics, Biogen, Bristol-Myers Squibb,
Hepatitis D vaccine -- Chiron Vaccines	Genentech, Korea Green Cross, NIS,
Hepatitis E vaccine recombinant --	Oncogen, Protein Sciences Corporation,
Genelabs/GlaxoSmithKline, Novavax	Terumo, Tonen Corporation, Wyeth-
hepatocyte growth factor -- Panorama,	Ayerst, Wyeth-Lederle Vaccines-Malvern,
Sosei	Advanced BioScience Laboratories,
hepatocyte growth factor kringle fragments -	Bavarian Nordic, Bavarian Nordic/Statens
- EntreMed	Serum Institute, GeneCure, Immune
Her-2/Neu peptides -- Corixa	Response, Progenics, Therion Biologics,
	United Biomedical, Chiron

FIG. 28M

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HIV vaccine vCP1433 -- Aventis Pasteur	Human monoclonal antibodies --
HIV vaccine vCP1452 -- Aventis Pasteur	Medarex/Northwest Biotherapeutics,
HIV vaccine vCP205 -- Aventis Pasteur	Medarex/Seattle Genetics
HL-9 -- American BioScience	human netrin-1 -- Exelixis
HM-9239 -- Cytran	human papillomavirus antibodies -- Epicyte
HML-103 -- Hemosol	Human papillomavirus vaccine -- Biotech
HML-104 -- Hemosol	Australia, IDEC, StressGen
HML-105 -- Hemosol	Human papillomavirus vaccine MEDI 501 --
HML-109 -- Hemosol	MedImmune/GlaxoSmithKline
HML-110 -- Hemosol	Human papillomavirus vaccine MEDI
HML-121 -- Hemosol	503/MEDI 504 --
hNLP -- Pharis	MedImmune/GlaxoSmithKline
Hookworm vaccine	Human papillomavirus vaccine TA-CIN --
host-vector vaccines -- Henogen	Cantab Pharmaceuticals
HPM 1 -- Chugai	Human papillomavirus vaccine TA-HPV --
HPV vaccine -- MediGene	Cantab Pharmaceuticals
HSA -- Meristem	Human papillomavirus vaccine TH-GW --
HSF -- StressGen	Cantab/GlaxoSmithKline
HSP carriers --Weizmann, Yeda, Peptor	human polyclonal antibodies -- Biosite/Eos
HSPPC-70 -- Antigenics	BioTech./ Medarex
HSPPC-96, pathogen-derived -- Antigenics	human type II anti factor VIII monoclonal
HSV 863 -- Novartis	antibodies -- ThromboGenics
HTLV-I DNA vaccine	humanised anti glycoprotein Ib murine
HTLV-I vaccine	monoclonal antibodies -- ThromboGenics
HTLV-II vaccine -- Access	HumaRAD -- Intracell
HU 901 -- Tanox	HuMax EGFR -- Genmab
Hu23F2G -- ICOS	HuMax-CD4 -- Medarex
HuHMFG1	HuMax-IL15 -- Genmab
HumaLYM -- Intracell	HYB 190 -- Hybridon
Human krebs statika -- Yamanouchi	HYB 676 -- Hybridon
human monoclonal antibodies --	I-125 MAb A33 -- Celltech
Abgenix/Biogen, Abgenix/ Corixa,	Ibritumomab tiuxetan -- IDEC
Abgenix/Immunex, Abgenix/Lexicon,	IBT-9401 -- Ibex
Abgenix/ Pfizer, Athersys/Medarex,	IBT-9402 -- Ibex
Biogen/MorphoSys, CAT/Searle,	IC 14 -- ICOS
Centocor/Medarex, Corixa/Kirin Brewery,	Idarubicin anti-Ly-2.1 --
Corixa/Medarex, Eos BioTech./Medarex,	IDEC 114 -- IDEC
Eos/Xenerex, Exelixis/Protein Design	IDEC 131 -- IDEC
Labs, ImmunoGen/ Raven, Medarex/	IDEC 152 -- IDEC
B.Twelve, MorphoSys/ImmunoGen, XTL	IDM 1 -- IDM
Biopharmaceuticals/Dyax,	IDPS -- Hollis-Eden Pharmaceuticals

**FIG. 28N**

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iduronate-2-sulfatase -- Transkaryotic Therapies	insulin -- AutoImmune, Altea, Biobras, BioSante, Bio-Tech. General, Chong Kun Dang, Emisphere, Flamel, Provalis, Rhein Biotech, TranXenoGen
IGF/IBP-2-13 -- Pharis	insulin (bovine) -- Novartis
IGN-101 -- Igeneon	insulin analogue -- Eli Lilly
IK HIR02 -- Iketon	Insulin Aspart -- Novo Nordisk
IL-11 -- Genetics Institute/AHP	insulin detemir -- Novo Nordisk
IL-13-PE38 -- NeoPharm	insulin glargine -- Aventis
IL-17 receptor -- Immunex	insulin inhaled -- Inhale Therapeutics Systems, Alkermes
IL-18BP -- Yeda	insulin oral -- Inovax
IL-1Hy1 -- Hyseq	insulin, AeroDose -- AeroGen
IL-1 $\beta$ -- Celltech	insulin, AERx -- Aradigm
IL-1 $\beta$ adjuvant -- Celltech	insulin, BEODAS -- Elan
IL-2 -- Chiron	insulin, Biphax -- Helix
IL-2 + IL-12 -- Hoffman La-Roche	insulin, buccal -- Generex
IL-6/sIL-6R fusion -- Hadasit	insulin, I2R -- Flemington
IL-6R derivative -- Tosoh	insulin, intranasal -- Bentley
IL-7-Dap 389 fusion toxin -- Ligand	insulin, oral -- Nobex, Unigene
IL-21 -- Novo Nordisk, ZymoGenetics	insulin, Orasome -- Endorex
IM-862 -- Cytran	insulin, ProMaxx -- Epic
IMC-1C11 -- ImClone	insulin, Quadrant -- Elan
imiglucerase -- Genzyme	insulin, recombinant -- Aventis
Immune globulin intravenous (human) -- Hoffman La Roche	insulin, Spiros -- Elan
immune privilege factor -- Proneuron	insulin, Transfersome -- IDEA
Immunocal -- Immunotec	insulin, Zymo, recombinant -- Novo Nordisk
Immunogene therapy -- Briana Bio-Tech	insulinotropin -- Scios
Immunoliposomal 5-fluorodeoxyuridine-dipalmitate --	Insulysin gene therapy --
immunosuppressant vaccine -- Aixlie	integrin antagonists -- Merck
immunotoxin -- Antisoma, NIH	interferon (Alpha2) -- SRC VB VECTOR, Viragen, Dong-A, Hoffman La-Roche, Genentech
ImmuRAIT-Re-188 -- Immunomedics	interferon -- BioMedicines, Human Genome Sciences
imreg-1 -- Imreg	interferon (Alfa-n3) -- Interferon Sciences Intl.
infertility -- Johnson & Johnson, E-TRANS	interferon (Alpha), Biphax -- Helix
Infliximab -- Centocor	
Influenza virus vaccine -- Aventis Pasteur, Protein Sciences	
inhibin -- Biotech Australia, Human Therapeutics	
Inhibitory G protein gene therapy	
INKP-2001 -- InKine	
Inolimomab -- Diaclone	

FIG. 280

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interferon (Alpha)—Amgen, BioNative, Novartis, Genzyme Transgenics, Hayashibara, Inhale Therapeutics Systems, Medusa, Flamel, Dong-A, GeneTrol, Nastech, Shantha, Wassermann, LG Chem, Sumitomo, Aventis, Behring EGIS, Pepgen, Servier, Rhein Biotech,	IL-2/ diphtheria toxin -- Ligand
interferon (Alpha2A)	Interleukin-3 -- Cangene
interferon (Alpha2B) -- Enzon, Schering- Plough, Biogen, IDEA	Interleukin-4 -- Immunology Ventures, Sanofi Winthrop, Schering-Plough, Immunex/ Sanofi Winthrop, Bayer, Ono
interferon (Alpha-N1) -- GlaxoSmithKline	interleukin-4 + TNF-Alpha -- NIH
interferon (beta) -- Rentschler, GeneTrol, Meristem, Rhein Biotech, Toray, Yeda, Daiichi, Mochida	interleukin-4 agonist -- Bayer
interferon (Beta1A) -- Serono, Biogen	interleukin-4 fusion toxin -- Ligand
interferon (beta1A),inhale -- Biogen	Interleukin-4 receptor -- Immunex, Immun
interferon (β1b)-- Chiron	Interleukin-6 -- Ajinomoto, Cangene, Yeda, Genetics Institute, Novartis
interferon (tau)-- Pepgen	interleukin-6 fusion protein
Interferon alfacon-1 -- Amgen	interleukin-6 fusion toxin -- Ligand, Serono
Interferon alpha-2a vaccine	interleukin-7 -- IC Innovations
Interferon Beta 1b -- Schering/Chiron, InterMune	interleukin-7 receptor -- Immunex
Interferon Gamma -- Boehringer Ingelheim, Sheffield, Rentschler, Hayashibara	interleukin-8 antagonists -- Kyowa Hakko/Millennium/Pfizer
interferon receptor , Type I -- Serono	interleukin-9 antagonists -- Genaera
interferon(Gamma1B) -- Genentech	Interleukin-10 -- DNAX, Schering-Plough
Interferon-alpha-2b + ribavirin -- Biogen, ICN	Interleukin-10 gene therapy --
Interferon-alpha-2b gene therapy -- Schering-Plough	interleukin-12 -- Genetics Institute, Hoffman La-Roche
Interferon-con1 gene therapy --	interleukin-13 -- Sanofi
interleukin-1 antagonists -- Dompe	interleukin-13 antagonists -- AMRAD
Interleukin-1 receptor antagonist -- Abbott Bioresearch, Pharmacia	Interleukin-13-PE38QQR
Interleukin-1 receptor type I -- Immunex	interleukin-15 -- Immunex
interleukin-1 receptor Type II -- Immunex	interleukin-16 -- Research Corp
Interleukin-1 trap -- Regeneron	interleukin-18 -- GlaxoSmithKline
Interleukin-1-alpha -- Immunex/Roche	Interleukin-18 binding protein -- Serono
interleukin-2 -- SRC VB VECTOR, Ajinomoto, Biomira, Chiron	lor-P3 -- Center of Molecular Immunology
	IP-10 -- NIH
	IPF -- Metabolex
	IR-501 -- Immune Response
	ISIS 9125 -- Isis Pharmaceuticals
	ISURF No. 1554 -- Millennium
	ISURF No. 1866 -- Iowa State Univer.
	ITF-1697 -- Italfarmaco
	IxC 162 -- Ixion
	J 695 -- Cambridge Antibody Tech., Genetics Inst., Knoll
	Jagged + FGF -- Repair

FIG. 28P

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JKC-362 -- Phoenix Pharmaceuticals	leptin, 2nd-generation -- Amgen
JTP-2942 -- Japan Tobacco	leridistim -- Pharmacia
Juman monoclonal antibodies -- Medarex/Raven	leuprolide, ProMaxx -- Epic
K02 -- Axys Pharmaceuticals	leuprorelin, oral -- Unigene
Keliximab -- IDEC	LeuTech -- Papatin
Keyhole limpet haemocyanin	LEX 032 -- SuperGen
KGF -- Amgen	LiDEPT -- Novartis
KM 871 -- Kyowa	Lintuzumab (anti-CD33 MAb) -- Protein Design Labs
KPI 135 -- Scios	lipase -- Altus Biologics
KPI-022 -- Scios	lipid A vaccine -- EntreMed
Kringle 5	lipid-linked anchor Tech. -- ICRT, ID Biomedical
KSB 304	liposome-CD4 Tech. -- Sheffield
KSB-201 -- KS Biomedix	Listeria monocytogenes vaccine
L 696418 -- Merck	LMB 1
L 703801 -- Merck	LMB 7
L1 -- Acorda	LMB 9 -- Battelle Memorial Institute, NIH
L-761191 -- Merck	LM-CD45 -- Cantab Pharmaceuticals
lactoferrin -- Meristem, Pharming, Agennix	lovastatin -- Merck
lactoferrin cardio -- Pharming	LSA-3
LAG-3 -- Serono	LT- $\beta$ receptor -- Biogen
LAIT -- GEMMA	lung cancer vaccine -- Corixa
LAK cell cytotoxin -- Arizona	lusupultide -- Scios
lamellarins -- PharmaMar/University of Malaga	L-Vax -- AVAX
laminin A peptides -- NIH	LY 355455 -- Eli Lilly
lanotepase -- Genetics Institute	LY 366405 -- Eli Lilly
laronidase -- BioMarin	LY-355101 -- Eli Lilly
Lassa fever vaccine	Lyme disease DNA vaccine -- Vical/Aventis Pasteur
LCAT -- NIH	Lyme disease vaccine -- Aquila
LDP 01 -- Millennium	Biopharmaceuticals, Aventis, Pasteur, Symbicom, GlaxoSmithKline, Hyland
LDP 02 -- Millennium	Immuno, MedImmune
Lecithinized superoxide dismutase -- Seikagaku	Lymphocytic choriomeningitis virus vaccine
LeIF adjuvant -- Corixa	lymphoma vaccine -- Biomira, Genitope
leishmaniasis vaccine -- Corixa	LYP18
lenercept -- Hoffman La-Roche	lys plasminogen, recombinant
Lenograstim -- Aventis, Chugai	Lysosomal storage disease gene therapy -- Avigen
lepirudin -- Aventis	lysostaphin -- Nutrition 21
leptin -- Amgen, IC Innovations	
Leptin gene therapy -- Chiron Corporation	

FIG. 28Q

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M 23 -- Gruenenthal	MEDI 507 -- BioTransplant
M1 monoclonal antibodies -- Acorda	melanin concentrating hormone --
Therapeutics	Neurocrine Biosciences
MA 16N7C2 -- Corvas Intl.	melanocortins -- OMRF
malaria vaccine -- GlaxoSmithKline,	Melanoma monoclonal antibodies -- Viragen
AdProTech, Antigenics, Apovia, Aventis	melanoma vaccine -- GlaxoSmithKline,
Pasteur, Axis Genetics, Behringwerke,	Akzo Nobel, Avant, Aventis Pasteur,
CDCP, Chiron Vaccines, Genzyme	Bavarian Nordic, Biovector, CancerVax,
Transgenics, Hawaii, MedImmune, NIH,	Genzyme Molecular Oncology, Humbolt,
NYU, Oxon, Roche/Saramane, Biotech	ImClone Systems, Memorial, NYU, Oxon
Australia, Rx Tech	Melanoma vaccine Magevac -- Therion
Malaria vaccine CDC/NIIMALVAC-1	memory enhancers -- Scios
malaria vaccine, multicomponent	meningococcal B vaccine -- Chiron
mammaglobin -- Corixa	meningococcal vaccine -- CAMR
mammastatin -- Biotherapeutics	Meningococcal vaccine group B conjugate -
mannan-binding lectin -- Natlmmu	- North American Vaccine
mannan-MUC1 -- Psiron	Meningococcal vaccine group B
MAP 30	recombinant -- BioChem Vaccines,
Marinovir -- Phytera	Microscience
MARstem -- Maret	Meningococcal vaccine group Y conjugate -
MB-015 -- Mochida	- North American Vaccine
MBP -- ImmuLogic	Meningococcal vaccine groups A B and C
MCI-028 -- Mitsubishi-Tokyo	conjugate -- North American Vaccine
MCIF -- Human Genome Sciences	Mepolizumab -- GlaxoSmithKline
MDC -- Advanced BioScience -- Akzo	Metastatin -- EntreMed, Takeda
Nobel, ICOS	Met-CkB7 -- Human Genome Sciences
MDX 11 -- Medarex	met-enkephalin -- TNI
MDX 210 -- Medarex	METH-1 -- Human Genome Sciences
MDX 22 -- Medarex	methioninase -- AntiCancer
MDX 22	Methionine lyase gene therapy --
MDX 240 -- Medarex	AntiCancer
MDX 33	Met-RANTES -- Genexa Biomedical,
MDX 44 -- Medarex	Serono
MDX 447 -- Medarex	Metreleptin
MDX H210 -- Medarex	Microtubule inhibitor MAb
MDX RA -- Houston BioTech., Medarex	Immunogen/Abgenix
ME-104 -- Pharmexa	MGDF -- Kirin
Measles vaccine	MGV -- Progenics
Mecasernin -- Cephalon/Chiron, Chiron	micrin -- Endocrine
MEDI 488 -- MedImmune	microplasmin -- ThromboGenics
MEDI 500	MIF -- Genetics Institute

FIG. 28R

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migration inhibitory factor -- NIH	MAb 45-2D9- -- haematoporphyrin conjugate
Mim CD4.1 -- Xyte Therapies	MAb 4B4
mirostipen -- Human Genome Sciences	MAb 4E3-CPA conjugate -- BCM Oncologia
Mitumomab (BEC-2) -- ImClone Systems, Merck KGaA	MAb 4E3-daunorubicin conjugate
MK 852 -- Merck	MAb 50-6
MLN 1202 (Anti-CCR2 monoclonal antibody) -- Millenium Pharmaceuticals	MAb 50-61A -- Institut Pasteur
Mobenakin -- NIS	MAb 5A8 -- Biogen
molgramostim -- Genetics Institute, Novartis	MAb 791T/36-methotrexate conjugate
monoclonal antibodies -- Abgenix/Celltech, Immusol/ Medarex, Viragen/ Roslin Institute, Cambridge Antibody Tech./Elan	MAb 7c11.e8
MAb 108 --	MAb 7E11 C5-selenocystamine conjugate
MAb 10D5 --	MAb 93KA9 -- Novartis
MAb 14.18-interleukin-2 immunocytokine -- Lexigen	MAb A5B7-cisplatin conjugate -- Biodynamics Research, Pharmacia
MAb 14G2a --	MAb A5B7-I-131
MAb 15A10 --	MAb A7
MAb 170 -- Biomira	MAb A717 -- Exocell
MAb 177Lu CC49 --	MAb A7-zinostatin conjugate
MAb 17F9	MAb ABX-RB2 -- Abgenix
MAb 1D7	MAb ACA 11
MAb 1F7 -- Immune Network	MAb AFP-I-131 -- Immunomedics
MAb 1H10-doxorubicin conjugate	MAb AP1
MAb 26-2F	MAb AZ1
MAb 2A11	MAb B3-LysPE40 conjugate
MAb 2E1 -- RW Johnson	MAb B4 -- United Biomedical
MAb 2F5	MAb B43 Genistein-conjugate
MAb 31.1 -- International BioImmune Systems	MAb B43.13-Tc-99m -- Biomira
MAb 32 -- Cambridge Antibody Tech., Peptech	MAb B43-PAP conjugate
MAb 323A3 -- Centocor	MAb B4G7-gelonin conjugate
MAb 3C5	MAb BCM 43-daunorubicin conjugate -- BCM Oncologia
MAb 3F12	MAb BIS-1
MAb 3F8	MAb BMS 181170 -- Bristol-Myers Squibb
MAb 42/6	MAb BR55-2
MAb 425 -- Merck KGaA	MAb BW494
MAb 447-52D -- Merck Sharp & Dohme	MAb C 242-DM1 conjugate -- ImmunoGen
	MAb C242-PE conjugate
	MAb c30-6
	MAb CA208-cytorhodin-S conjugate -- Hoechst Japan
	MAb CC49 -- Enzon

FIG. 28S

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MAB ch14.18 --	MAB LL2-I-131 -- Immunomedics
MAB CH14.18-GM-CSF fusion protein --	MAB LL2-Y-90
Lexigen	MAB LS2D617 -- Hybritech
MAB chCE7	MAB LYM-1-gelonin conjugate
MAB CI-137 -- AMRAD	MAB LYM-1-I-131
MAB cisplatin conjugate	MAB LYM-1-Y-90
MAB CLB-CD19	MAB LYM-2 -- Peregrine
MAB CLB-CD19v	MAB M195
MAB CLL-1 -- Peregrine	MAB M195-bismuth 213 conjugate --
MAB CLL-1-GM-CSF conjugate	Protein Design Labs
MAB CLL-1-IL-2 conjugate -- Peregrine	MAB M195-gelonin conjugate
MAB CLN IgG -- doxorubicin conjugates	MAB M195-I-131
MAB conjugates -- Tanox	MAB M195-Y-90
MAB D612	MAB MA 33H1 -- Sanofi
MAB Dal B02	MAB MAD11
MAB DC101 -- ImClone	MAB MGb2
MAB EA 1 --	MAB MINT5
MAB EC708 -- Biovation	MAB MK2-23
MAB EP-5C7 -- Protein Design Labs	MAB MOC31 ETA(252-613) conjugate
MAB ERIC-1 -- ICRT	MAB MOC-31-In-111
MAB F105 gene therapy	MAB MOC-31-PE conjugate
MAB FC 2.15	MAB MR6 --
MAB G250 -- Centocor	MAB MRK-16 -- Aventis Pasteur
MAB GA6	MAB MS11G6
MAB GA733	MAB MX-DTPA BrE-3
MAB Gliomab-H -- Viventia Biotech	MAB MY9
MAB HB2-saporin conjugate	MAB Nd2 -- Tosoh
MAB HD 37 --	MAB NG-1 -- Hygeia
MAB HD37-ricin chain-A conjugate	MAB NM01 -- Nissin Food
MAB HNK20 -- Acambis	MAB OC 125
MAB huN901-DM1 conjugate --	MAB OC 125-CMA conjugate
ImmunoGen	MAB OKI-1 -- Ortho-McNeil
MAB I-131 CC49 -- Corixa	MAB OX52 -- Bioproducts for Science
MAB ICO25	MAB PMA5
MAB ICR12-CPG2 conjugate	MAB PR1
MAB ICR-62	MAB prost 30
MAB IRac-ricin A conjugate	MAB R-24
MAB K1	MAB R-24 $\alpha$ Human GD3 -- Celltech
MAB KS1-4-methotrexate conjugate	MAB RFB4-ricin chain A conjugate
MAB L6 -- Bristol-Myers Squibb, Oncogen	MAB RFT5-ricin chain A conjugate
MAB LiCO 16-88	MAB SC 1

FIG. 28T



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MAB SM-3 -- ICRT	Muc-1 vaccine -- Corixa
MAB SMART 1D10 -- Protein Design Labs	mucosal tolerance -- Aberdeen
MAB SMART ABL 364 -- Novartis	mullerian inhibiting subst
MAB SN6f	muplestim -- Genetics Institute, Novartis,
MAB SN6f-deglycosylated ricin A chain	DSM Anti-Infectives
conjugate --	murine MAB -- KS Biomedix
MAB SN6j	Mutant somatropin -- JCR Pharmaceutical
MAB SN7-ricin chain A conjugate	MV 833 -- Toagosei
MAB T101-Y-90 conjugate -- Hybritech	Mycoplasma pulmonis vaccine
MAB T-88 -- Chiron	Mycoprex -- XOMA
MAB TB94 -- Cancer ImmunoBiology	myeloperoxidase -- Henogen
MAB TEC 11	myostatin -- Genetics Institute
MAB TES-23 -- Chugai	Nacolomab tafenatox -- Pharmacia
MAB TM31 -- Avant	Nagrecor -- Scios
MAB TNT-1 -- Cambridge Antibody Tech.,	nagrestipen -- British Biotech
Peregrine	NAP-5 -- Corvas Intl.
MAB TNT-3	NAPc2 -- Corvas Intl.
MAB TNT-3 -- IL2 fusion protein --	nartograstim -- Kyowa
MAB TP3-At-211	Natalizumab -- Protein Design Labs
MAB TP3-PAP conjugate --	Nateplase -- NIH, Nihon Schering
MAB UJ13A -- ICRT	nateplase -- Schering AG
MAB UN3	NBI-3001 -- Neurocrine Biosci.
MAB ZME-018-gelonin conjugate	NBI-5788 -- Neurocrine Biosci.
MAB-BC2 -- GlaxoSmithKline	NBI-6024 -- Neurocrine Biosci.
MAB-DM1 conjugate -- ImmunoGen	Nef inhibitors -- BRI
MAB-ricin-chain-A conjugate -- XOMA	Neisseria gonorrhoea vaccine -- Antex
MAB-temoporphin conjugates	Biologics
Monopharm C -- Viventia Biotech	Neomycin B-arginine conjugate
monteplase -- Eisai	Nerelimomab -- Chiron
montirelin hydrate -- Gruenenthal	Nerve growth factor -- Amgen -- Chiron,
moroctocog alfa -- Genetics Institute	Genentech
Moroctocog-alfa -- Pharmacia	Nerve growth factor gene therapy
MP 4	nesiritide citrate -- Scios
MP-121 -- Biopharm	neuregulin-2 -- CeNeS
MP-52 -- Biopharm	neurocan -- NYU
MRA -- Chugai	neuronal delivery system -- CAMR
MS 28168 -- Mitsui Chemicals, Nihon	Neutrophil inhibitory Factor -- Corvas
Schering	Neuroprotective vaccine -- University of
MSH fusion toxin -- Ligand	Auckland
MSI-99 -- Genaera	neurotrophic chimaeras -- Regeneron
MT 201 -- Micromet	neurotrophic factor -- NsGene, CereMedix

FIG. 28U

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NeuroVax -- Immune Response	Oncophage -- Antigenics
neurturin -- Genentech	Oncostatin M -- Bristol-Myers Squibb
neutral endopeptidase -- Genentech	OncoVax-CL -- Jenner Biotherapies
NGF enhancers -- NeuroSearch	OncoVax-P -- Jenner Biotherapies
NHL vaccine -- Large Scale Biology	onercept -- Yeda
NIP45 -- Boston Life Sciences	onychomycosis vaccine -- Boehringer
NKI-B20	Ingelheim
NM 01 -- Nissin Food	opebecan -- XOMA
NMI-139 -- NitroMed	opioids -- Arizona
NMMP -- Genetics Institute	Oprelvekin -- Genetics Institute
NN-2211 -- Novo Nordisk	Oregovomab -- AltaRex
Noggin -- Regeneron	Org-33408 b-- Akzo Nobel
Nonacog alfa	Orolip DP -- EpiCept
Norelin -- Biostar	oryzacystatin
Norwalk virus vaccine	OSA peptides -- GenSci Regeneration
NRLU 10 -- NeoRx	osteoblast-cadherin GF -- Pharis
NRLU 10 PE -- NeoRx	Osteocalcin-thymidine kinase gene therapy
NT-3 -- Regeneron	osteogenic protein -- Curis
NT-4/5 -- Genentech	osteopontin -- OraPharma
NU 3056	osteoporosis peptides -- Integra, Telios
NU 3076	osteoprotegerin -- Amgen, SnowBrand
NX 1838 -- Gilead Sciences	otitis media vaccines -- Antex Biologics
NY ESO-1/CAG-3 antigen -- NIH	ovarian cancer -- University of Alabama
NYVAC-7 -- Aventis Pasteur	OX40-IgG fusion protein -- Cantab, Xenova
NZ-1002 -- Novazyme	P 246 -- Diatide
obesity therapy -- Nobex	P 30 -- Alfacell
OC 10426 -- Ontogen	p1025 -- Active Biotech
OC 144093 -- Ontogen	P-113 <sup>^</sup> -- Demegen
OCIF -- Sankyo	P-16 peptide -- Transition Therapeutics
Oct-43 -- Otsuka	p43 -- Ramot
Odulimomab -- Immunotech	P-50 peptide -- Transition Therapeutics
OK PSA - liposomal	p53 + RAS vaccine -- NIH, NCI
OKT3-gamma-1-ala-ala	PACAP(1-27) analogue
OM 991	paediatric vaccines -- Chiron
OM 992	Pafase -- ICOS
Omalizumab -- Genentech	PAGE-4 plasmid DNA -- IDEC
oncoimmunin-L -- NIH	PAI-2 -- Biotech Australia, Human
Oncolysin B -- ImmunoGen	Therapeutics
Oncolysin CD6 -- ImmunoGen	Palifermin (keratinocyte growth factor) --
Oncolysin M -- ImmunoGen	Amgen
Oncolysin S -- ImmunoGen	Palivizumab -- MedImmune

FIG. 28V

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PAM 4 -- Merck	PEG-uricase -- Mountain View
pamiteplase -- Yamanouchi	Pegvisomant -- Genentech
pancreatin, Minitabs -- Eurand	PEGylated proteins, PolyMASC -- Valentis
Pangen -- Fournier	PEGylated recombinant native human leptin
Pantarin -- Selective Genetics	-- Roche
Parainfluenza virus vaccine -- Pharmacia,	Pemtumomab
Pierre Fabre	Penetratin -- Cyclacel
paraoxanase -- Esperion	Pepscan -- Antisoma
parathyroid hormone -- Abiogen, Korea	peptide G -- Peptech, ICRT
Green Cross	peptide vaccine -- NIH, NCI
Parathyroid hormone (1-34) --	Pexelizumab
Chugai/Suntory	pexiganan acetate -- Genaera
Parkinson's disease gene therapy -- Cell	Pharmaprojects No. 3179 -- NYU
Genesys/ Ceregene	Pharmaprojects No. 3390 -- Ernest Orlando
Parvovirus vaccine -- MedImmune	Pharmaprojects No. 3417 -- Sumitomo
PCP-Scan -- Immunomedics	Pharmaprojects No. 3777 -- Acambis
PDGF -- Chiron	Pharmaprojects No. 4209 -- XOMA
PDGF cocktail -- Theratechnologies	Pharmaprojects No. 4349 -- Baxter Intl.
peanut allergy therapy -- Dynavax	Pharmaprojects No. 4651
PEG anti-ICAM MAb -- Boehringer	Pharmaprojects No. 4915 -- Avanir
Ingelheim	Pharmaprojects No. 5156 -- Rhizogenics
PEG asparaginase -- Enzon	Pharmaprojects No. 5200 -- Pfizer
PEG glucocerebrosidase	Pharmaprojects No. 5215 -- Origene
PEG hirudin -- Knoll	Pharmaprojects No. 5216 -- Origene
PEG interferon-alpha-2a -- Roche	Pharmaprojects No. 5218 -- Origene
PEG interferon-alpha-2b + ribavirin --	Pharmaprojects No. 5267 -- ML
Biogen, Enzon, ICN Pharmaceuticals,	Laboratories
Schering-Plough	Pharmaprojects No. 5373 -- MorphoSys
PEG MAb A5B7 --	Pharmaprojects No. 5493 -- Metabolex
Pegacaristim -- Amgen -- Kirin Brewery --	Pharmaprojects No. 5707 -- Genentech
ZymoGenetics	Pharmaprojects No. 5728 -- Autogen
Pegaldesleukin -- Research Corp	Pharmaprojects No. 5733 -- BioMarin
pegaspargase -- Enzon	Pharmaprojects No. 5757 -- NIH
pegfilgrastim -- Amgen	Pharmaprojects No. 5765 -- Gryphon
PEG-interferon Alpha -- Viragen	Pharmaprojects No. 5830 -- AntiCancer
PEG-interferon Alpha 2A -- Hoffman La-	Pharmaprojects No. 5839 -- Dyax
Roche	Pharmaprojects No. 5849 -- Johnson &
PEG-interferon Alpha 2B -- Schering-	Johnson
Plough	Pharmaprojects No. 5860 -- Mitsubishi-
PEG-r-hirudin -- Abbott	Tokyo
PEG-rHuMGDF -- Amgen	

FIG. 28W

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Pharmaprojects No. 5869 -- Oxford GlycoSciences	Plasminogen activators -- Abbott Laboratories, American Home Products, Boehringer Mannheim, Chiron Corporation, DuPont Pharmaceuticals, Eli Lilly, Shionogi, Genentech, Genetics Institute, GlaxoSmithKline, Hemispherx Biopharma, Merck & Co, Novartis, Pharmacia Corporation, Wakamoto, Yeda
Pharmaprojects No. 5883 -- Asahi Brewery	plasminogen-related peptides -- Bio-Tech. General/MGH
Pharmaprojects No. 5947 -- StressGen	platelet factor 4 -- RepliGen
Pharmaprojects No. 5961 -- Theratechnologies	Platelet-derived growth factor -- Amgen -- ZymoGenetics
Pharmaprojects No. 5962 -- NIH	plusonemin-- Hayashibara
Pharmaprojects No. 5966 -- NIH	PMD-2850 -- Protherics
Pharmaprojects No. 5994 -- Pharming	Pneumococcal vaccine -- Antex Biologics, Aventis Pasteur
Pharmaprojects No. 5995 -- Pharming	Pneumococcal vaccine intranasal -- BioChem Vaccines/Biovector
Pharmaprojects No. 6023 -- IMMUCON	PR1A3
Pharmaprojects No. 6063 -- Cytoclonal	PR-39
Pharmaprojects No. 6073 -- SIDDCO	pralmorelin -- Kaken
Pharmaprojects No. 6115 -- Genzyme	Pretarget-Lymphoma -- NeoRx
Pharmaprojects No. 6227 -- NIH	Priliximab -- Centocor
Pharmaprojects No. 6230 -- NIH	PRO 140 -- Progenics
Pharmaprojects No. 6236 -- NIH	PRO 2000 -- Procept
Pharmaprojects No. 6243 -- NIH	PRO 367 -- Progenics
Pharmaprojects No. 6244 -- NIH	PRO 542 -- Progenics
Pharmaprojects No. 6281 -- Senetek	pro-Apo A-I -- Esperion
Pharmaprojects No. 6365 -- NIH	prolactin -- Genzyme
Pharmaprojects No. 6368 -- NIH	Prosaptide TX14(A) -- Bio-Tech. General
Pharmaprojects No. 6373 -- NIH	prostate cancer antibodies -- Immunex, UroCor
Pharmaprojects No. 6408 -- Pan Pacific	prostate cancer antibody therapy -- Genentech/UroGenesys, Genotherapeutics
Pharmaprojects No. 6410 -- Athersys	prostate cancer immunotherapeutics -- The PSMA Development Company
Pharmaprojects No. 6421 -- Oxford GlycoSciences	prostate cancer vaccine -- Aventis Pasteur, Zonagen, Corixa, Dendreon, Jenner Biotherapies, Therion Biologics
Pharmaprojects No. 6522 -- Maxygen	
Pharmaprojects No. 6523 -- Pharis	
Pharmaprojects No. 6538 -- Maxygen	
Pharmaprojects No. 6554 -- APALEXO	
Pharmaprojects No. 6560 -- Ardana	
Pharmaprojects No. 6562 -- Bayer	
Pharmaprojects No. 6569 -- Eos	
Phenoxazine	
Phenylase -- Ibex	
Pigment epithelium derived factor -- plasminogen activator inhibitor-1, recombinant -- DuPont Pharmaceuticals	

FIG. 28X

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prostate-specific antigen -- EntreMed	RD 62198
protein A -- RepliGen	rDnase -- Genentech
protein adhesives -- Enzon	RDP-58 -- SangStat
protein C -- Baxter Intl., PPL Therapeutics, ZymoGenetics	RecepTox-Fce -- Keryx
protein C activator -- Gilead Sciences	RecepTox-GnRH -- Keryx, MTR Technologies
protein kinase R antags -- NIH	RecepTox-MBP -- Keryx, MTR Technologies
protirelin -- Takeda	recFSH -- Akzo Nobel, Organon
protocadherin 2 -- Caprion	REGA 3G12
Pro-urokinase -- Abbott, Bristol-Myers Squibb, Dainippon, Tosoh -- Welfide	Regavirumab -- Teijin
P-selectin glycoprotein ligand-1 -- Genetics Institute	relaxin -- Connetics Corp
pseudomonal infections -- InterMune	Renal cancer vaccine -- Macropharm
Pseudomonas vaccine -- Cytovax	repifermin -- Human Genome Sciences
PSGL-Ig -- American Home Products	Respiratory syncytial virus PFP-2 vaccine -- Wyeth-Lederle
PSP-94 -- Procyon	Respiratory syncytial virus vaccine -- GlaxoSmithKline, Pharmacia, Pierre Fabre
PTH 1-34 -- Nobex	Respiratory syncytial virus vaccine inactivated
Quilimmune-M -- Antigenics	Respiratory syncytial virus-parainfluenza virus vaccine -- Aventis Pasteur, Pharmacia
R 744 -- Roche	Reteplase -- Boehringer Mannheim, Hoffman La-Roche
R 101933	Retropep -- Retroscreen
R 125224 -- Sankyo	RFB4 (dsFv) PE38
RA therapy -- Cardion	RFI 641 -- American Home Products
Rabies vaccine recombinant -- Aventis Pasteur, BioChem Vaccines, Kaketsuken Pharmaceuticals	RFTS -- UAB Research Foundation
RadioTheraCIM -- YM BioSciences	RG 12986 -- Aventis Pasteur
Ramot project No. 1315 -- Ramot	RG 83852 -- Aventis Pasteur
Ramot project No. K-734A -- Ramot	RG-1059 -- RepliGen
Ramot project No. K-734B -- Ramot	rGCR -- NIH
Ranibizumab (Anti-VEGF fragment) -- Genentech	rGLP-1 -- Restoragen
RANK -- Immunex	rGRF -- Restoragen
ranpirnase -- Alfacell	rh Insulin -- Eli Lilly
ranpirnase-anti-CD22 MAb -- Alfacell	RHAMM targeting peptides -- Cangene
RANTES inhibitor -- Milan	rHb1.1 -- Baxter Intl.
RAPID drug delivery systems -- ARIAD	rhCC10 -- Claragen
rasburicase -- Sanofi	rhCG -- Serono
rBPI-21, topical -- XOMA	Rheumatoid arthritis gene therapy
RC 529 -- Corixa	
rCFTR -- Genzyme Transgenics	

FIG. 28Y

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Rheumatoid arthritis vaccine -- Veterans Affairs Medical Center	SB RA 31012 --
rhLH -- Serono	SC 56929 -- Pharmacia
Ribozyme gene therapy -- Genset	SCA binding proteins -- Curis, Enzon
Rickettsial vaccine recombinant	scFv(14E1)-ETA Berlex Laboratories, Schering AG
RIGScan CR -- Neoprobe	ScFv(FRP5)-ETA --
RIP-3 -- Rigel	ScFv6C6-PE40 --
Rituximab -- Genentech	SCH 55700 -- Celltech
RK-0202 -- RxKinetix	Schistosomiasis vaccine -- Glaxo Wellcome/Medeva, Brazil
RLT peptide -- Esperion	SCPF -- Advanced Tissue Sciences
rM/NEI -- IVAX	scuPA-suPAR complex -- Hadasit
rmCRP -- Immtech	SD-9427 -- Pharmacia
RN-1001 -- Renovo	SDF-1 -- Ono
RN-3 -- Renovo	SDZ 215918 -- Novartis
RNAse conjugate -- Immunomedics	SDZ 280125 -- Novartis
RO 631908 -- Roche	SDZ 89104 -- Novartis
Rotavirus vaccine -- Merck	SDZ ABL 364 -- Novartis
RP 431 -- DuPont Pharmaceuticals	SDZ MMA 383 -- Novartis
RP-128 -- Resolution	Secretin -- Ferring, Repligen
RPE65 gene therapy --	serine protease inhbs -- Pharis
RPR 110173 -- Aventis Pasteur	sermorelin acetate -- Serono
RPR 115135 -- Aventis Pasteur	SERP-1 -- Viron
RPR 116258A -- Aventis Pasteur	sertenef -- Dainippon
rPSGL-Ig -- American Home Products	serum albumin, Recombinant human -- Aventis Behring
r-SPC surfactant -- Byk Gulden	serum-derived factor -- Hadasit
RSV antibody -- Medimmune	Sevirumab -- Novartis
Ruplizumab -- Biogen	SGN 14 -- Seattle Genetics
rV-HER-2/neu -- Therion Biologics	SGN 15 -- Seattle Genetics
SA 1042 -- Sankyo	SGN 17/19 -- Seattle Genetics
sacrosidase -- Orphan Medical	SGN 30 -- Seattle Genetics
Sant 7	SGN-10 -- Seattle Genetics
Sargramostim -- Immunex	SGN-11 -- Seattle Genetics
saruplase -- Gruenenthal	SH 306 -- DuPont Pharmaceuticals
Satumomab -- Cytogen	Shanvac-B -- Shantha
SB 1 -- COR Therapeutics	Shigella flexneri vaccine -- Avant, Acambis, Novavax
SB 207448 -- GlaxoSmithKline	Shigella sonnei vaccine --
SB 208651 -- GlaxoSmithKline	sICAM-1 -- Boehringer Ingelheim
SB 240683 -- GlaxoSmithKline	Silteplase -- Genzyme
SB 249415 -- GlaxoSmithKline	
SB 249417 -- GlaxoSmithKline	
SB 6 -- COR Therapeutics	

FIG. 28Z

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SIV vaccine -- Endocon, Institut Pasteur	Staphylococcus aureus vaccine conjugate --
SK 896 -- Sanwa Kagaku Kenkyusho	Nabi
SK-827 -- Sanwa Kagaku Kenkyusho	Staphylococcus therapy -- Tripep
Skeletex -- CellFactors	Staphylokinase -- Biovation, Prothera,
SKF 106160 -- GlaxoSmithKline	Thrombogenetics
S-nitroso-AR545C --	Streptococcal A vaccine -- M6
SNTP -- Active Biotech	Pharmaceuticals, North American Vaccine
somatomedin-1 -- GroPep, Mitsubishi-	Streptococcal B vaccine -- Microscience
Tokyo, NIH	Streptococcal B vaccine recombinant --
somatomedin-1 carrier protein -- Insmed	Biochem Vaccines
somatostatin -- Ferring	Streptococcus pyogenes vaccine
Somatotropin/	STRL-33 -- NIH
Human Growth Hormone -- Bio-Tech.	Subalin -- SRC VB VECTOR
General, Eli Lilly	SUIS -- United Biomedical
somatropin -- Bio-Tech. General, Alkermes,	SUIS-LHRH -- United Biomedical
ProLease, Aventis Behring, Biovector,	SUN-E3001 -- Suntory
Cangene, Dong-A, Eli Lilly, Emisphere,	super high affinity monoclonal antibodies --
Enact, Genentech, Genzyme Transgenics,	YM BioSciences
Grandis/InfiMed, CSL, InfiMed, MacroMed,	Superoxide dismutase -- Chiron, Enzon,
Novartis, Novo Nordisk, Pharmacia	Ube Industries, Bio-Tech, Yeda
Serono, TranXenoGen	superoxide dismutase-2 -- OXIS
somatropin derivative -- Schering AG	suppressin -- UAB Research Foundation
somatropin, AIR -- Eli Lilly	SY-161-P5 -- ThromboGenics
Somatropin, inhaled -- Eli Lilly/Alkermes	SY-162 -- ThromboGenics
somatropin, Kabi -- Pharmacia	Systemic lupus erythematosus vaccine --
somatropin, Orasome -- Novo Nordisk	MedClone/VivoRx
Sonermin -- Dainippon Pharmaceutical	T cell receptor peptides -- Xoma
SP(V5.2)C -- Supertek	T cell receptor peptide vaccine
SPf66	T4N5 liposomes -- AGI Dermatics
sphingomyelinase -- Genzyme	TACI, soluble -- ZymoGenetics
SR 29001 -- Sanofi	targeted apoptosis -- Antisoma
SR 41476 -- Sanofi	tasonermin -- Boehringer Ingelheim
SR-29001 -- Sanofi	TASP
SS1(dsFV)-PE38 -- NeoPharm	TASP-V
$\beta$ 2 microglobulin -- Avidex	Tat peptide analogues -- NIH
$\beta$ 2-microglobulin fusion proteins -- NIH	TBP I -- Yeda
$\beta$ -amyloid peptides -- CeNeS	TBP II
$\beta$ -defensin -- Pharis	TBV25H -- NIH
Staphylococcus aureus infections --	Tc 99m ior cea1 -- Center of Molecular
Inhibitex/ZLB	Immunology
	Tc 99m P 748 -- Diatide

FIG. 28AA

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Tc 99m votumumab -- Intracell	Tissue factor -- Genentech
Tc-99m rh-Annexin V -- Theseus Imaging	Tissue factor pathway inhibitor
teceleukin -- Biogen	TJN-135 -- Tsumura
tenecteplase -- Genentech	TM 27 -- Avant
Teriparatide -- Armour Pharmaceuticals, Asahi Kasei, Eli Lilly	TM 29 -- Avant
terlipressin -- Ferring	TMC-151 -- Tanabe Seiyaku
testisin -- AMRAD	TNF tumour necrosis factor -- Asahi Kasei
Tetrafibricin -- Roche	TNF Alpha -- CytImmune
TFPI -- EntreMed	TNF antibody -- Johnson & Johnson
tgD-IL-2 -- Takeda	TNF binding protein -- Amgen
TGF-Alpha -- ZymoGenetics	TNF degradation product -- Oncotech
TGF- $\beta$ -- Kolon	TNF receptor -- Immunex
TGF- $\beta$ 2 -- Insmmed	TNF receptor 1, soluble -- Amgen
TGF- $\beta$ 3 -- OSI	TNF Tumour necrosis factor-alpha -- Asahi Kasei, Genetech, Mochida
Thalassaemia gene therapy -- Crucell	TNF-Alpha inhibitor -- Tripep
TheraCIM-h-R3 -- Center of Molecular Immunology, YM BioSciences	TNFR:Fc gene therapy -- Targeted Genetics
Theradigm-HBV -- Epimmune	TNF-SAM2
Theradigm-HPV -- Epimmune	Tolerimab -- Innogenetics
Theradigm-malaria -- Epimmune	Toxoplasma gondii vaccine -- GlaxoSmithKline
Theradigm-melanoma -- Epimmune	TP 9201 -- Telios
TheraFab -- Antisoma	TP10 -- Avant
ThGRF 1-29 -- Theratechnologies	TP20 -- Avant
ThGRF 1-44 -- Theratechnologies	tPA -- Centocor
Thrombin receptor activating peptide -- Abbott	trafermin -- Scios
thrombomodulin -- Iowa, Novocastra	TRAIL/Apo2L -- Immunex
Thrombopoietin -- Dragon Pharmaceuticals, Genentech	TRAIL-R1 MAb -- Cambridge Antibody Technologies
thrombopoietin, Pliva -- Recepton	transferrin-binding proteins -- CAMR
Thrombospondin 2 --	Transforming growth factor-beta-1 -- Genentech
thrombostatin -- Thromgen	transport protein -- Genesis
thymalfasin -- SciClone	Trastuzumab -- Genetech
thymocartin -- Gedeon Richter	TRH -- Ferring
thymosin Alpha1 -- NIH	Triabin -- Schering AG
thyroid stimulating hormone -- Genzyme	Triconal
tICAM-1 -- Bayer	Triflavin
Tick anticoagulant peptide -- Merck	troponin I -- Boston Life Sciences
TIF -- Xoma	TRP-2 <sup>^</sup> -- NIH
Tifacogin -- Chiron, NIS, Pharmacia	trypsin inhibitor -- Mochida

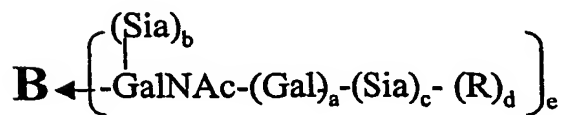
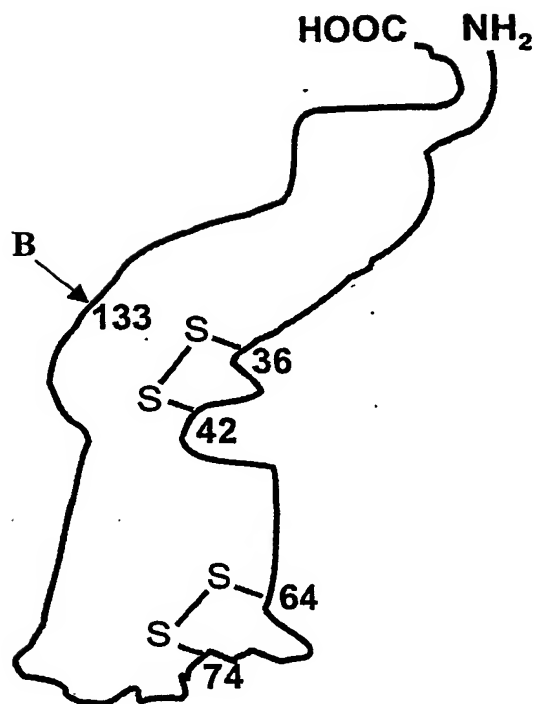
FIG. 28BB



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TSP-1 gene therapy --	Vascular endothelial growth factors -- R&D
TT-232	Systems
TTS-CD2 -- Active Biotech	vascular targeting agents -- Peregrine
Tuberculosis vaccine -- Aventis Pasteur,	vasopermeation enhancement agents --
Genesis	Peregrine
Tumor Targeted Superantigens -- Active	vasostatin -- NIH
Biotech -- Pharmacia	VCL -- Bio-Tech. General
tumour vaccines -- PhotoCure	VEGF -- Genentech, Scios
tumour-activated prodrug antibody	VEGF inhibitor -- Chugai
conjugates -- Millennium/ImmunoGen	VEGF-2 -- Human Genome Sciences
tumstatin -- ILEX	VEGF-Trap -- Regeneron
Tuvirumab -- Novartis	viscumin, recombinant -- Madaus
TV-4710 -- Teva	Vitaxin
TWEAK receptor -- Immunex	Vitrax -- ISTA Pharmaceuticals
TXU-PAP	West Nile virus vaccine -- Bavarian Nordic
TY-10721 -- TOA Eiyo	WP 652
Type I diabetes vaccine -- Research Corp	WT1 vaccine -- Corixa
Typhoid vaccine CVD 908	WX-293 -- Willex BioTech.
U 143677 -- Pharmacia	WX-360 -- Willex BioTech.
U 81749 -- Pharmacia	WX-UK1 -- Willex BioTech.
UA 1248 -- Arizona	XMP-500 -- XOMA
UGIF -- Sheffield	XomaZyme-791 -- XOMA
UIC 2	XTL 001 -- XTL Biopharmaceuticals
UK 101	XTL 002 -- XTL Biopharmaceuticals
UK-279276 -- Corvas Intl.	yeast delivery system -- Globelimmune
urodilatin -- Pharis	Yersinia pestis vaccine
urofollitrophin -- Sero	YIGSR-Stealth -- Johnson & Johnson
Urokinase -- Abbott	Yissum Project No. D-0460 -- Yissum
uteroferrin -- Pepgen	YM 207 -- Yamanouchi
V 20 -- GLYCODESIGN	YM 337 -- Protein Design Labs
V2 vasopressin receptor gene therapy	Yttrium-90 labelled biotin
vaccines -- Active Biotech	Yttrium-90-labeled anti-CEA MAb T84.66 --
Varicella zoster glycoprotein vaccine --	ZD 0490 -- AstraZeneca
Research Corporation Technologies	ziconotide -- Elan
Varicella zoster virus vaccine live -- Cantab	ZK 157138 -- Berlex Laboratories
Pharmaceuticals	Zolimomab aritox
Vascular endothelial growth factor --	Zorcell -- Immune Response
Genentech, University of California	ZRXL peptides -- Novartis

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, sialyl or oligosialyl

FIG. 29A

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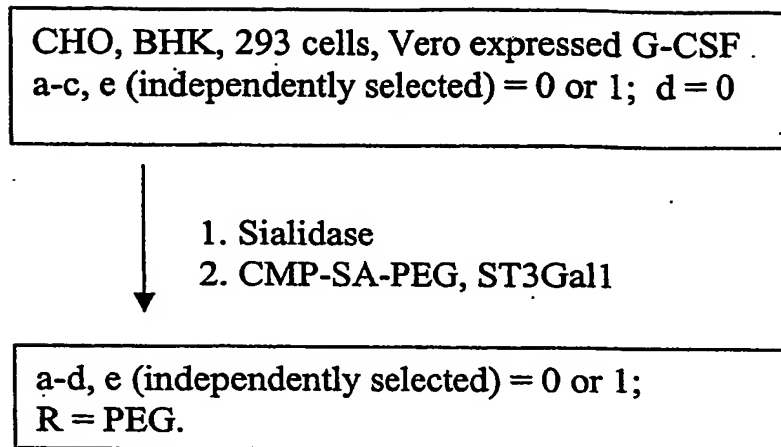


FIG. 29B

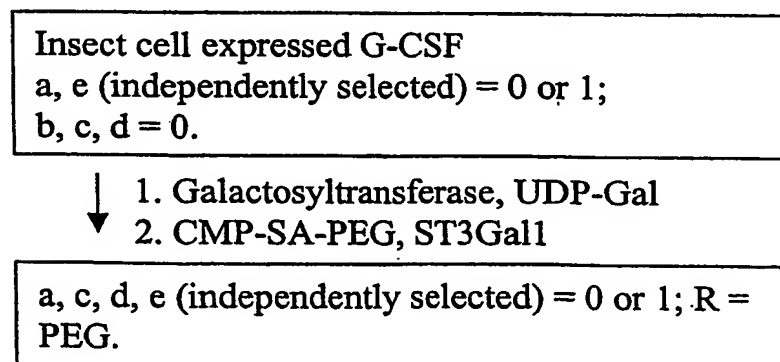


FIG. 29C

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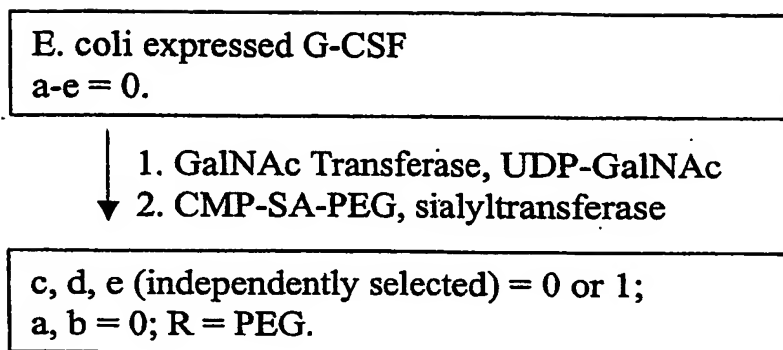


FIG. 29D

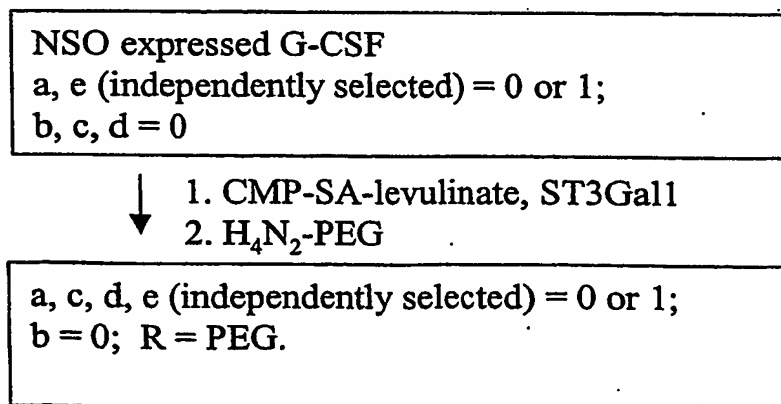


FIG. 29E

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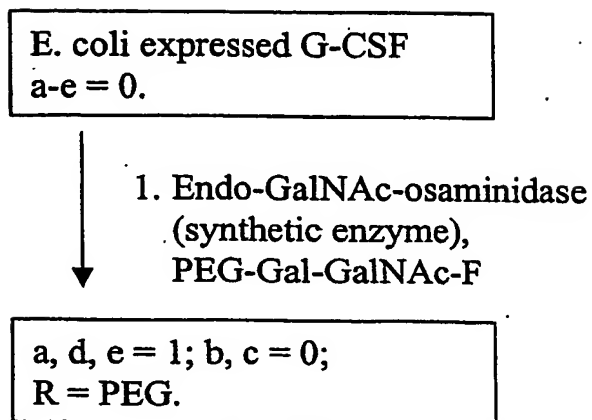


FIG. 29F

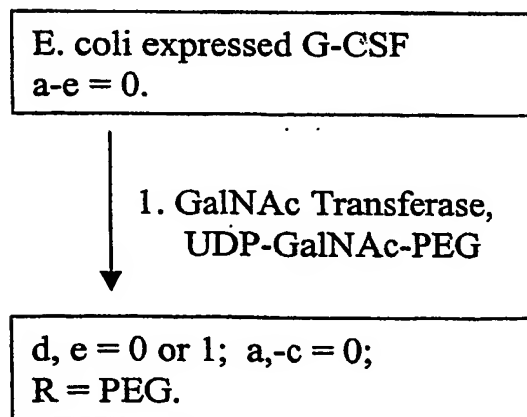
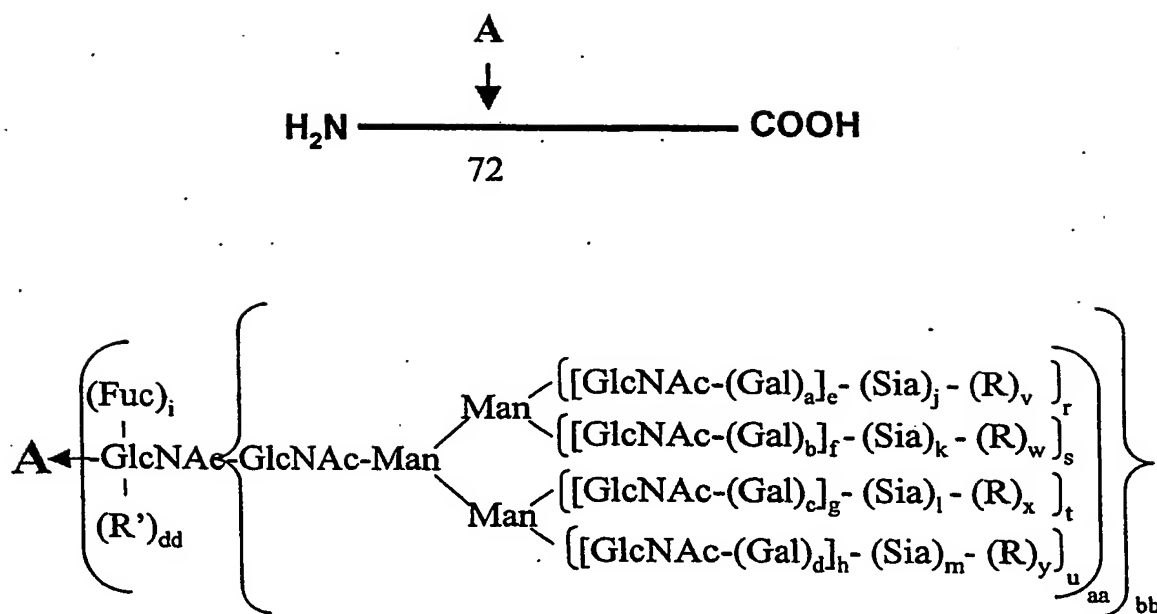


FIG. 29G

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a-d, i, n-u (independently selected) = 0 or 1.

aa, bb, cc, dd, ee (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 30A

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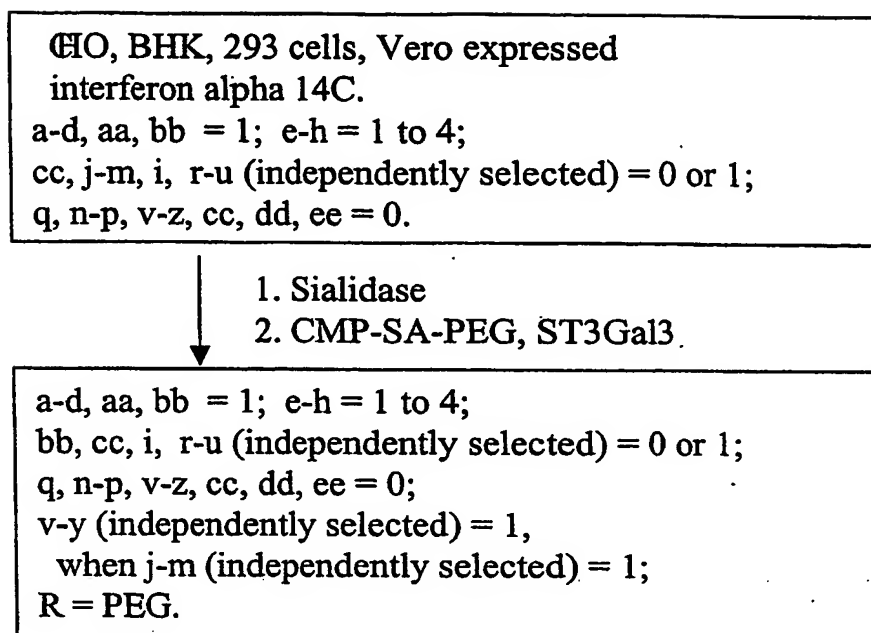


FIG. 30B

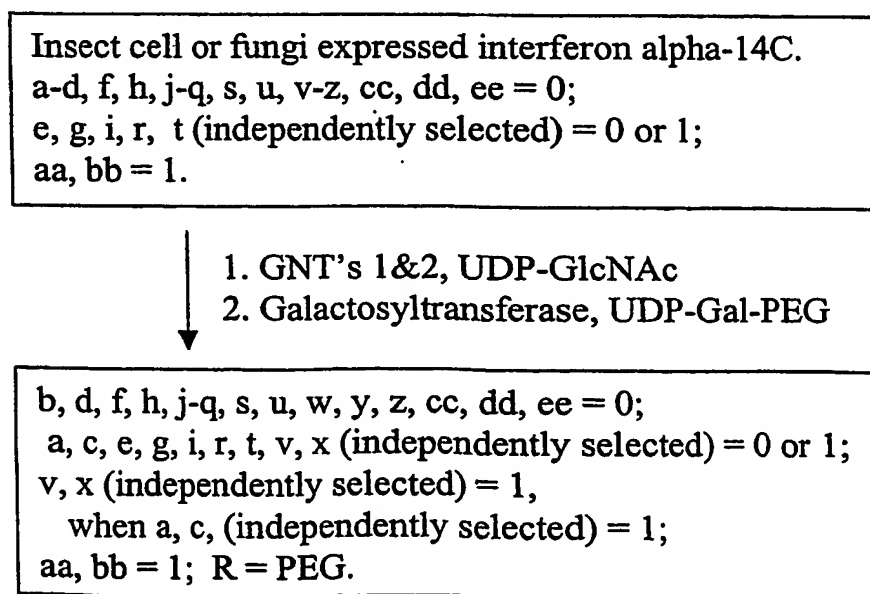


FIG. 30C

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Yeast expressed interferon alpha-14C.

a-q, cc, dd, ee, v-z = 0;

r-y (independently selected) = 0 to 1;

aa, bb = 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

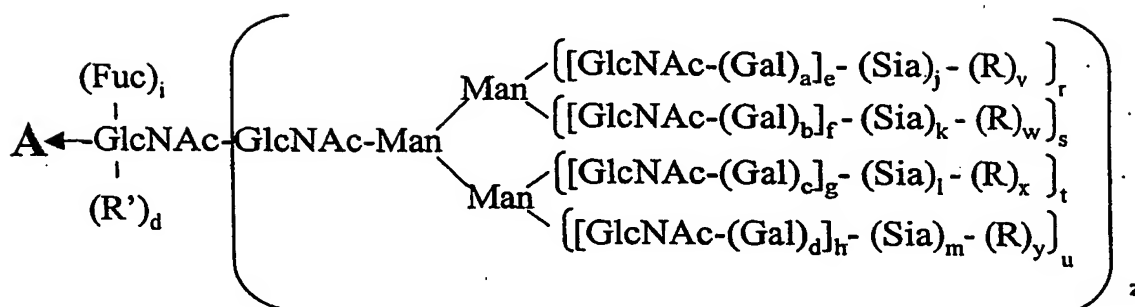
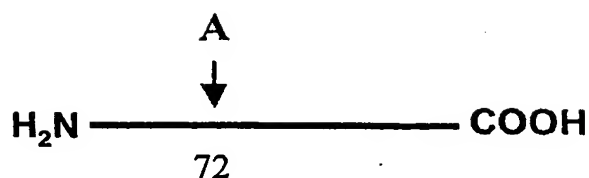
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-z, bb = 0; aa = 1; R' = -Gal-Sia-PEG.

FIG. 30D



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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1.

R = polymer; R' = sugar, glycoconjugate.

FIG. 30E

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CHO, BHK, 293 cells, Vero expressed  
interferon alpha-14C.  
h = 1 to 3;  
a-g, j-m, i (independently selected) = 0 or 1;  
r-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1.



1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
a-g, i (independently selected) = 0 or 1;  
r-u (independently selected) = 0 or 1;  
j-m, v-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 30F

Insect cell or fungi expressed  
interferon alpha-14C.  
a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, r, t (independently selected) = 0 or 1;  
z = 1.



1. GNT's 1,2,4,5, UDP-GlcNAc  
2. Galactosyltransferase, UDP-Gal  
3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 30G

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Yeast expressed interferon alpha-14C.  
a-n = 0; r-y (independently selected) = 0 to 1;  
z = 1; R (branched or linear) = Man,  
oligomannose.

1. mannosidases  
2. GNT's 1,2,4,5, UDP-GlcNAc  
3. Galactosyltransferase, UDP-Gal  
↓  
4.. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 30H

NSO expressed interferon alpha 14C.  
a-i, r-u (independently selected) = 0 or 1;  
j-m, n, v-y = 0; z = 1.

1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt  
↓  
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-i, j-m, r-y (independently selected) = 0 or 1;  
n = 0; z = 1; R = PEG.

FIG. 30I

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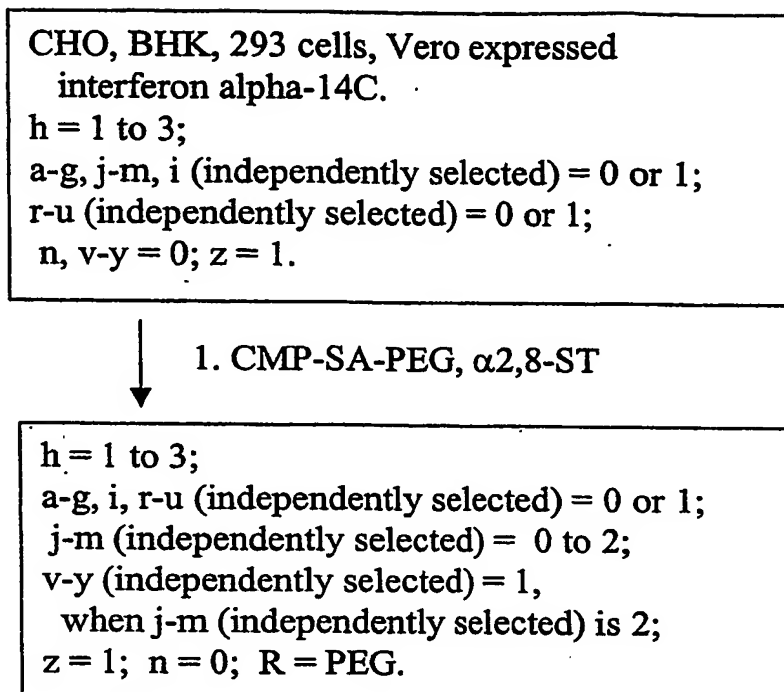


FIG. 30J

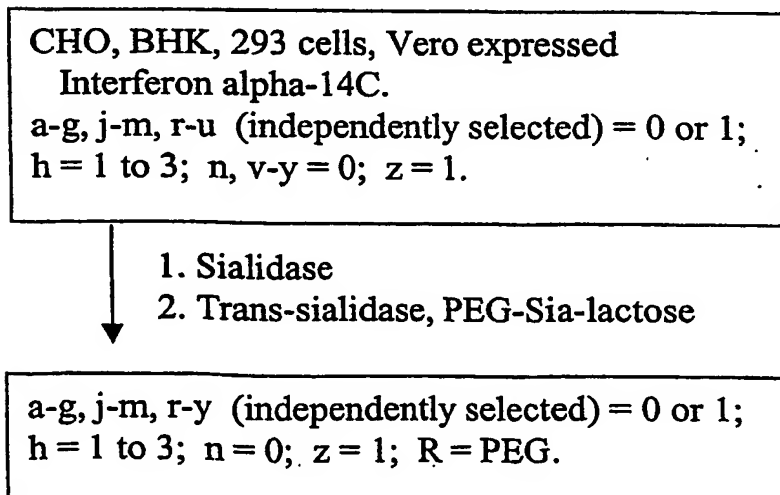


FIG. 30K

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CHO, BHK, 293 cells, Vero expressed  
interferon alpha-14C.

$h = 1$  to  $3$ ;

$a-g, j-m, i$  (independently selected) =  $0$  or  $1$ ;

$r-u$  (independently selected) =  $0$  or  $1$ ;

$n, v-y = 0$ ;  $z = 1$ .

1. CMP-SA,  $\alpha 2,8$ -ST

$h = 1$  to  $3$ ;

$a-g, i, r-u$  (independently selected) =  $0$  or  $1$ ;

$j-m$  (independently selected) =  $0$  to  $40$ ;

$z = 1$ ;  $v-y, n = 0$ .

FIG. 30L

Insect cell or fungi expressed interferon alpha-14C.

$a-d, f, h, j-n, s, u, v-y = 0$ ;

$e, g, i, r, t$  (independently selected) =  $0$  or  $1$ ;

$z = 1$ .

1. GNT's 1 & 2, UDP-GlcNAc

2. Galactosyltransferase,  
UDP-Gal-linker-SA-CMP

3. ST3Gal3, transferrin

$a, c, e, g, i, r, t, v, x$  (independently selected) =  $0$  or  $1$ ;

$z = 1$ ;  $b, d, f, h, j-n, s, u, w, y = 0$ ;

$R = \text{transferrin}$ .

FIG. 30M

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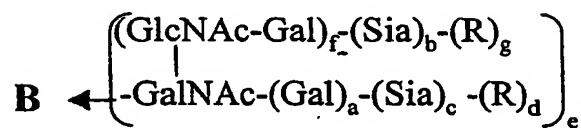
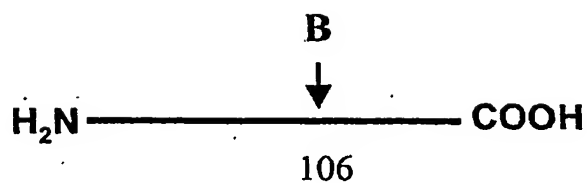
Insect cell or fungi expressed interferon alpha-14C.  
a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, r, t (independently selected) = 0 or 1; z = 1.

- ↓
1. endoglycanase
  2. Galactosyltransferase,  
UDP-Gal-linker-SA-CMP
  3. ST3Gal3, transferrin

i (independently selected) = 0 or 1;  
a-h, j-m, r-z = 0;  
n = 1; R' = -Gal-linker-transferrin.

FIG. 30N

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a-c, e, f (independently selected) = 0 or 1;  
 d, g = 0; R = polymer, glycoconjugate.

FIG. 300

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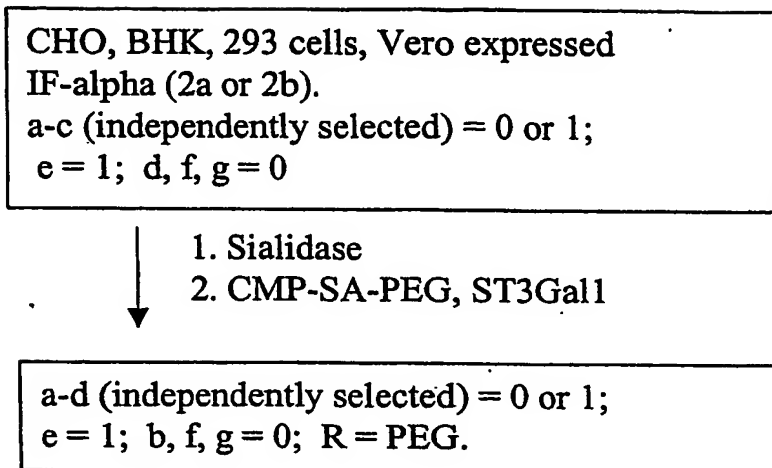


FIG. 30P

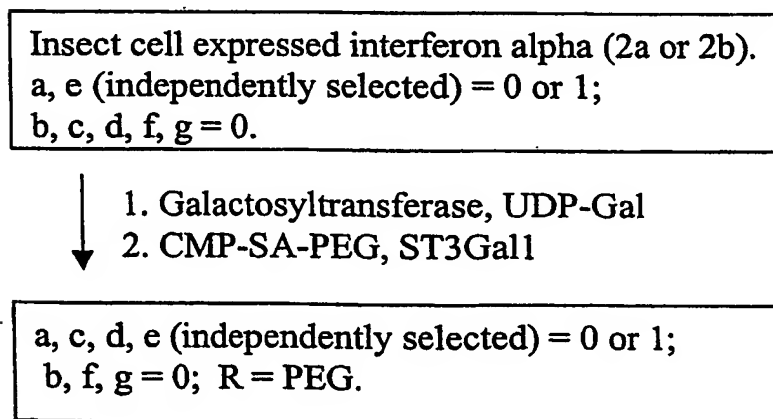


FIG. 30Q



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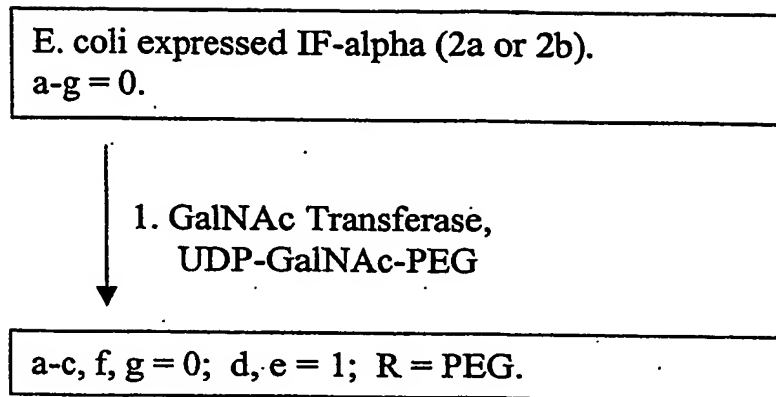


FIG. 30R

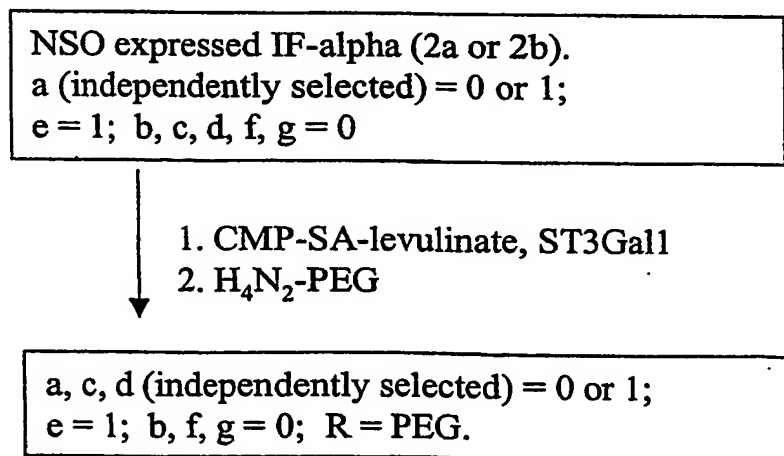


FIG. 30S

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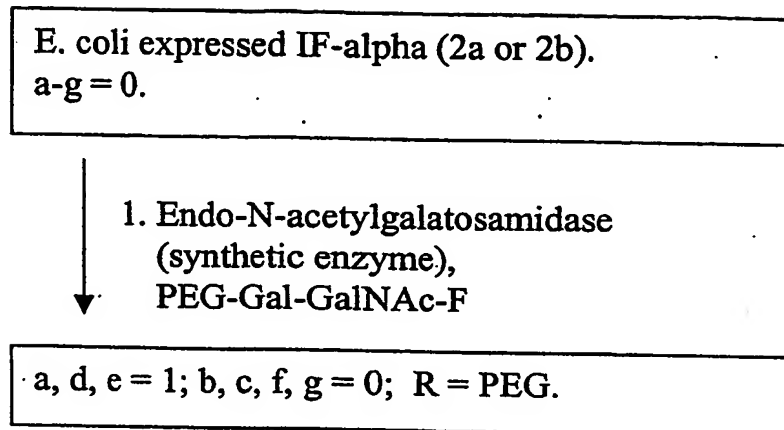


FIG. 30T

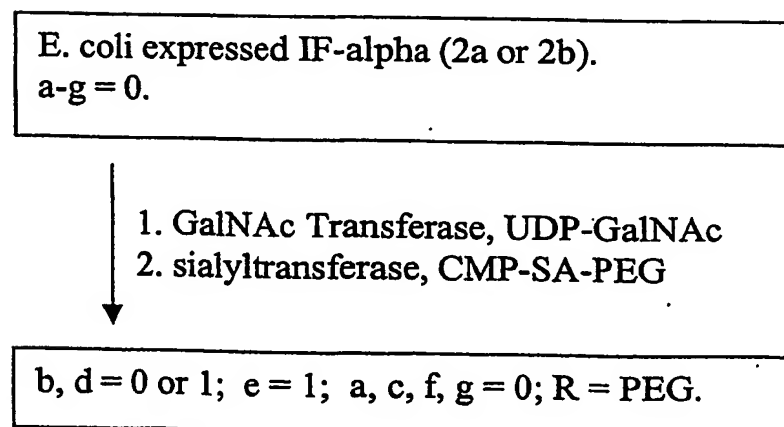


FIG. 30U

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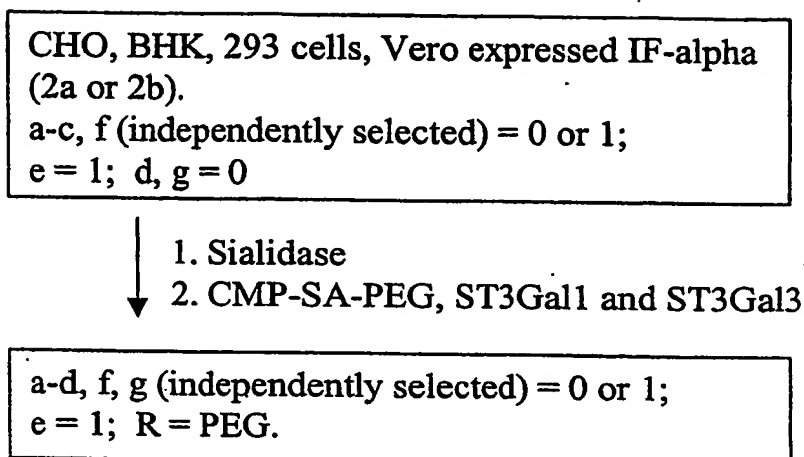


FIG. 30V

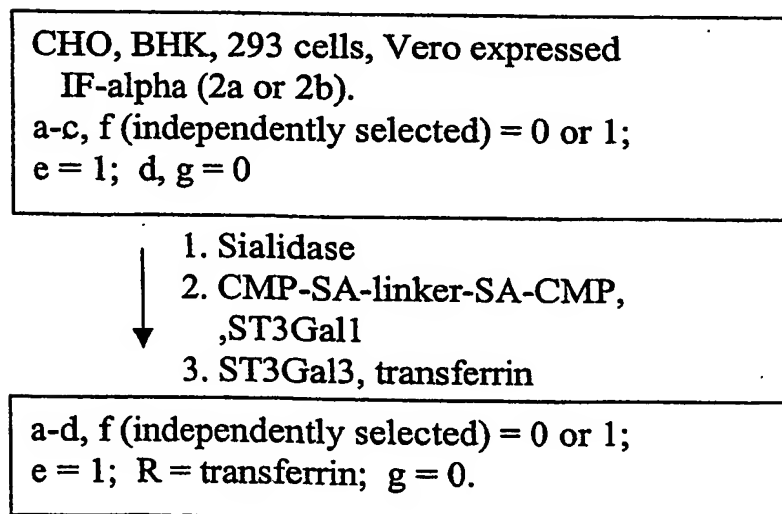
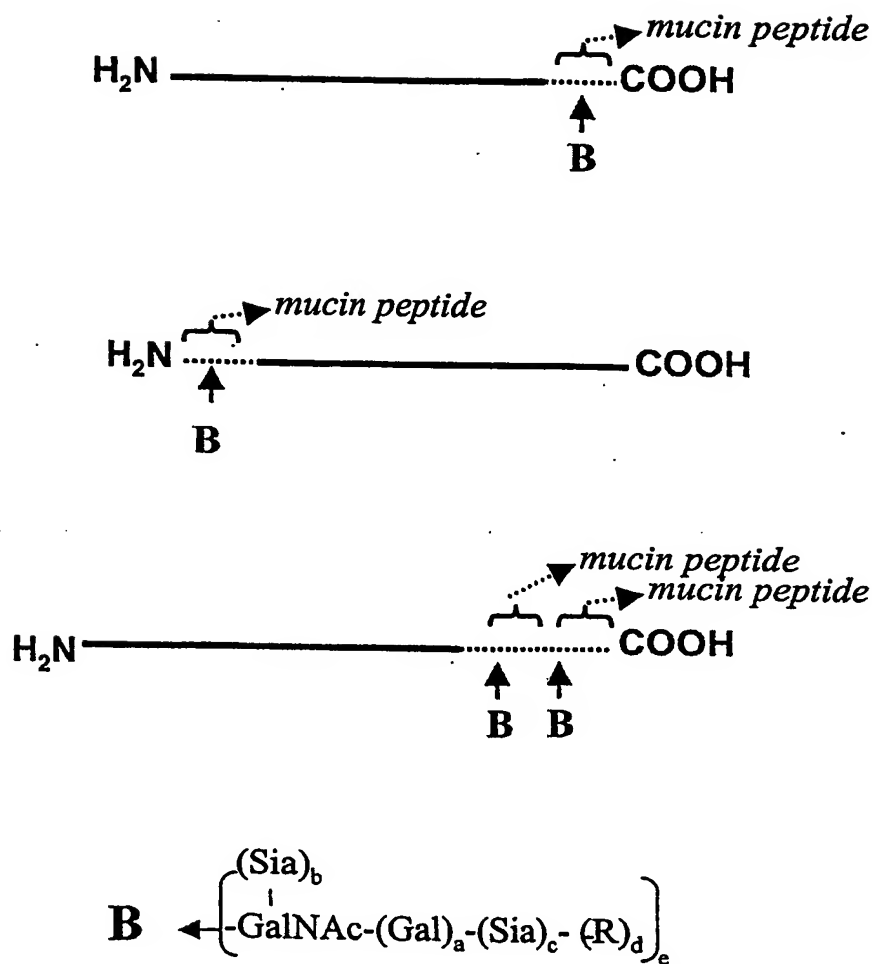


FIG. 30W

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a-c, e (independently selected) = 0 or 1;  
 d = 0; R = polymer, glycoconjugate.

FIG. 30X

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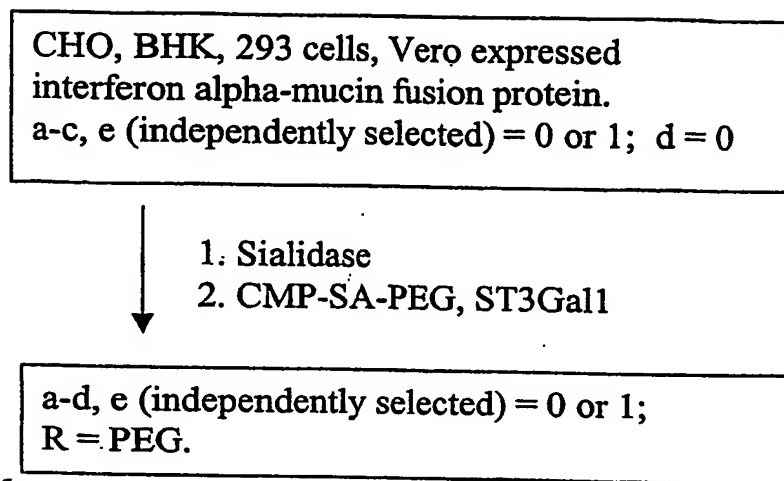


FIG. 30Y

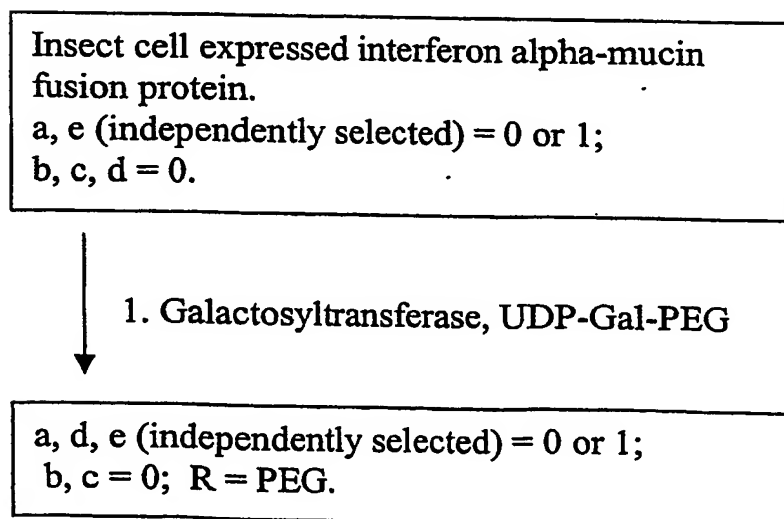


FIG. 30Z

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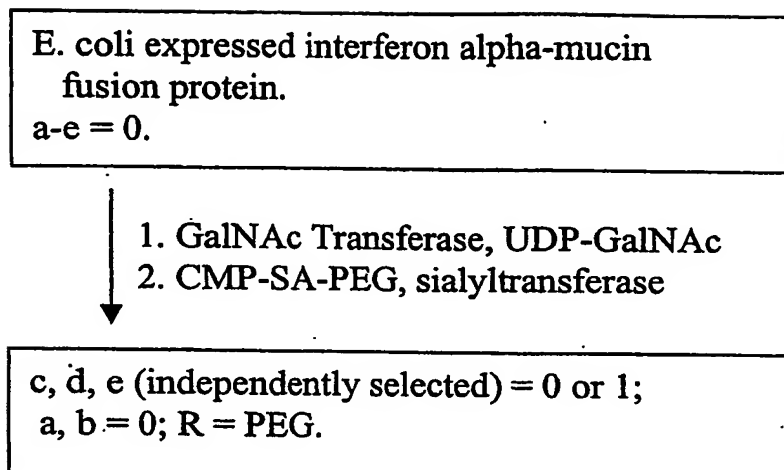
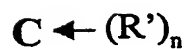
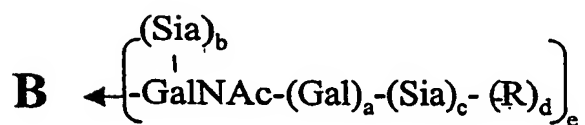
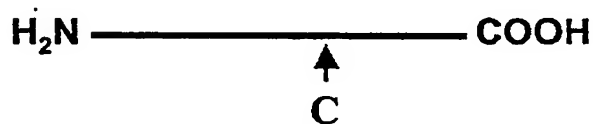
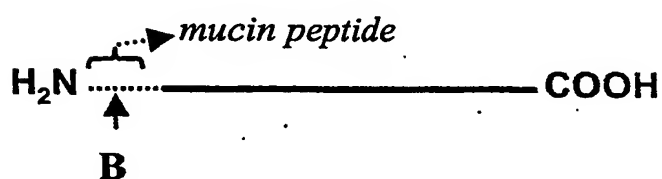
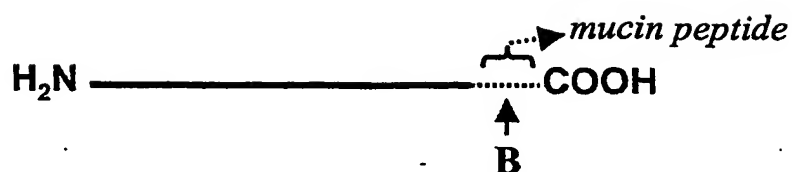


FIG. 30AA

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 30BB

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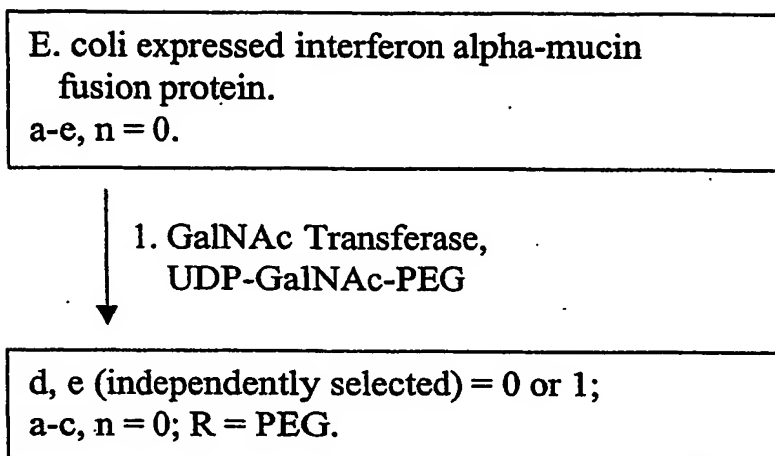


FIG. 30CC

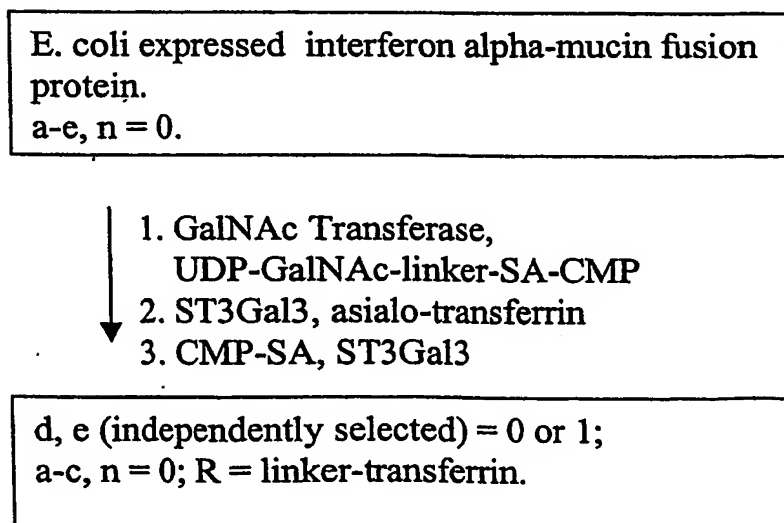


FIG. 30DD



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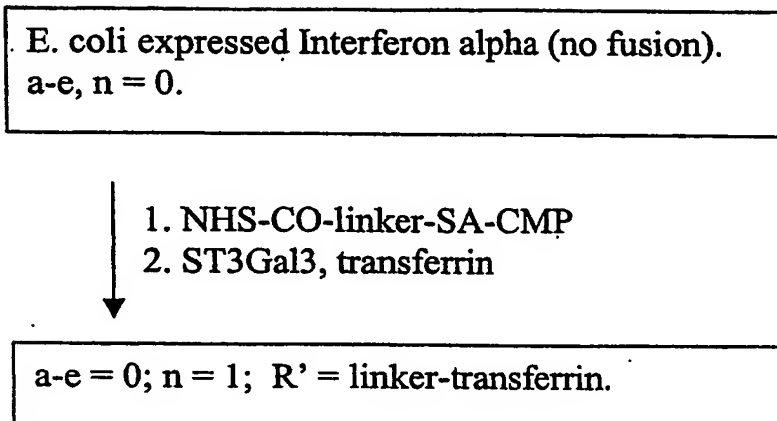
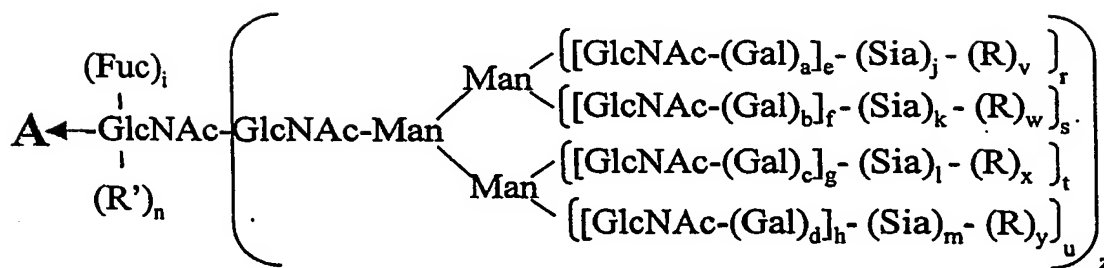


FIG. 30EE

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a-d, i, r-u (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 4.  
 j-m (independently selected) = 0 or 1.  
 n, v-y = 0; z = 0 or 1; R = polymer

FIG. 31A

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CHO, BHK, 293 cells, Vero expressed IF-beta  
 h = 1 to 3;  
 a-g, j-m, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1.

1. Sialidase  
 2. CMP-SA-PEG, ST3Gal3

h = 1 to 3;  
 a-g, i (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 z = 1; n = 0; R = PEG.

FIG. 31B

Insect cell expressed IF-beta  
 a-d, f, h, j-n, s, u, v-y = 0;  
 e, g, i, r, t (independently selected) = 0 or 1;  
 z = 1.

1. GNT's 1&2, UDP-GlcNAc  
 2. Galactosyltransferase, UDP-Gal  
 2. CMP-SA-PEG, ST3Gal3,  
 buffer, salt

b, d, f, h, k, m, n, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 j, l, v, x (independently selected) = 0 or 1;  
 z = 1; R = PEG.

FIG. 31C

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Yeast expressed IF-beta

a-n = 0; z = 1;

r-y (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose or polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z = 0; n = 1; R' = -Gal-Sia-PEG.

FIG. 31D

CHO, BHK, 293 cells, Vero expressed IF-beta

h = 1 to 3;

a-g, j-m, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

n, v-y = 0; z = 1.

- ↓
1. CMP-SA-PEG, ST3Gal3

h = 1 to 3;

a-g, i (independently selected) = 0 or 1;

r-u (independently selected) = 0 or 1;

j-m, v-y (independently selected) = 0 or 1;

z = 1; n = 0; R = PEG.

FIG. 31E

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Insect cell expressed IF-beta  
a-d, f, h, j-n, s, u, v-y = 0; e, g, i, r, t  
(independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 31F

Yeast expressed IF-beta  
a-n = 0; z = 1;  
r-y (independently selected) = 0 to 1;  
R (branched or linear) = Man, oligomannose.

- ↓
1. mannosidases
  2. GNT's 1,2,4,5, UDP-GlcNAc
  3. Galactosyltransferase, UDP-Gal
  4. CMP-SA-PEG, ST3Gal3

a-m, r-y (independently selected) = 0 or 1;  
z = 1; n = 0; R = PEG.

FIG. 31G

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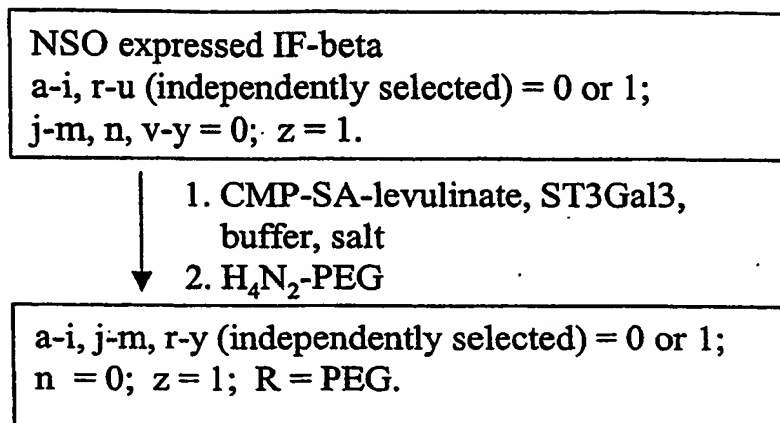


FIG. 31H

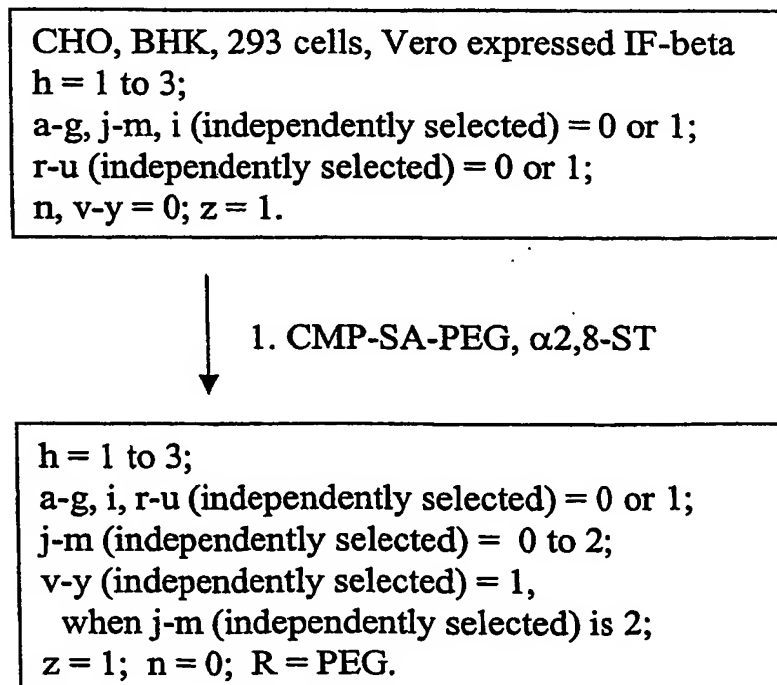


FIG. 31I

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CHO, BHK, 293 cells, Vero expressed IF-beta  
a-g, j-m, r-u (independently selected) = 0 or 1;  
h = 1 to 3; n, v-y = 0; z = 1.



1. Sialidase
2. Trans-sialidase, PEG-Sia-lactose

a-g, j-m, r-y (independently selected) = 0 or 1;  
h = 1 to 3; n = 0; z = 1; R = PEG.

FIG. 31J

CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, r-u, z (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.



1. Sialidase
2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;  
e-h = 1; n=0;  
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31K

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NSO expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2.  $\alpha$ -Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; R = PEG

n = 0; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;

FIG. 31L

CHO, BHK, 293 cells, Vero expressed Ifn-beta.

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, r-u, z (independently selected) = 0 or 1;

e-h = 1; n = 0;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 31M



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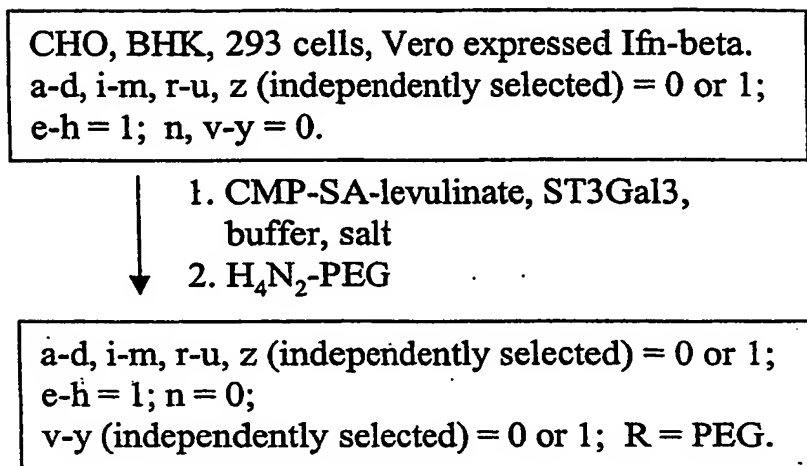


FIG. 31N

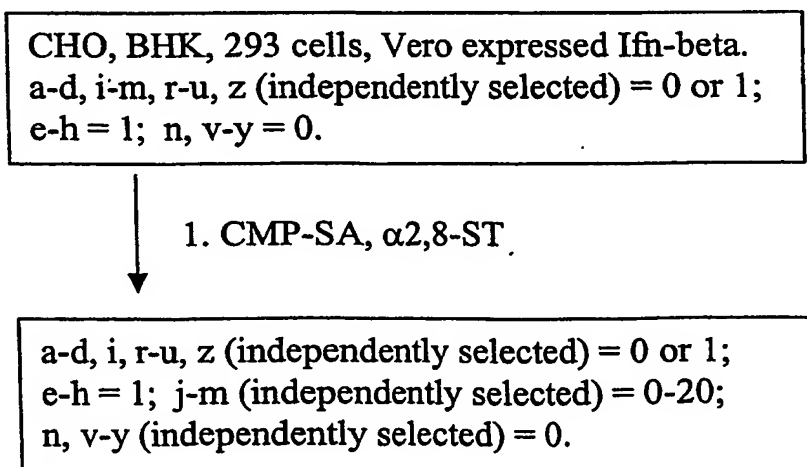
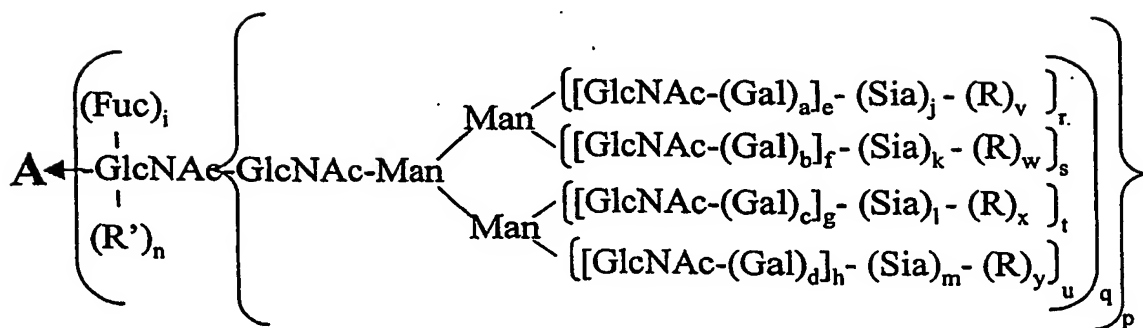
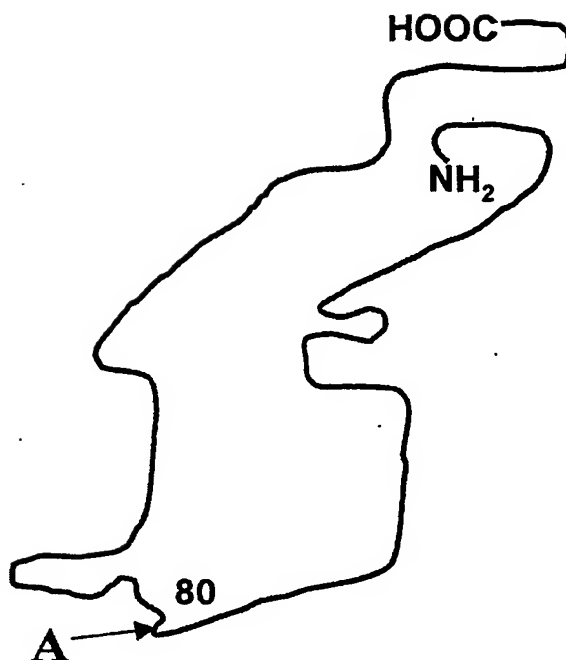


FIG. 31O

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group;

R' = H, glycosyl group, modifying group,  
glycoconjugate.

FIG. 31P

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Insect cell expressed Ifn-beta.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 31Q

Yeast expressed Ifn-beta.

a-m = 0; q-y (independently selected) = 0 to 1;

p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0;

n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 31R

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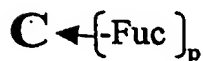
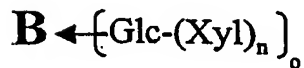
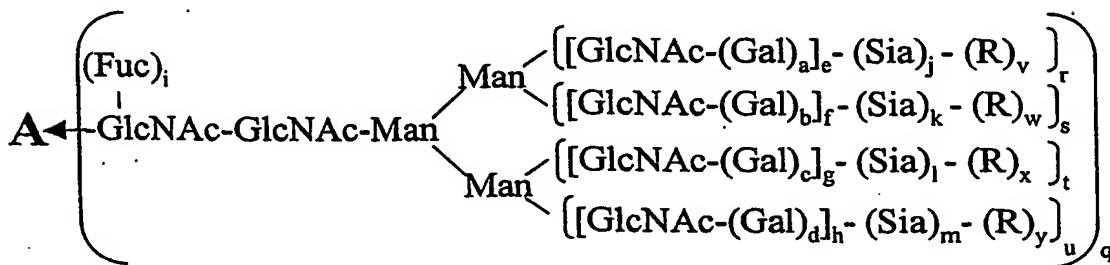
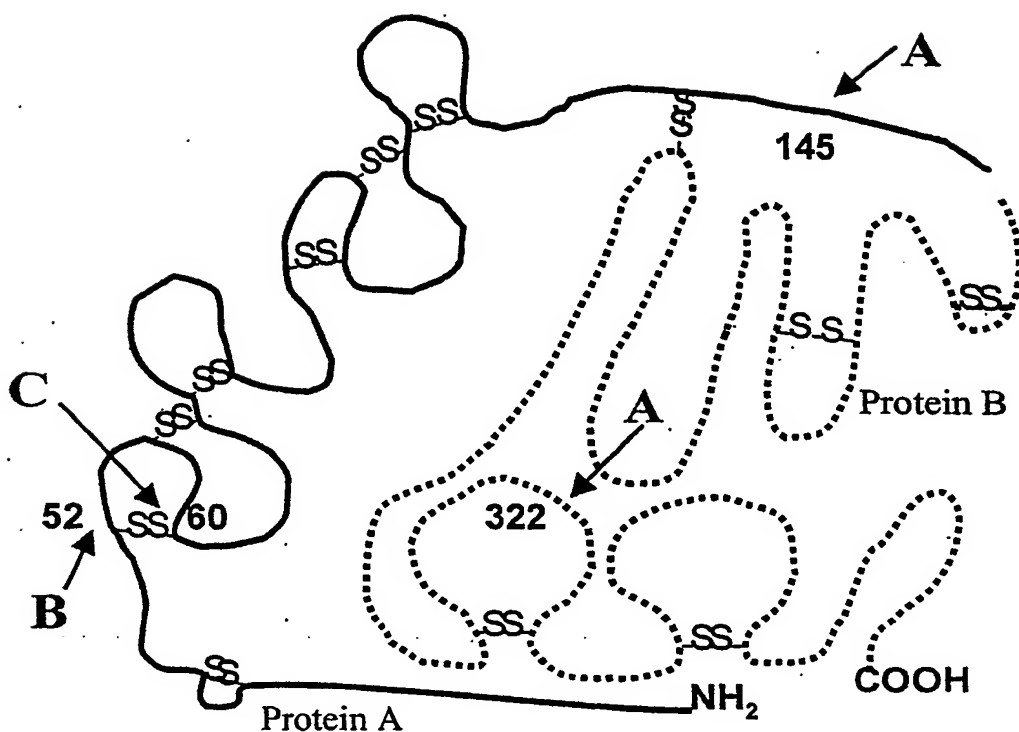
CHO, BHK, 293 cells, Vero expressed Ifn-beta.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 31S

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a-d, i, q-u (independently selected) = 0 or 1.

o, p (independently selected) = 0 or 1.

e-h, n (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-y = 0;

R = modifying group, mannose, oligo-mannose, Sia-Lewis X, Sia-Lewis A..

FIG. 32A

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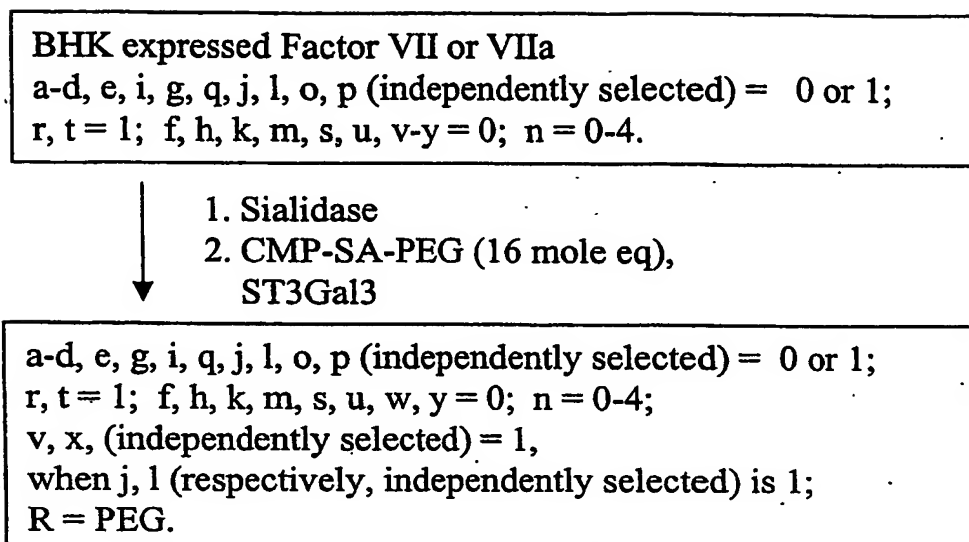


FIG. 32B

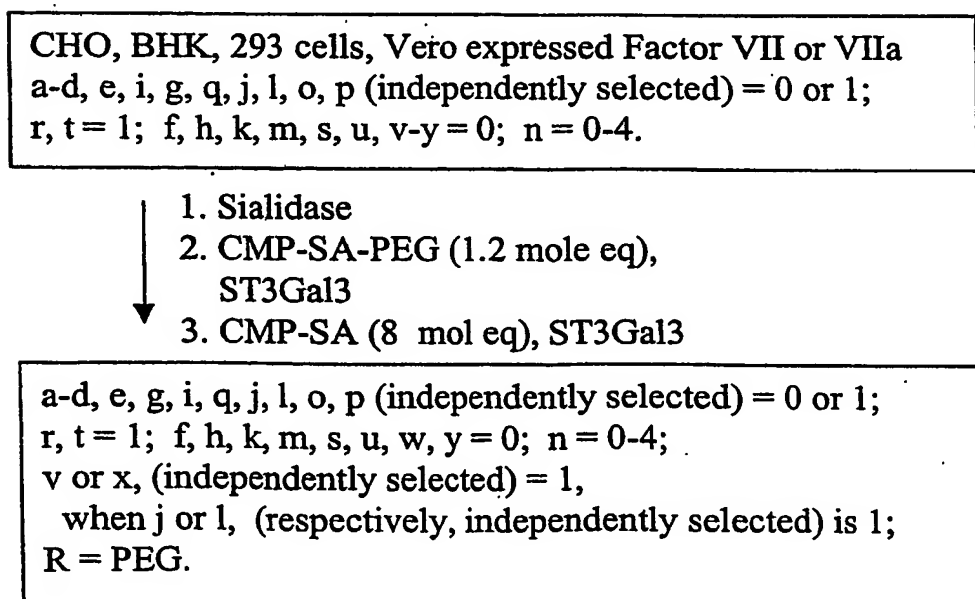


FIG. 32C

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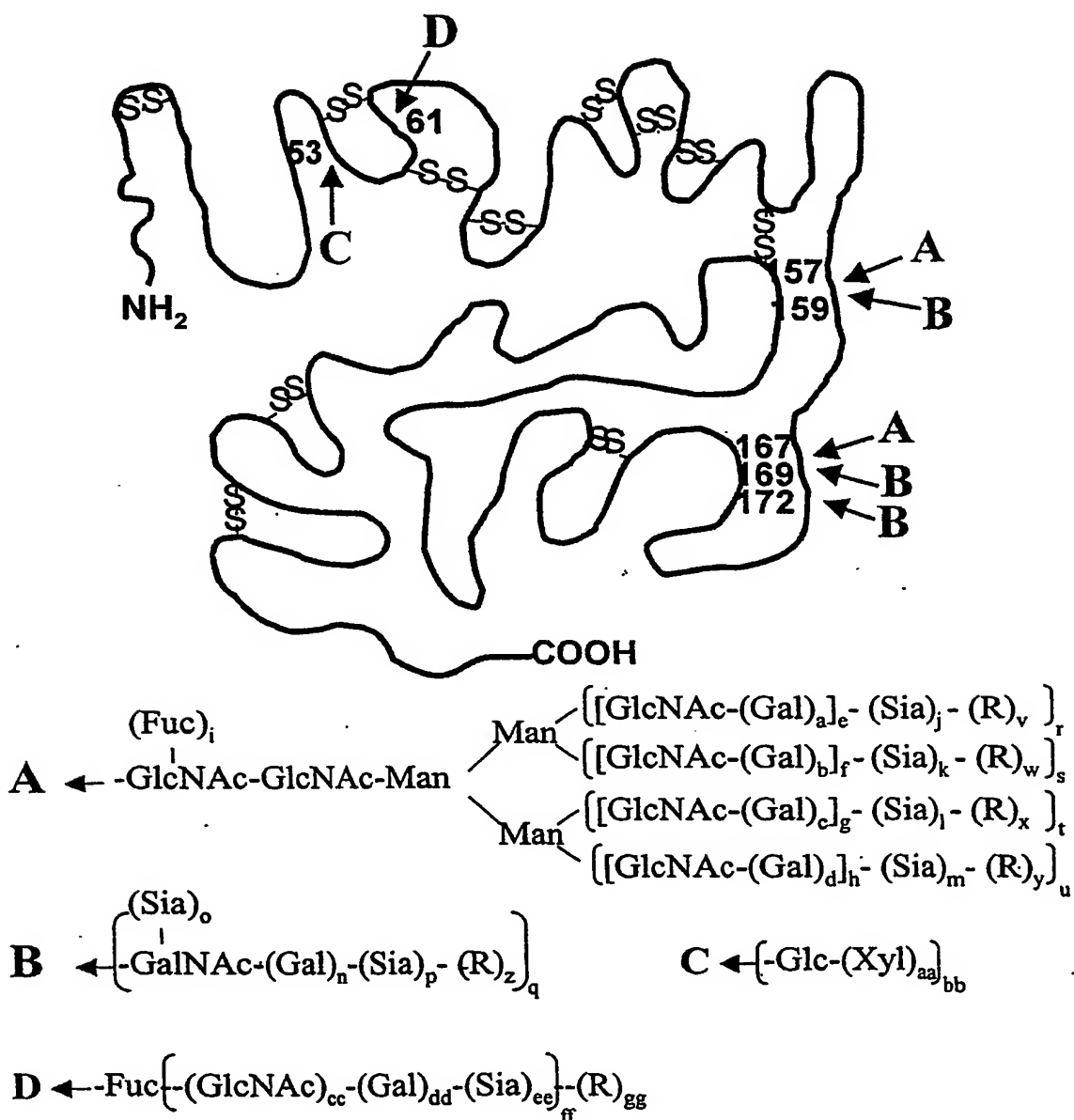
NSO expressed Factor VII or VIIa  
a--u (independently selected) = 0 or 1;  
v-y = 0; n = 0-4;  
Sia (independently selected) = Sia or Gal.

- ↓  
1. Sialidase and  $\alpha$ -galactosidase  
2. Galactosyltransferase, UDP-Gal  
↓ 3. CMP-SA-PEG, ST3Gal3

a-m, o-u (independently selected) = 0 or 1;  
n = 0-4; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
Sia = Sia; R = PEG.

FIG. 32D

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a-d, i, n-u (independently selected) = 0 or 1.

bb, cc, dd, ee, ff, gg (independently selected) = 0 or 1.

e-h, aa (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0; R = modifying group, mannose, oligo-mannose.

FIG. 33A



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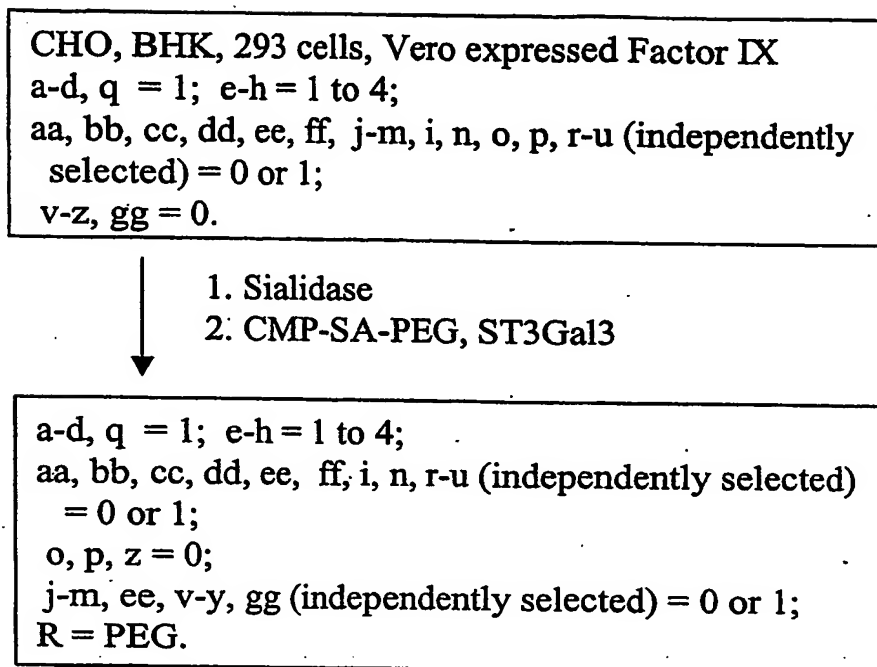


FIG. 33B

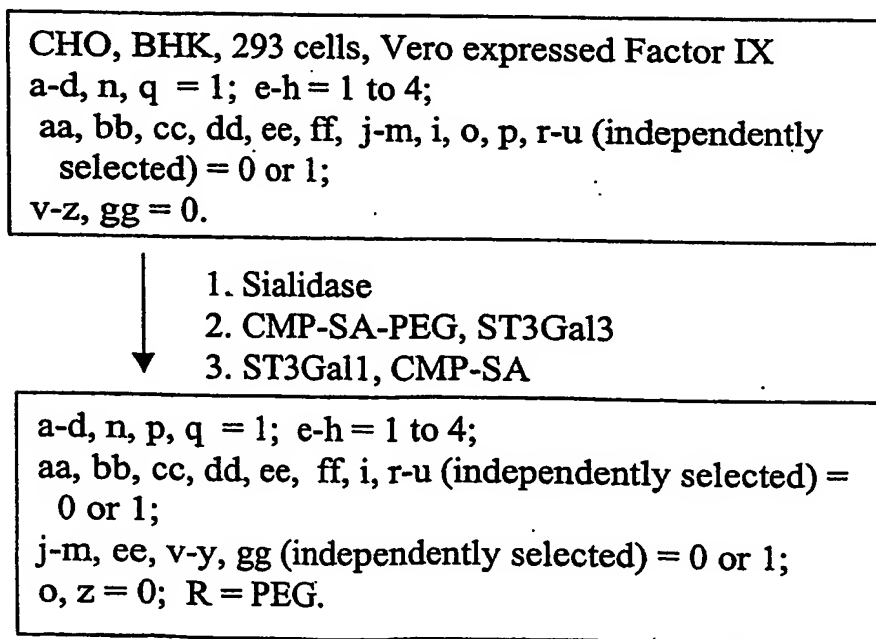


FIG. 33C

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CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, n, q, bb, cc, dd, ff = 1; e-h, aa = 1 to 4; ee, j-m, i,  
 o, p, r-u (independently selected) = 0 or 1; v-z, gg = 0.

- ↓
1. sialidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA, ST3Gal3
  4. CMP-SA-PEG, ST3Gal1

a-d, n, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, r-u (independently selected) =  
 0 or 1; R = PEG;  
 o, v-y, gg = 0;  
 j-m, p, ee (independently selected) = 0 or 1, but when  
 p = 1, z = 1.

FIG. 33D

CHO, BHK, 293 cells, Vero expressed Factor IX  
 a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, j-m, i, n, o, p, r-u (independently  
 selected) = 0 or 1;  
 v-z, gg = 0.

- ↓
- CMP-SA-PEG, ST3Gal3

a-d, q = 1; e-h = 1 to 4;  
 aa, bb, cc, dd, ee, ff, i, n, r-u (independently selected)  
 = 0 or 1; R = PEG;  
 o, p, z = 0; j-m, ee, v-y, gg (independently selected) =  
 0 or 1.

FIG. 33E

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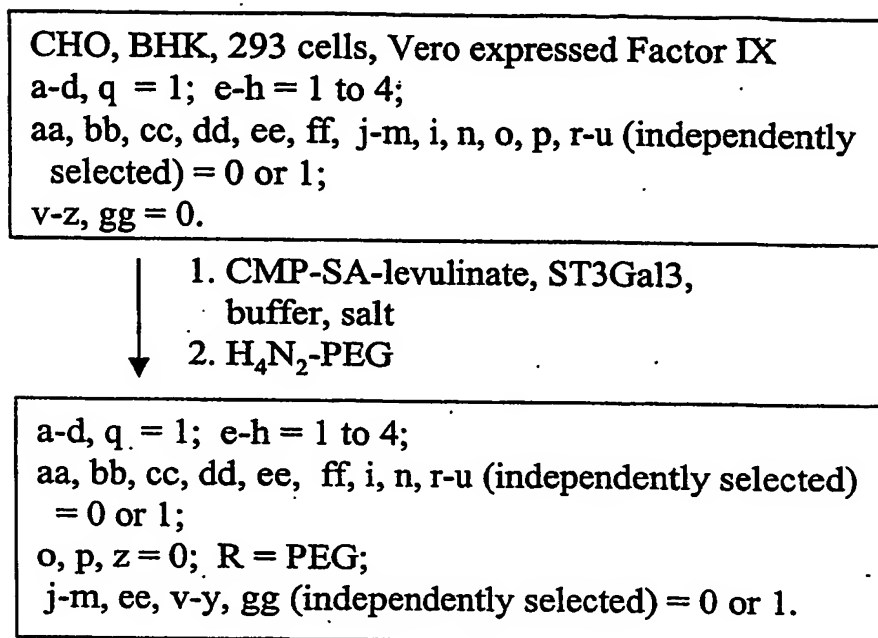


FIG. 33F

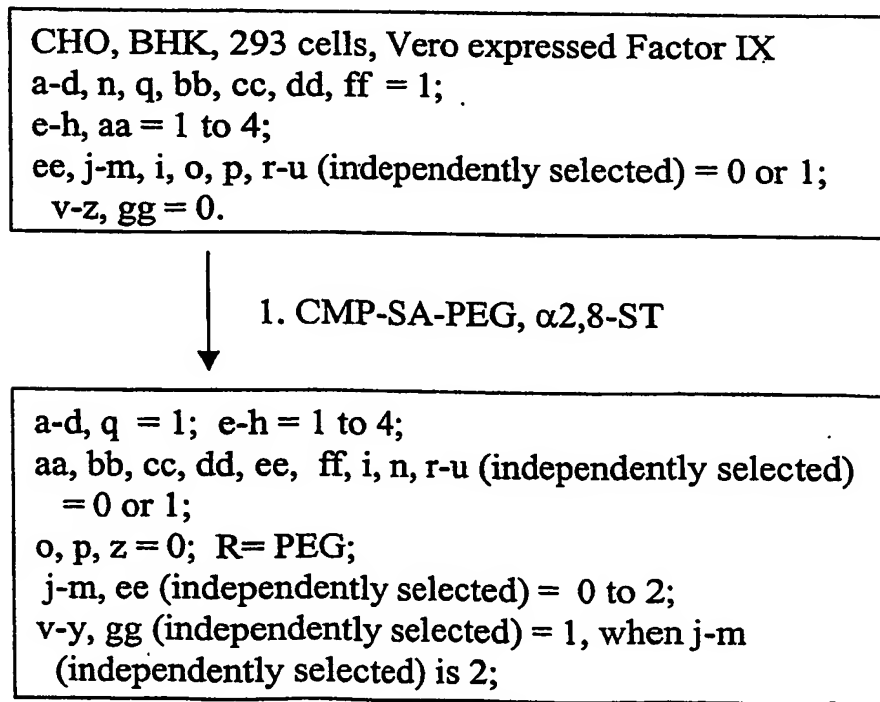
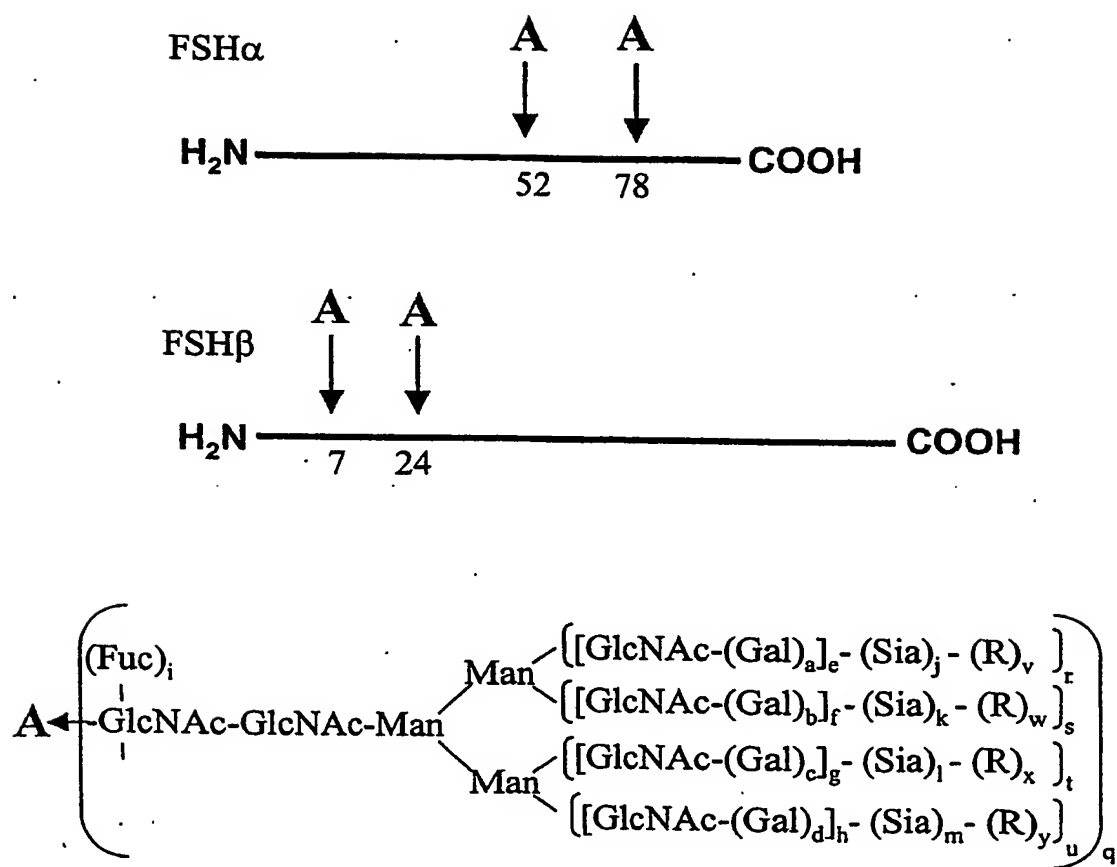


FIG. 33G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 34A

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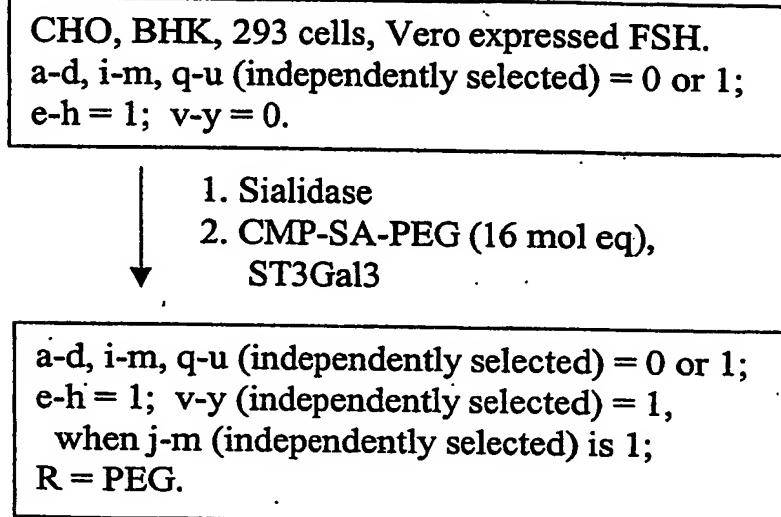


FIG. 34B

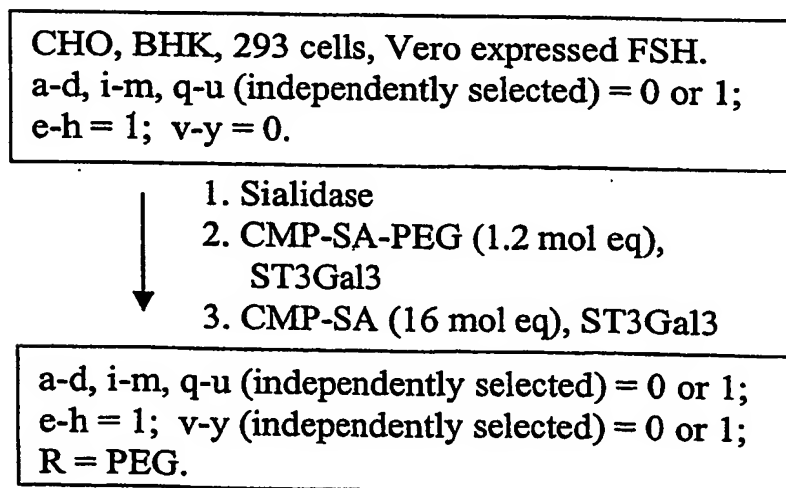


FIG. 34C

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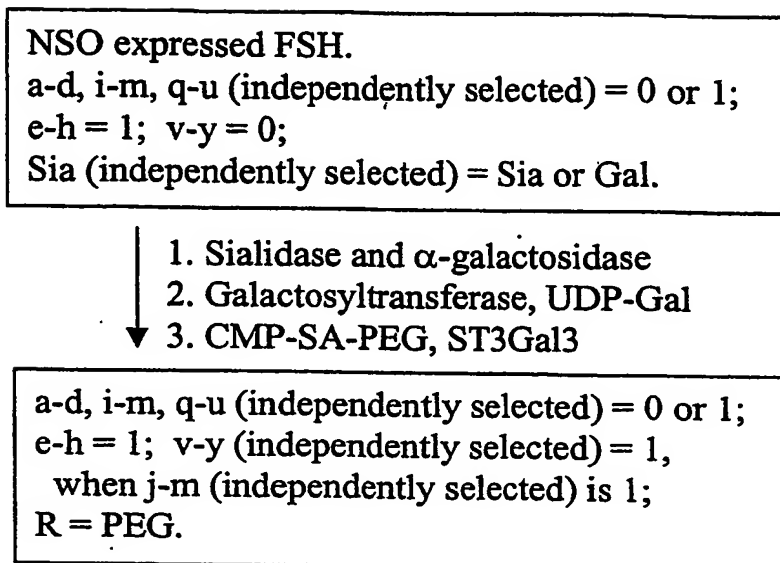


FIG. 34D

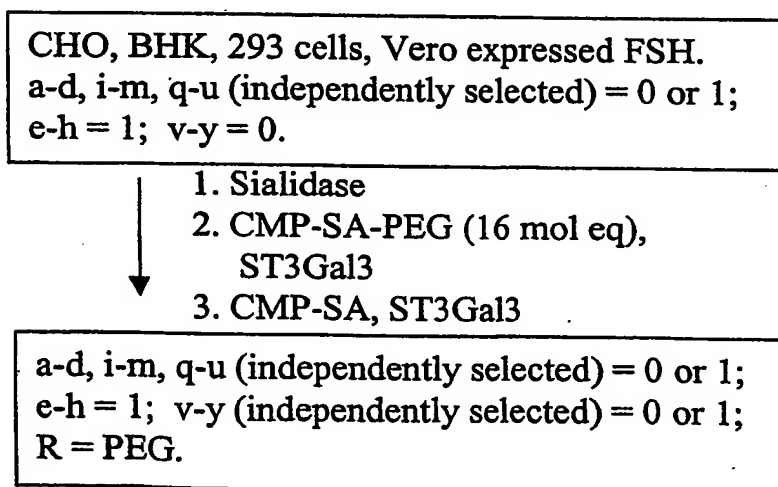


FIG. 34E

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CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 34F

CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 34G

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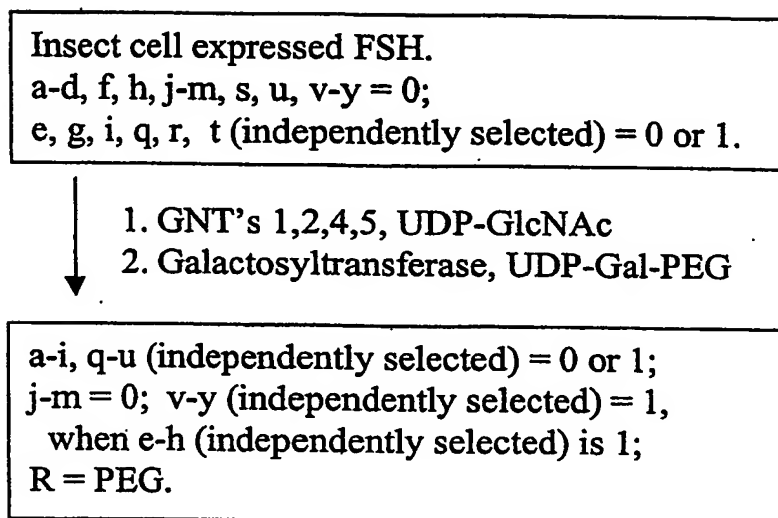


FIG. 34H

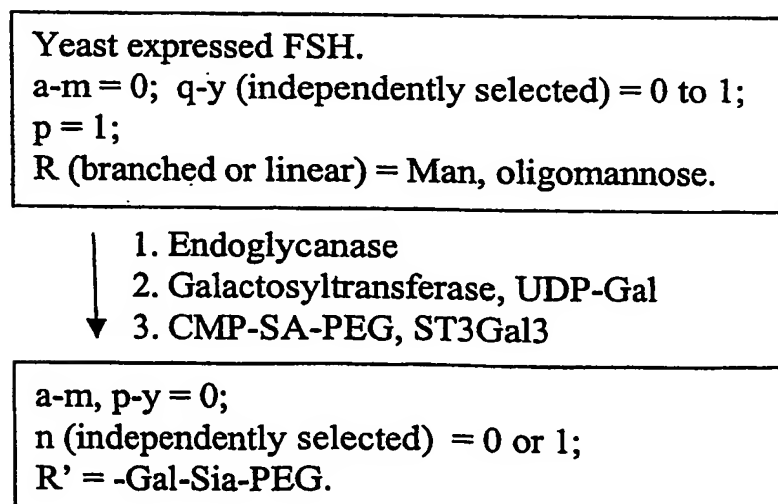


FIG. 34I



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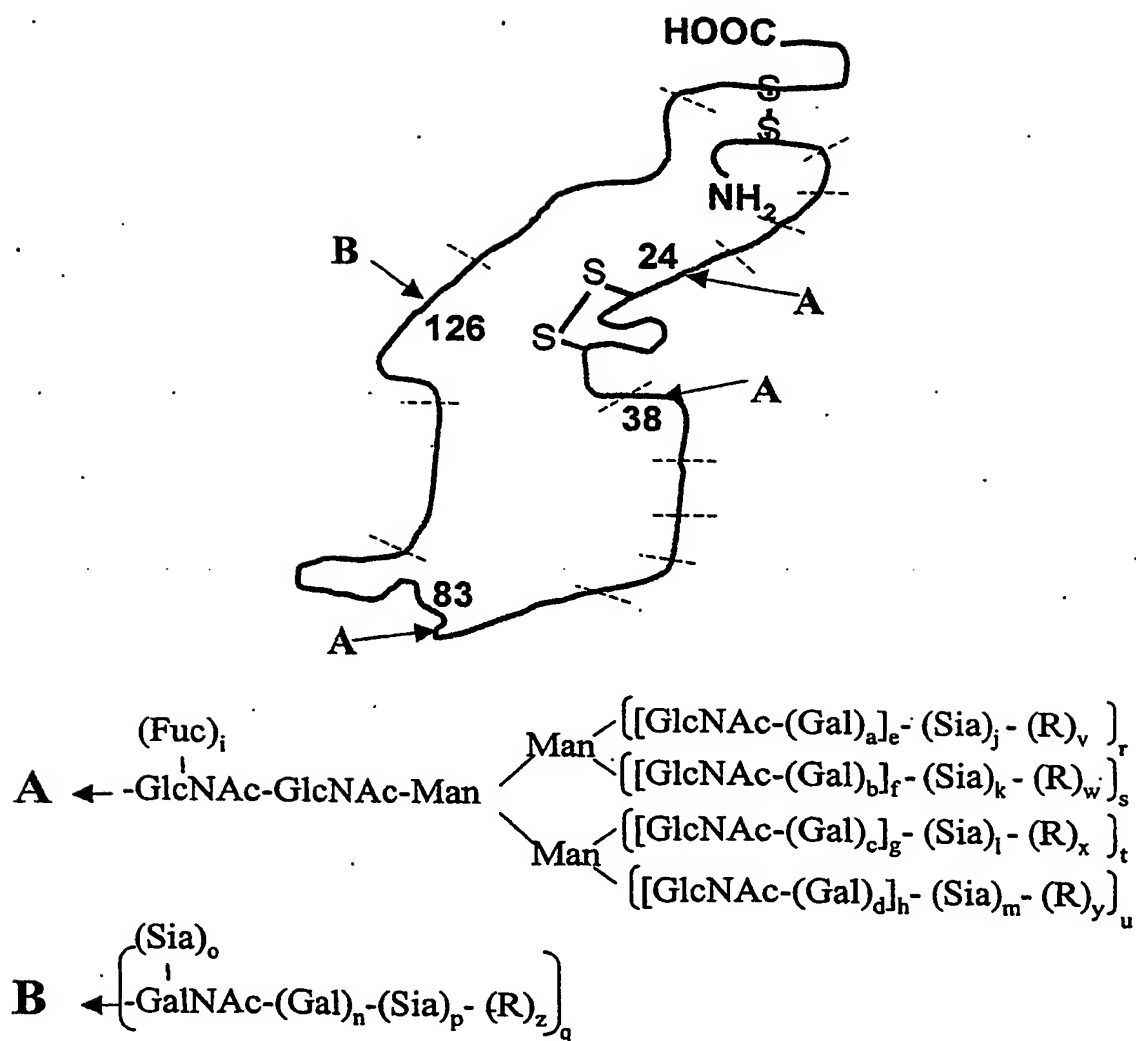
CHO, BHK, 293 cells, Vero expressed FSH.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated chorionic gonadrophin (CG) produced in CHO.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-CG.

FIG. 34J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35A

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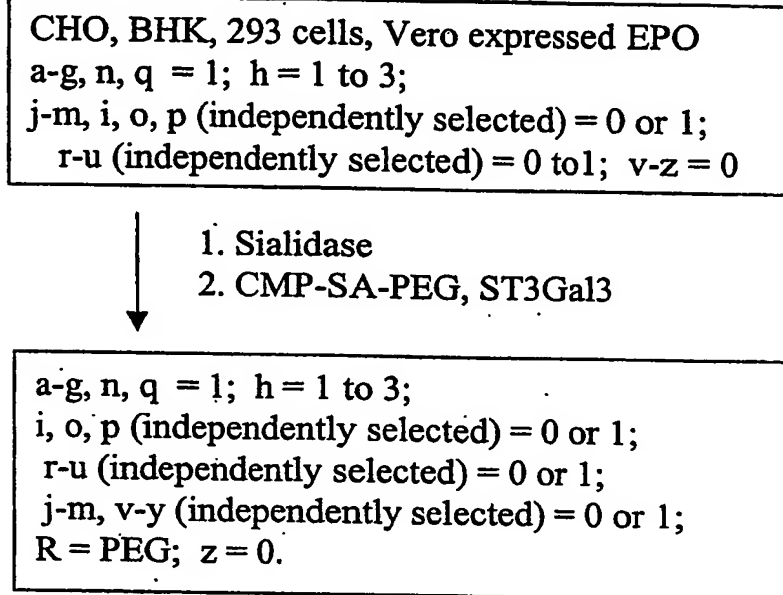


FIG. 35B

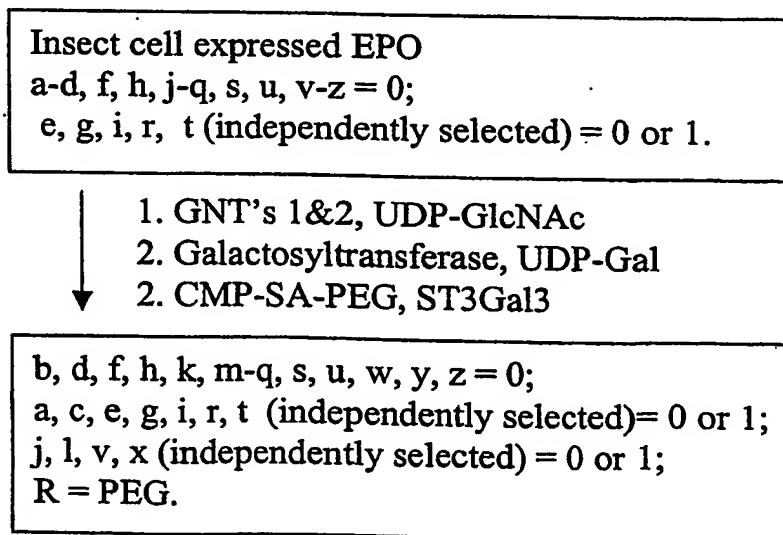


FIG. 35C

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CHO, BHK, 293 cells, Vero expressed EPO  
 a-q, r-u (independently selected) = 0 or 1;  
 v-z = 0.

1. sialidase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA, ST3Gal3
- ↓ 4. CMP-SA-PEG, ST3Gal1

a-h, n, q = 1;  
 i-m, o, r-u (independently selected) = 0 or 1;  
 v-y = 0; p, z = 0 or 1; R = PEG.

FIG. 35D

CHO, BHK, 293 cells, Vero expressed EPO  
 a-g, n, q = 1; h = 1 to 3;  
 j-m, i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 or 1;  
 v-z = 0

1. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3;  
 i, o, p (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1;  
 j-m, v-y (independently selected) = 0 or 1;  
 R = PEG; z = 0.

FIG. 35E

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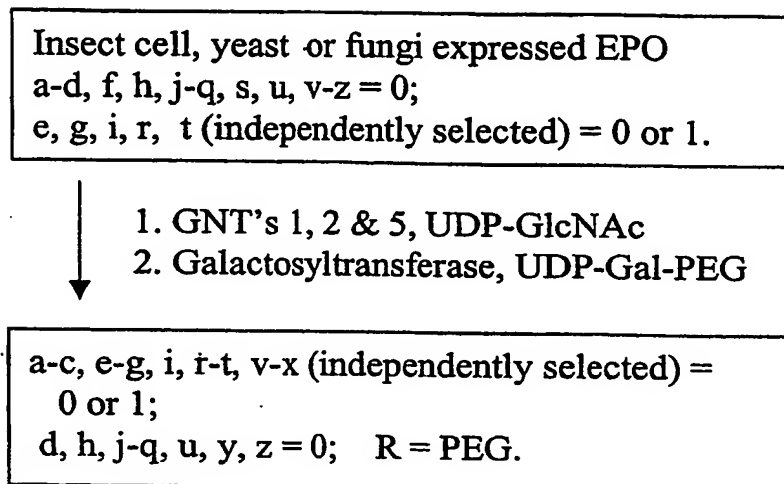


FIG. 35F

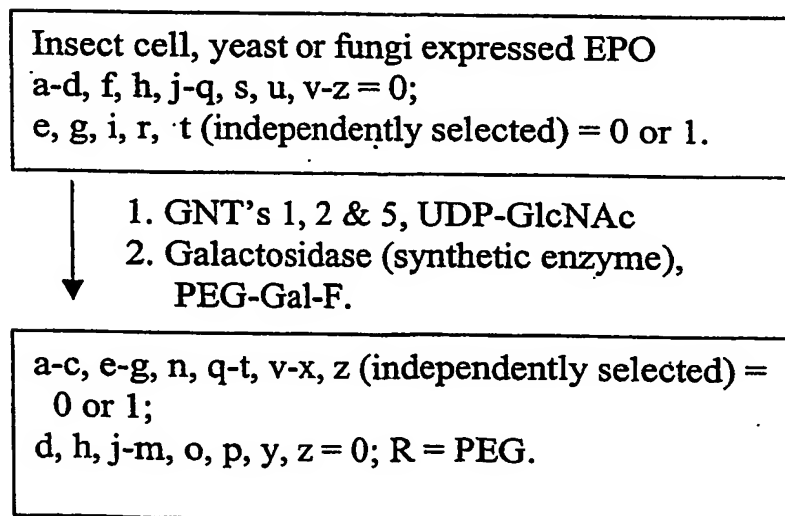


FIG. 35G

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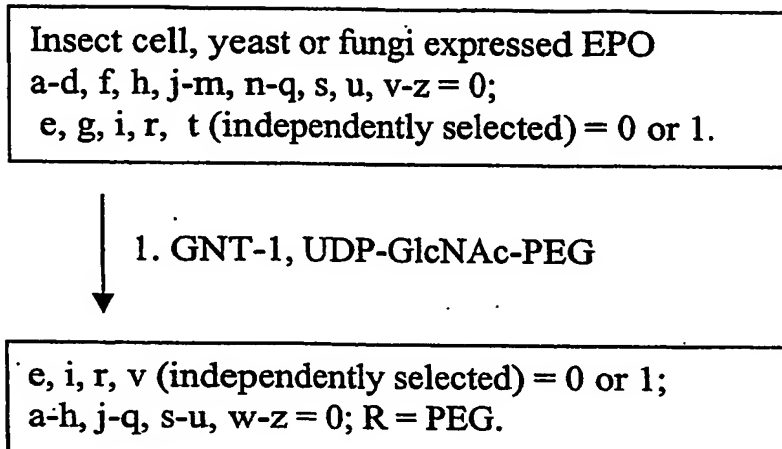


FIG. 35H

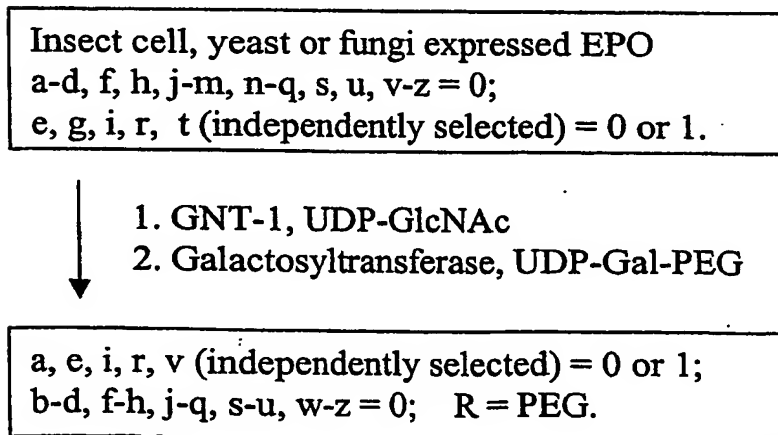


FIG. 35I

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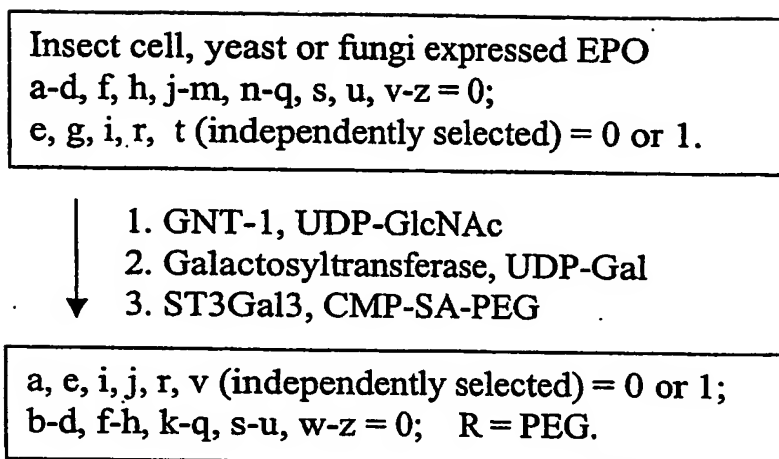


FIG. 35J

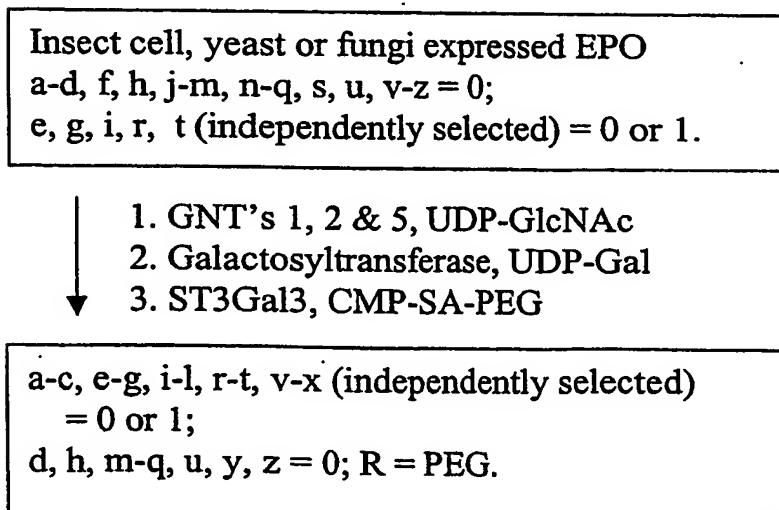


FIG. 35K

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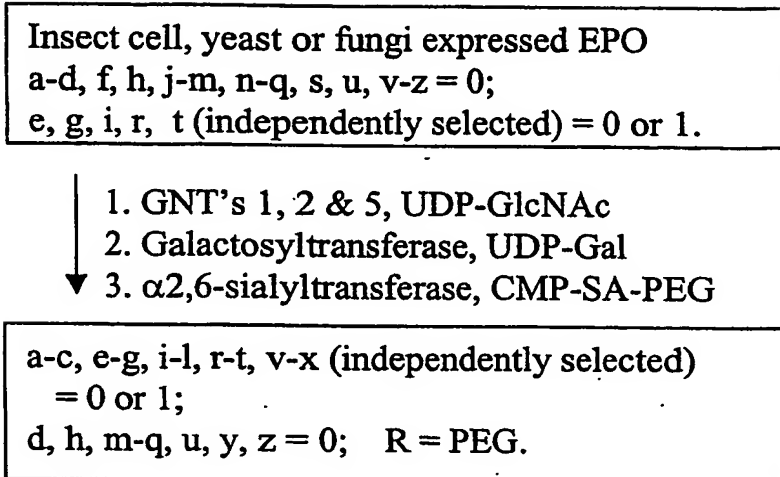


FIG. 35L

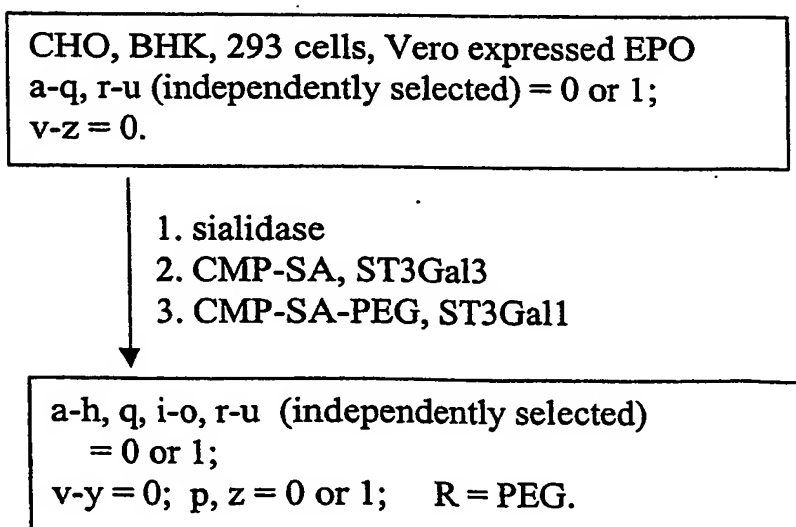


FIG. 35M



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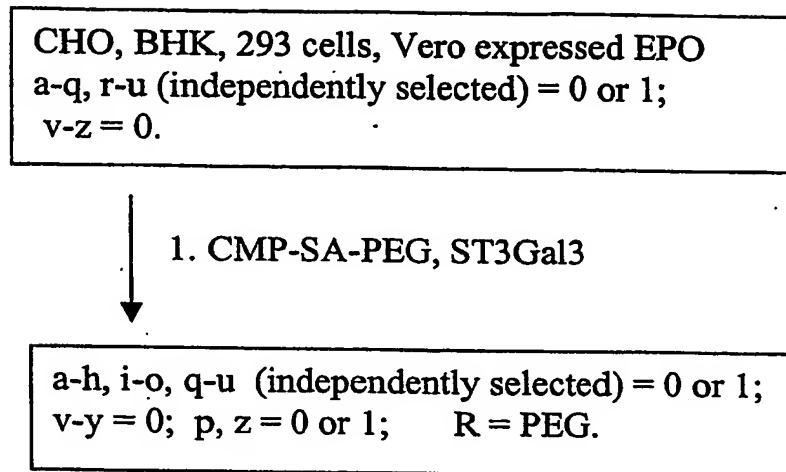


FIG. 35N

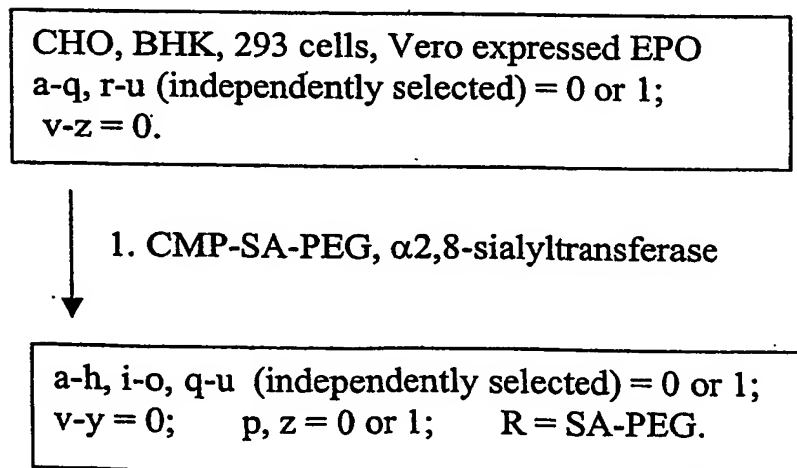


FIG. 35O

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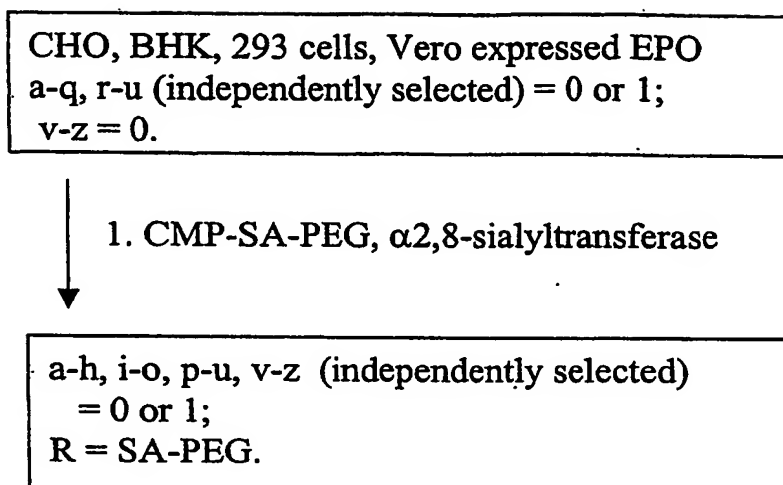


FIG. 35P

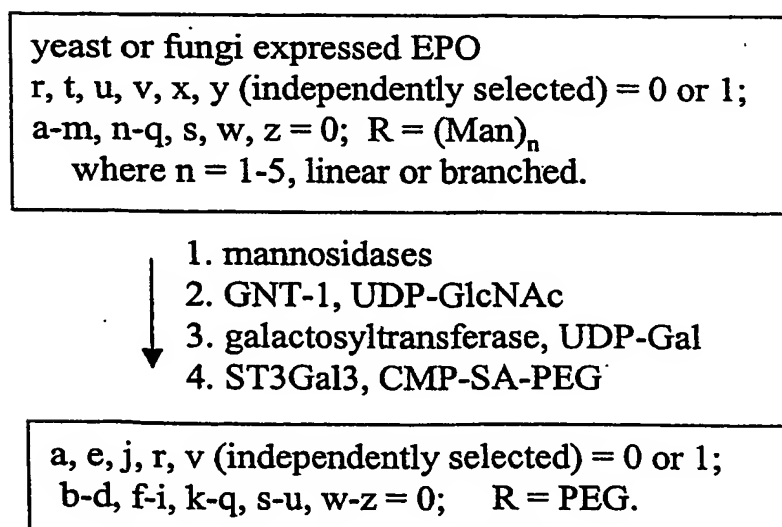


FIG. 35Q

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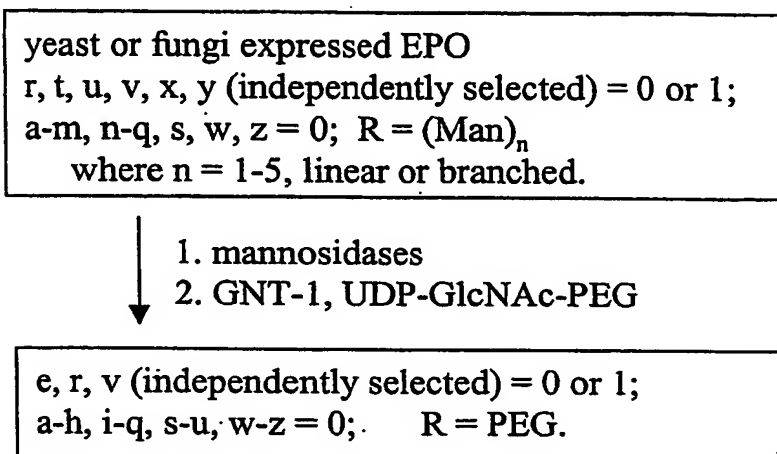


FIG. 35R

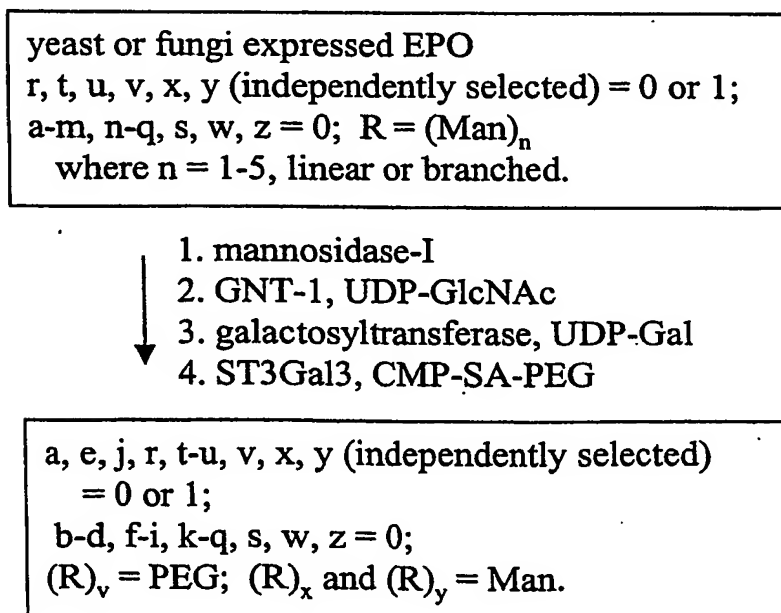
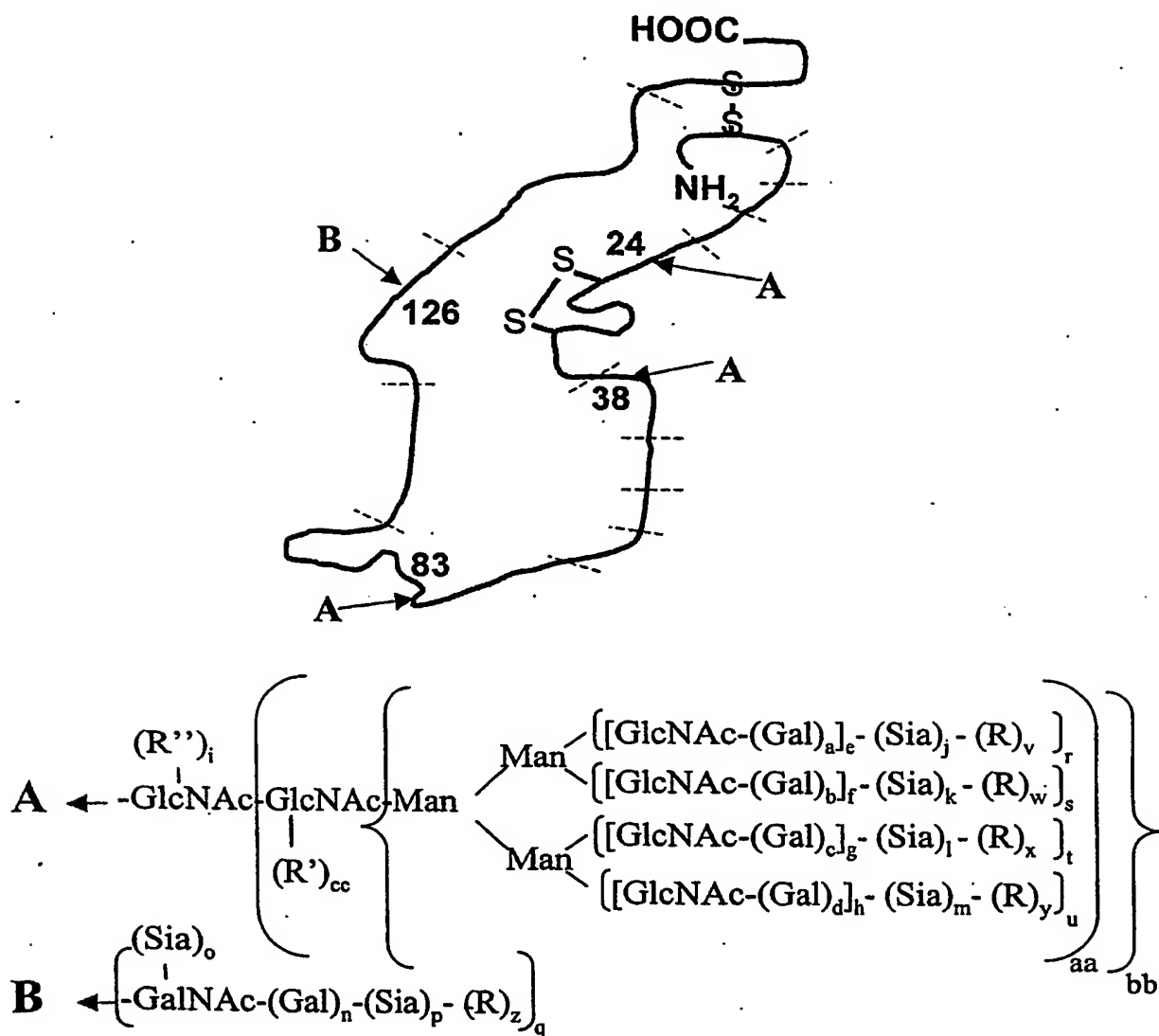


FIG. 35S

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; aa, bb = 1; cc = 0;

R = polymer; R'' and R' = sugar-polymer or Fuc.

FIG. 35T

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yeast or fungi expressed EPO

r, t, u, v, x, y (independently selected) = 0 or 1;

cc, a-m, n-q, s, w, z = 0;

aa, bb = 1;

R = (Man)<sub>n</sub> where n = 1-100, linear or branched.



1. endo-H

2. galactosyltransferase, UDP-Gal-PEG

i (independently selected) = 0 or 1;

aa, bb, cc, a-h, j-z = 0; R'' = Gal-PEG.

FIG. 35U

yeast or fungi expressed EPO

r, t, u, v, x, y (independently selected) = 0 or 1;

cc, a-m, n-q, s, w, z = 0; aa, bb = 1;

R = (Man)<sub>n</sub> where n = 1-100, linear or branched.



1. endo-H

2. galactosyltransferase, UDP-Gal

3. ST3Gal3, CMP-SA-PEG

i (independently selected) = 0 or 1;

aa, bb, cc, a-h, j-z = 0; R'' = Gal-SA-PEG.

FIG. 35V

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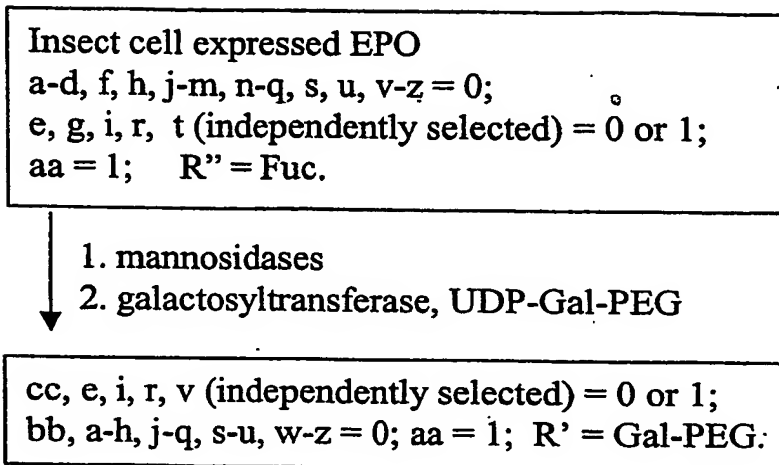
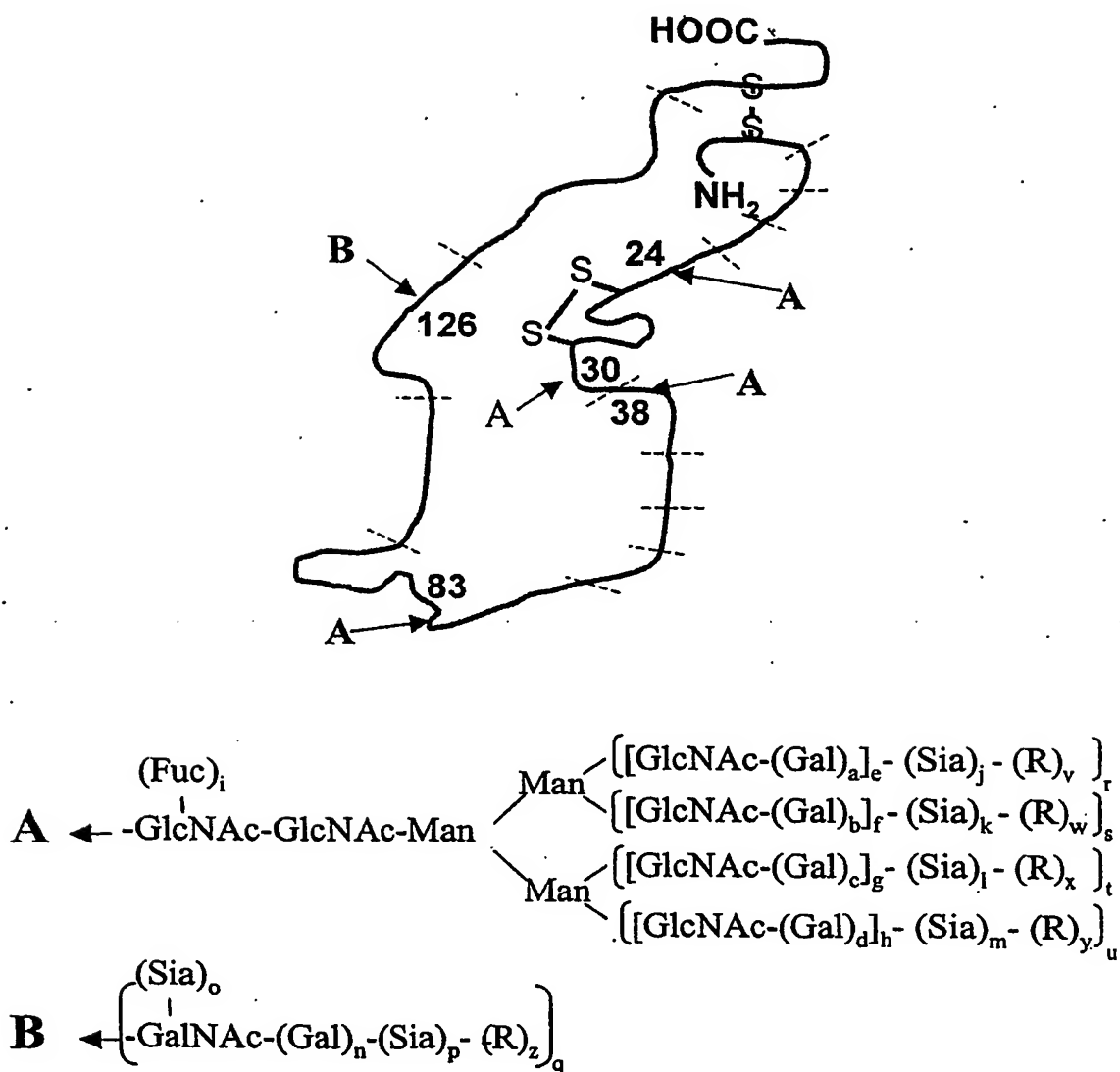


FIG. 35W

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = polymer.

FIG. 35X

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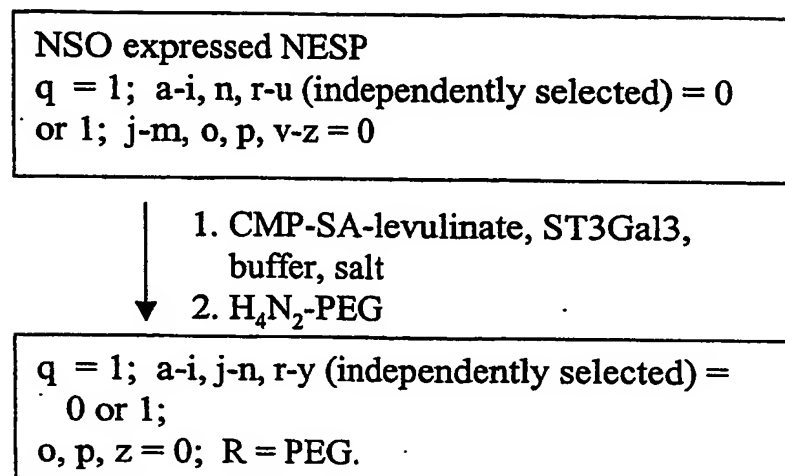


FIG. 35Y

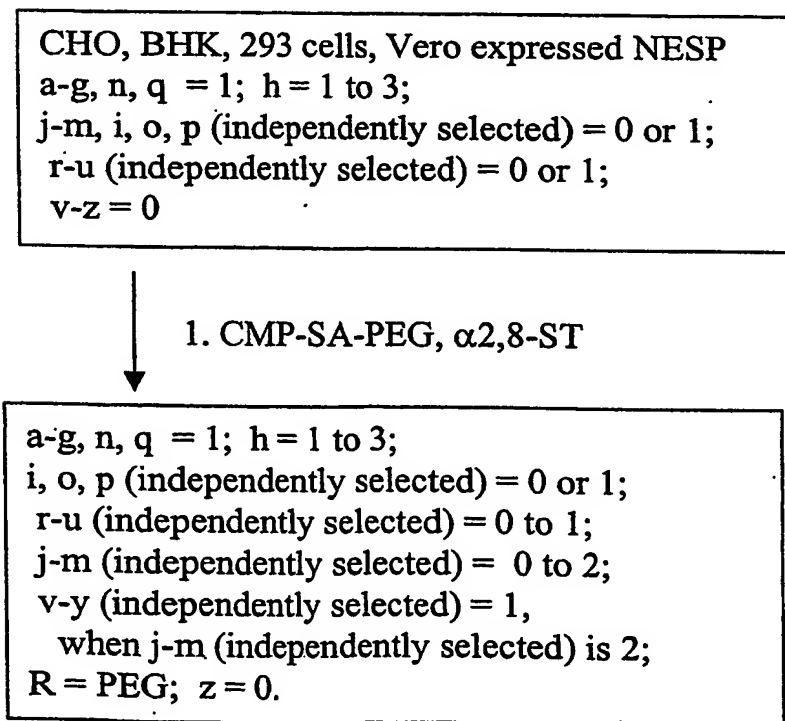


FIG. 35Z



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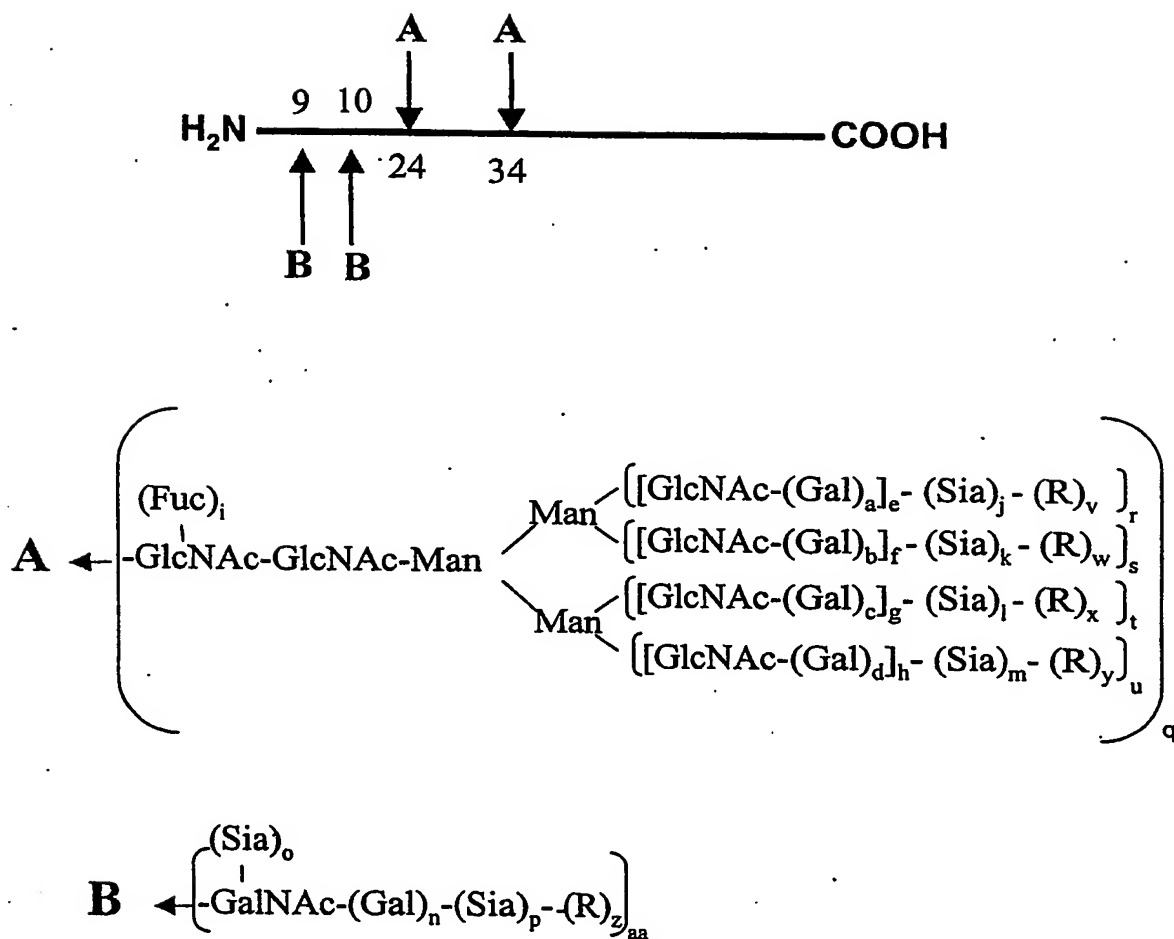
CHO, BHK, 293 cells, Vero expressed NESP  
a-g, n, q = 1; h = 1 to 3;  
j-m, i, o, p (independently selected) = 0 or 1;  
r-u (independently selected) = 0 to 1; v-z = 0

↓  
1 CMP-SA, poly- $\alpha$ 2,8-ST

a-g, n, q = 1; h = 1 to 3;  
i, j-m, o, p, r-u, (independently selected) = 0 or 1;  
v-z (independently selected) = 0-40; R = Sia.

FIG. 35AA

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a-d, i, n-u, aa (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 100.  
 v-y = 0; R = polymer, glycoconjugate.

FIG. 36A

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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 36B

CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3 &  
ST3Gal1

a-d, i-m, p-u, aa (independently selected) = 0 or 1;  
o, z = 0; n, e-h = 1;  
v-y (independently selected) = 0 or 1; R = PEG.

FIG. 36C

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NSO expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-PEG, ST3Gal1

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;  
n, e-h = 1; o, v-y = 0; z = 1, when p = 1; R = PEG.

FIG. 36D

CHO, BHK, 293 cells, Vero expressed GM-CSF.

a-d, i-m, o-u, aa (independently selected) = 0 or 1;

n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-y, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1; R = PEG.

FIG. 36E

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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = PEG.

FIG. 36F

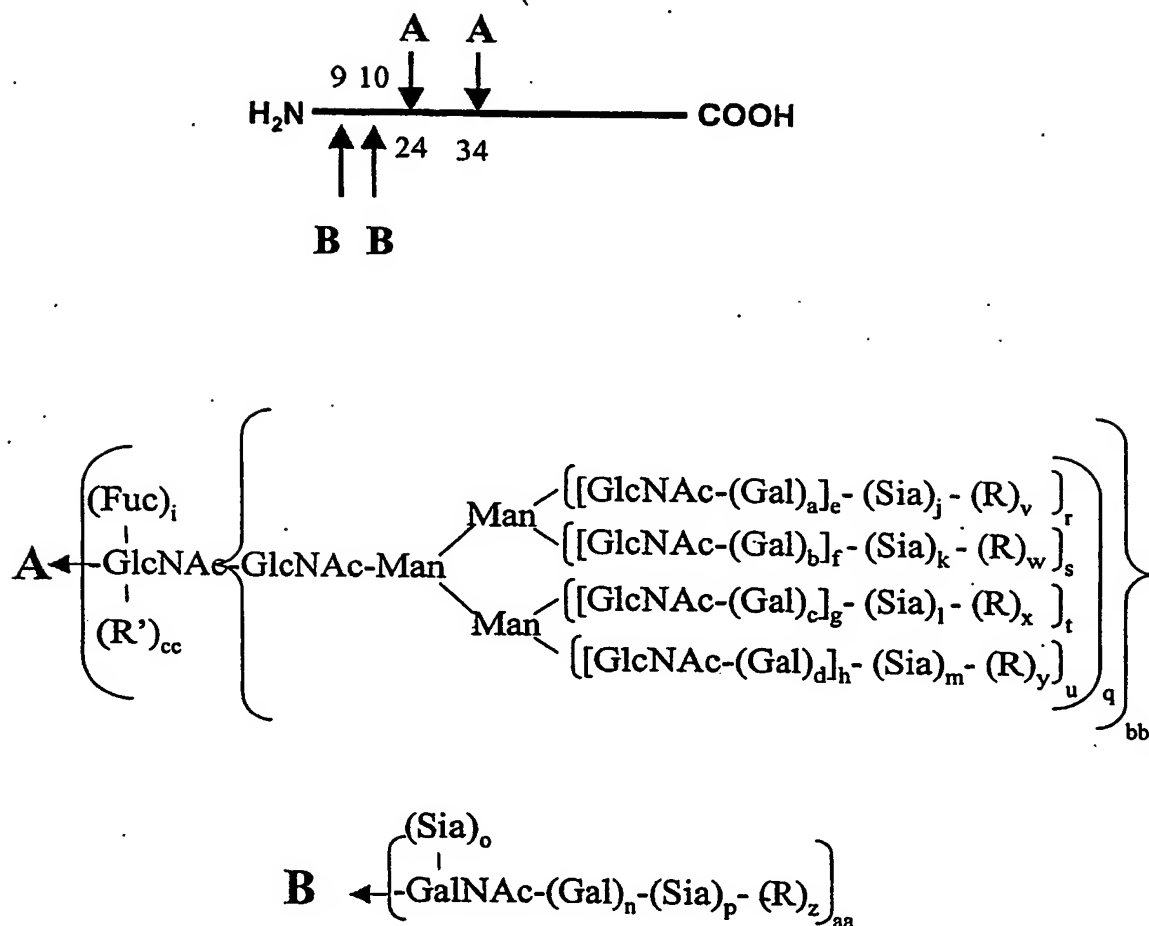
CHO, BHK, 293 cells, Vero expressed GMCSF.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; j-m (independently selected) = 0-20;  
v-z (independently selected) = 0.

FIG. 36G

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a-d, i, n-u, aa, bb, cc (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group. glycoconjugate.

FIG. 36H

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Insect cell expressed GM-CSF.  
 a-d, f, h, j-m, o, p, s, u, v-z = 0;  
 e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.

- ↓
1. GNT's 1,2,4,5, UDP-GlcNAc
  2. Galactosyltransferase, UDP-Gal-PEG

a-i, n, q-u (independently selected) = 0 or 1;  
 j-m = 0; v-y (independently selected) = 1,  
 when e-h (independently selected) is 1;  
 R = PEG.

FIG. 36I

Yeast expressed GM-CSF.  
 a-p, z, cc = 0;  
 q-y, aa (independently selected) = 0 to 1;  
 bb = 1; R (branched or linear) = Man, oligomannose;  
 GalNAc = Man.

- ↓
1. Endoglycanase
  2. mannosidase (if aa = 1).
  3. Galactosyltransferase, UDP-Gal-PEG

a-p, r-z, aa, bb = 0;  
 q, cc (independently selected) = 0 or 1;  
 R' = -Gal-PEG.

FIG. 36J

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CHO, BHK, 293 cells, Vero expressed GM-CSF.  
a--m, o-u, aa, bb (independently selected) = 0 or 1;  
n, v-z, cc = 0.

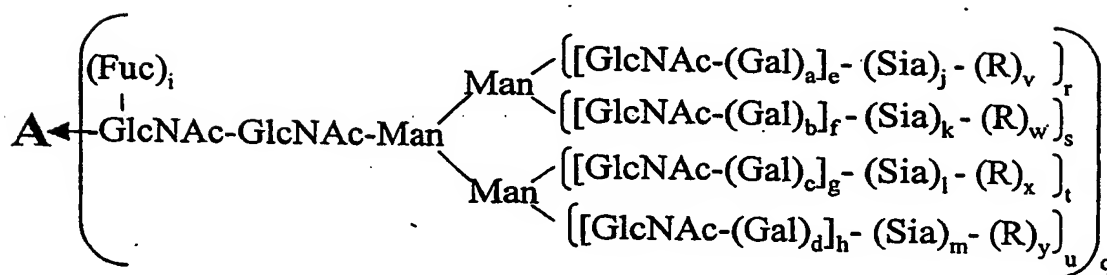
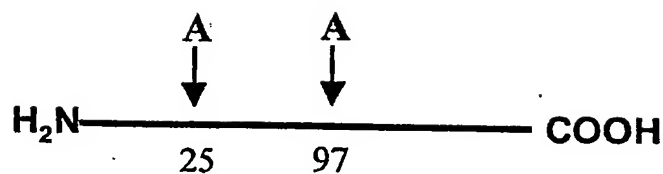
- ↓
1. sialidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-linker-SA-CMP, ST3Gal1
  3. ST3Gal3, transferrin

a--m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y, cc = 0; bb, n = 1; R = transferrin.

FIG. 36K



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 37A

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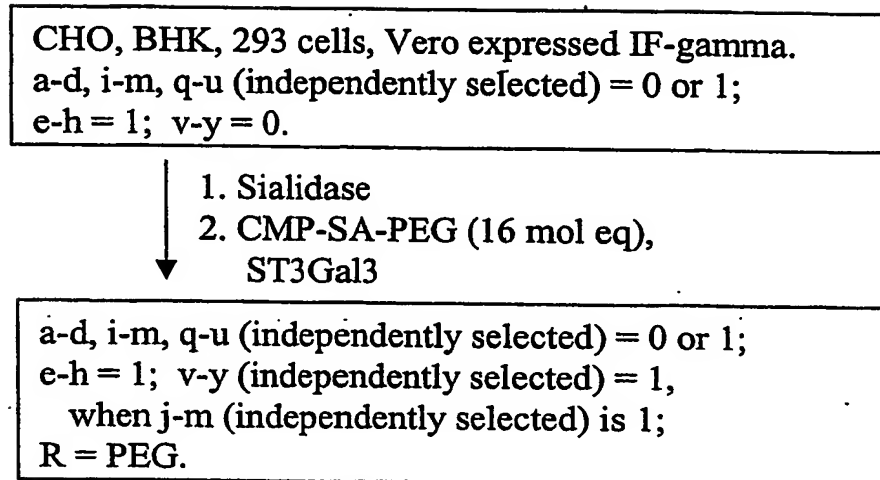


FIG. 37B

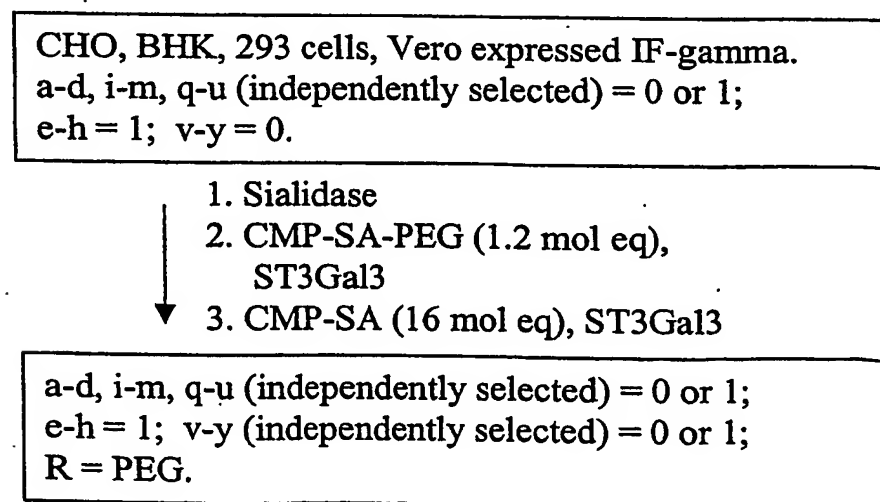


FIG. 37C

133/498

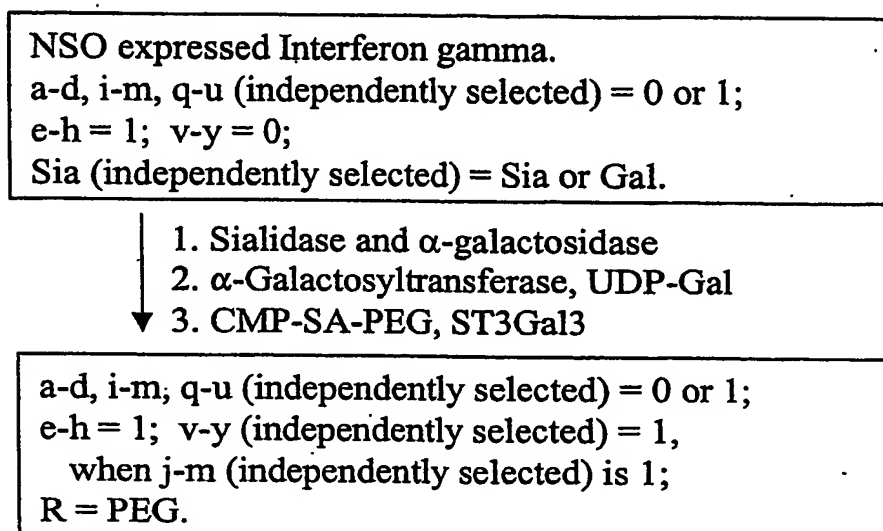


FIG. 37D

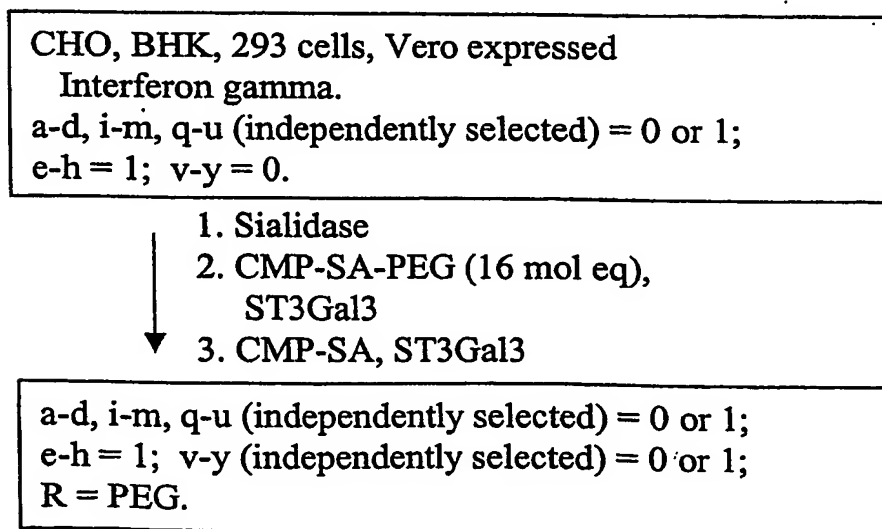


FIG. 37E

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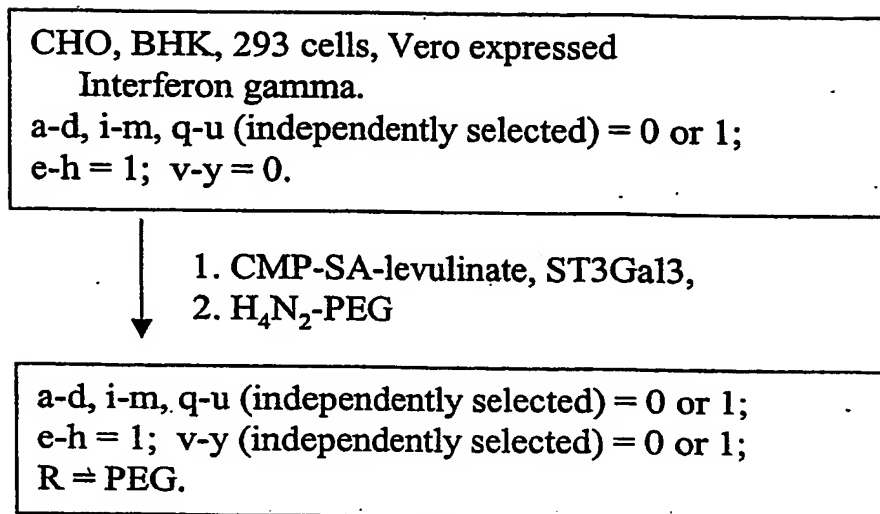


FIG. 37F

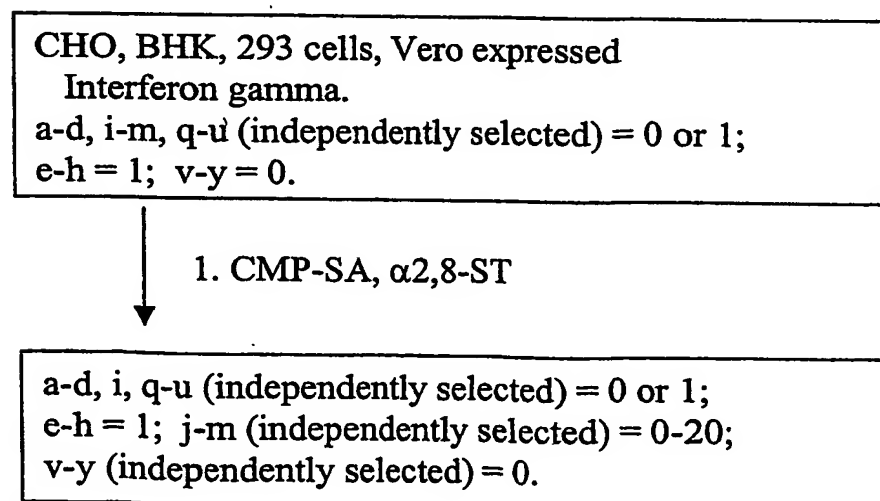
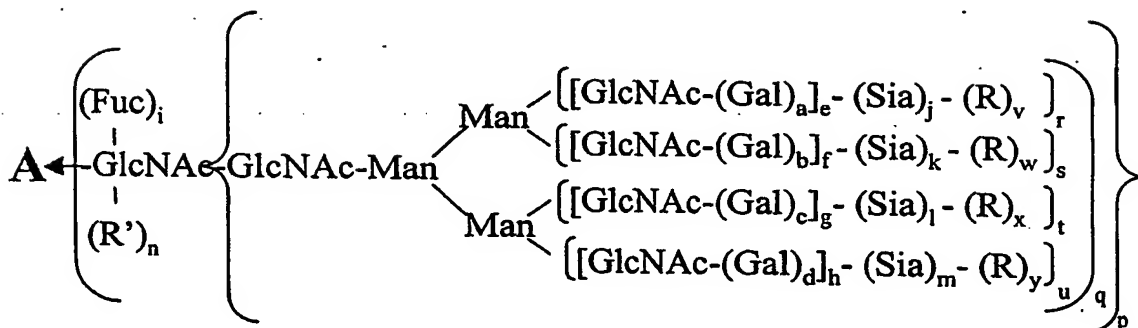
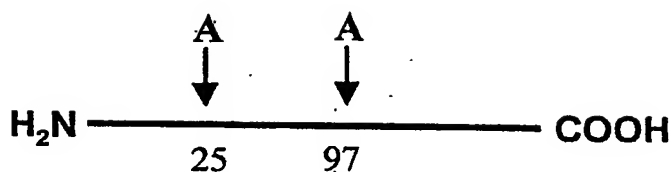


FIG. 37G

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 37H

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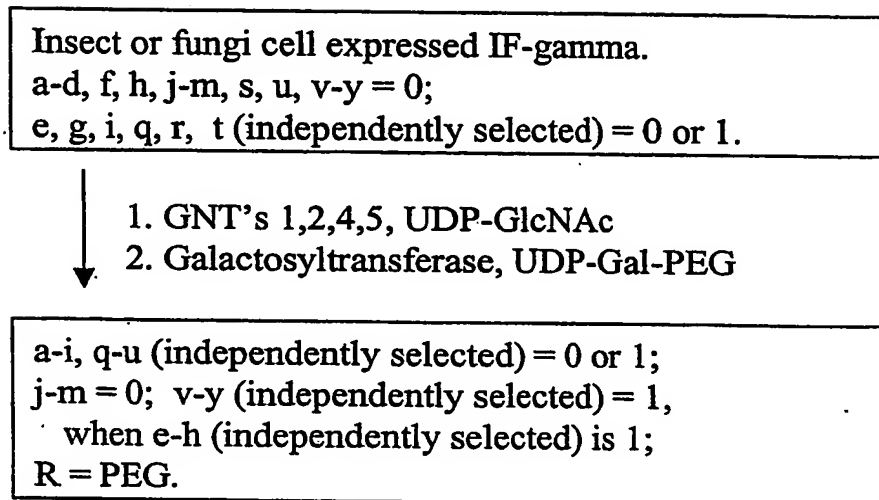


FIG. 37I

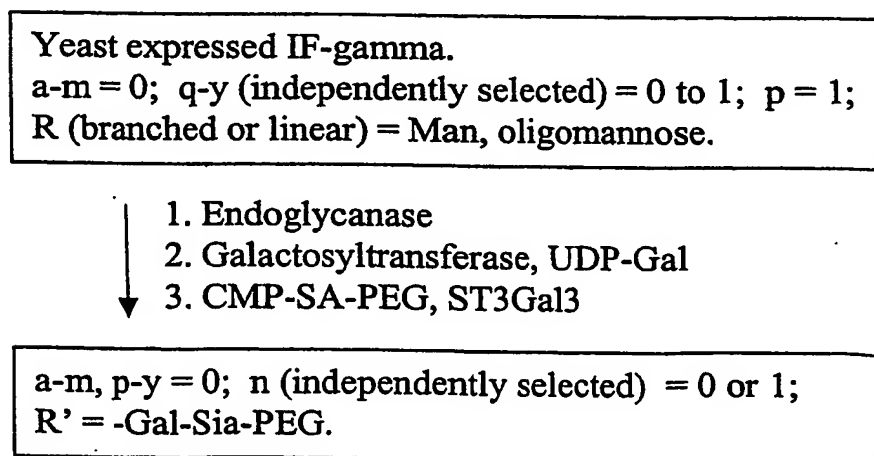


FIG. 37J

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CHO, BHK, 293 cells, Vero expressed IF-gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP, ST3Gal3
  2. Galactosyltransferase, transferrin treated with endoglycanase.

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 37K

CHO, BHK, 293 cells, Vero expressed  
Interferon gamma.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h, p = 1; n, v-y = 0.

- ↓
1. CMP-SA-PEG,  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h, p = 1;  
n, v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 37L

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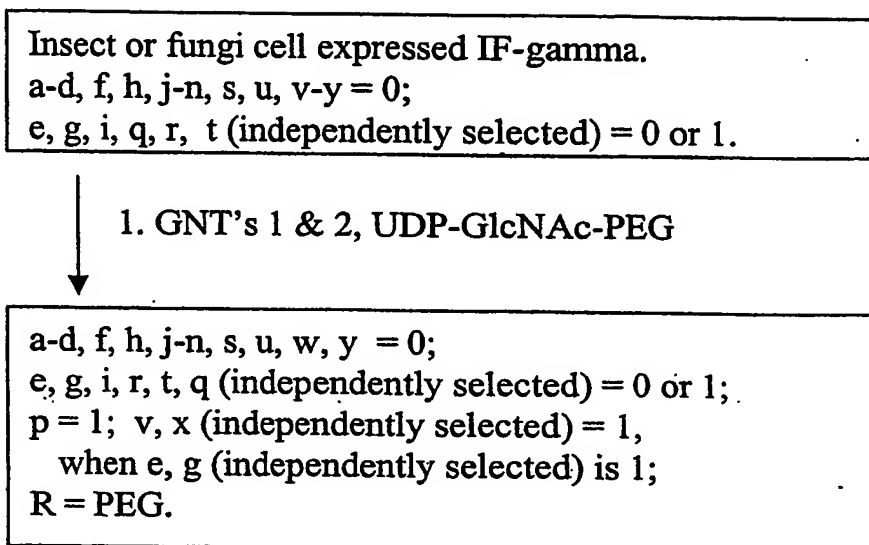


FIG. 37M

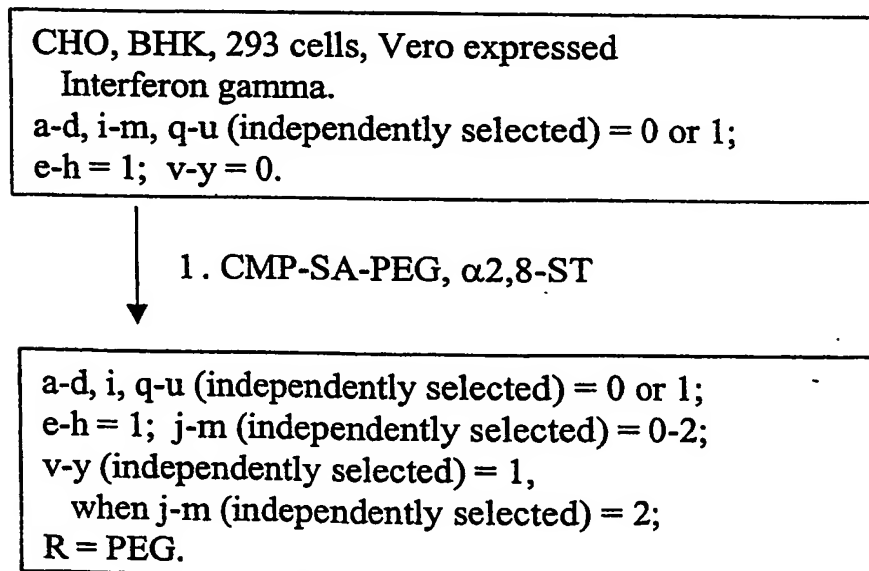
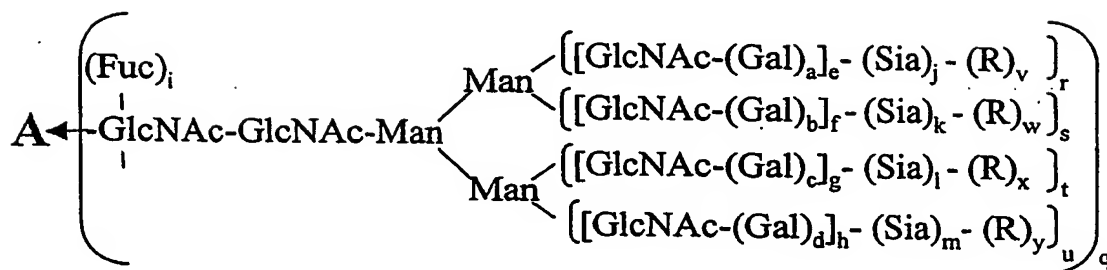
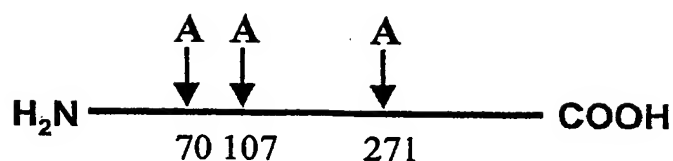


FIG. 37N



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 38A

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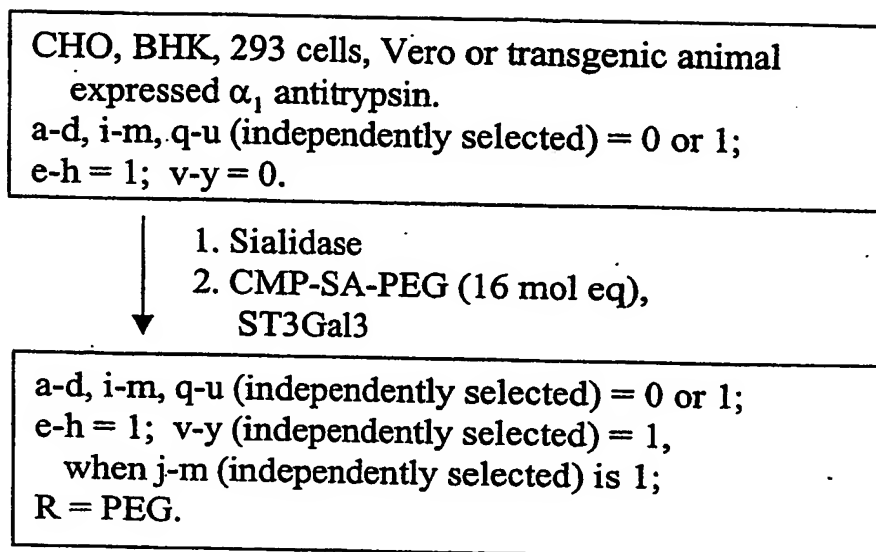


FIG. 38B

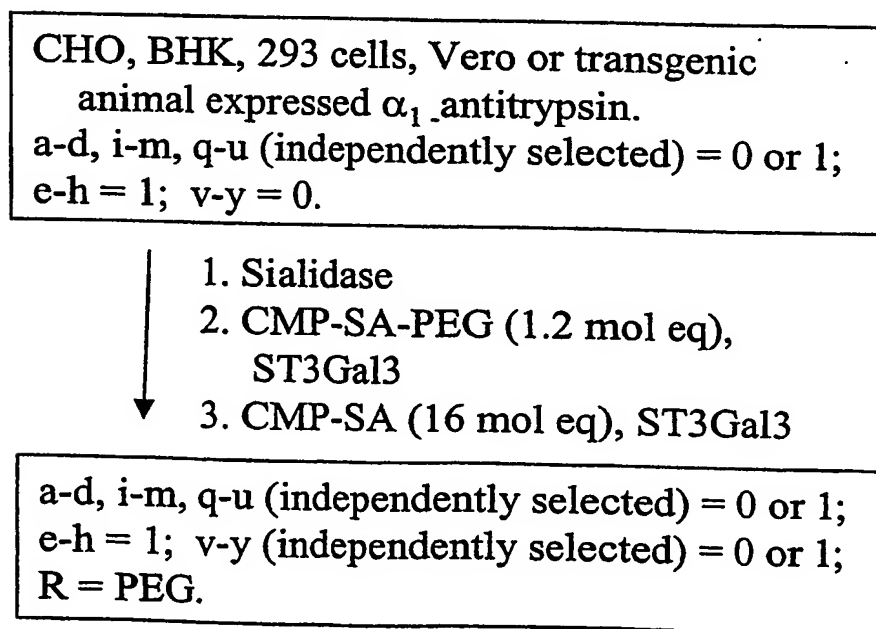


FIG. 38C

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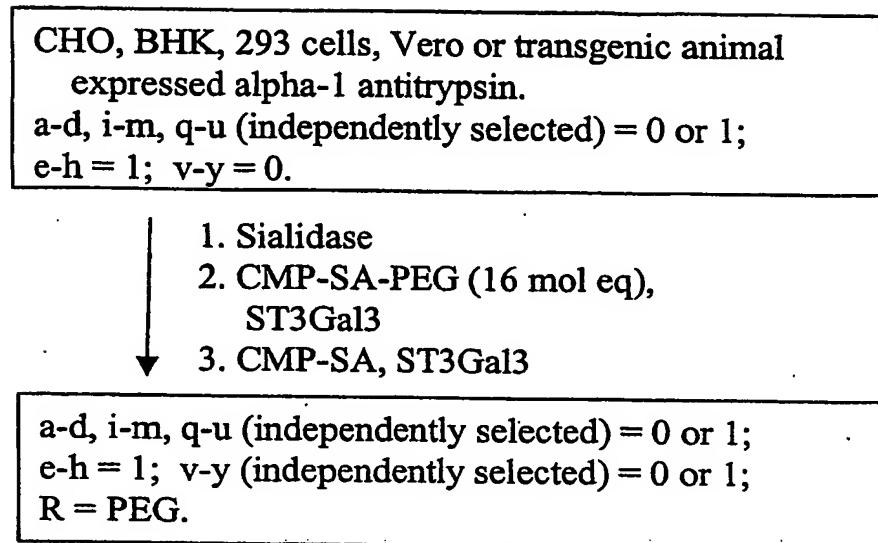


FIG. 38D

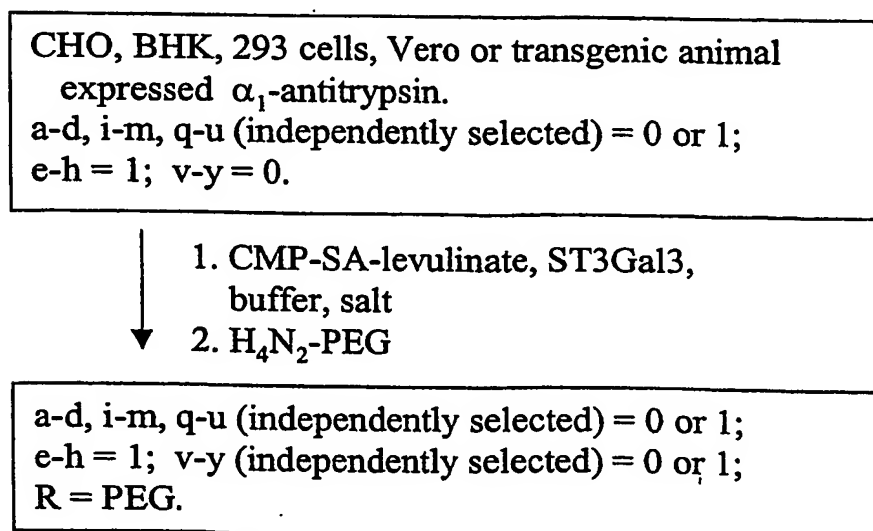


FIG. 38E

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CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

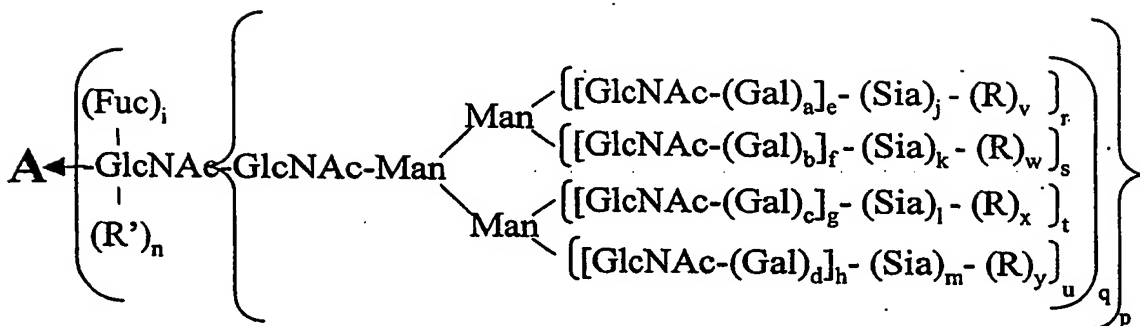
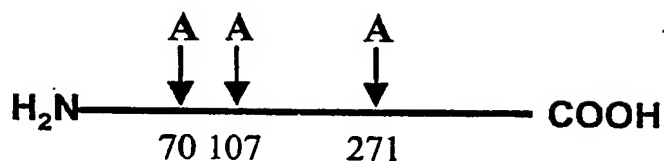


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1; e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 38F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 38G

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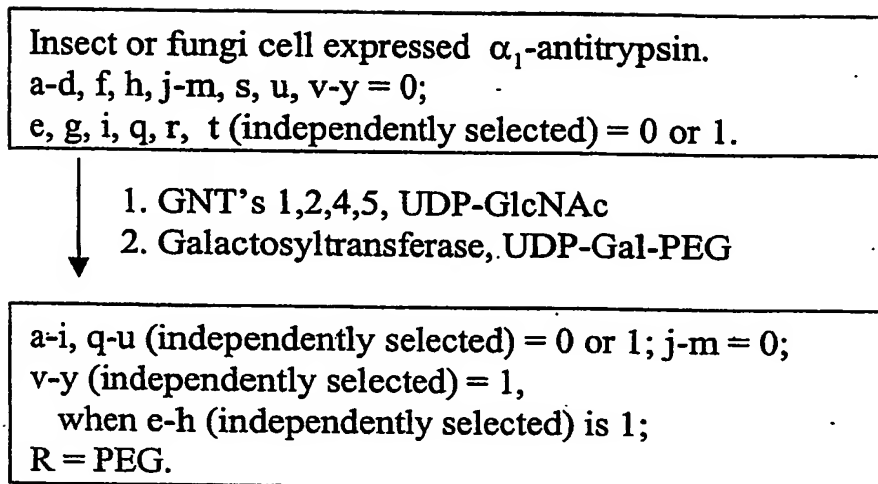


FIG. 38H

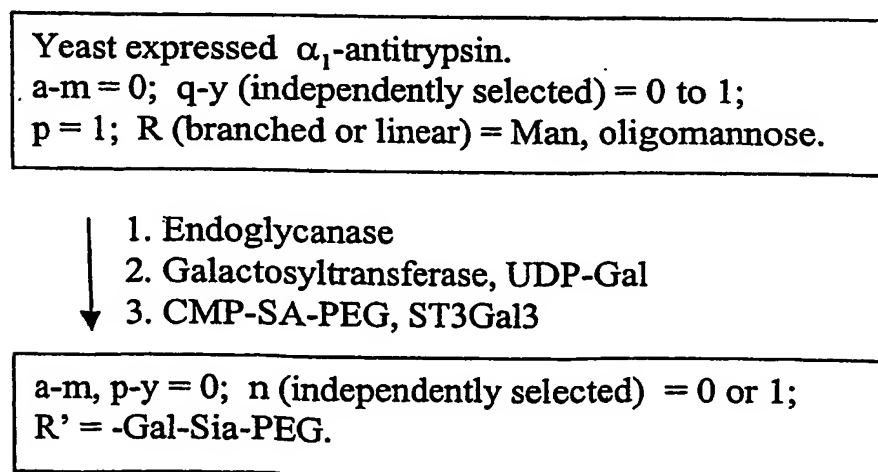


FIG. 38I

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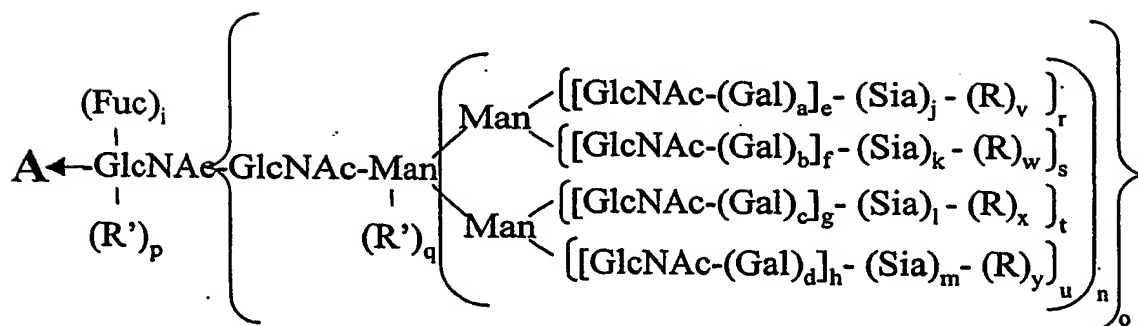
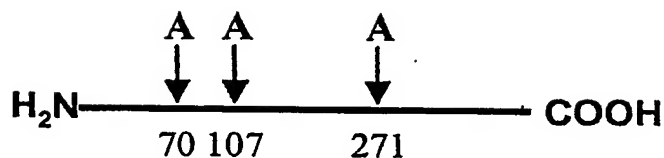
CHO, BHK, 293 cells, Vero expressed  $\alpha_1$ -antitrypsin.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin treated  
with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 38J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer;

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 38K



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Yeast expressed alpha-1 antitrypsin.

a-h, i-m, p, q = 0;

R (independently selected) = mannose, oligomannose, polymannose;

r-u, v-y (independently selected) = 0 or 1; n, o = 1.

- ↓ 1. endoglycanase  
 ↓ 2. Galactosyltransferase, UDP-Gal-PEG

a-h, i-o, q, r-u, v-y = 0; p = 1.

R'' = Gal-PEG.

FIG. 38L

Plant expressed alpha-1 antitrypsin.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1;

n = 1; R' = xylose

- ↓ 1. hexosaminidase,  
 ↓ 2. alpha mannosidase and xylosidase  
 ↓ 3. GlcNAc transferase, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, r, t (independently selected) = 0;

q = 1; R' = GlcNAc-PEG.

FIG. 38M

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CHO, BHK, 293 cells, Vero, transgenic animal  
expressed  $\alpha_1$  antitrypsin.

a-h, i-o, r-u (independently selected) = 0 or 1;

p, q, v-y = 0.



1. CMP-SA-PEG,  
ST3Gal3

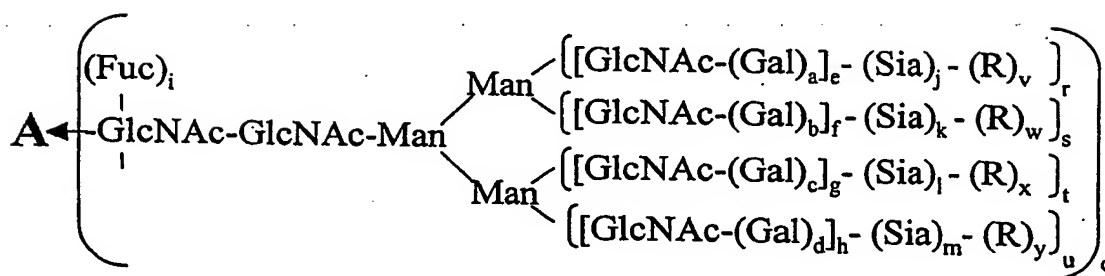
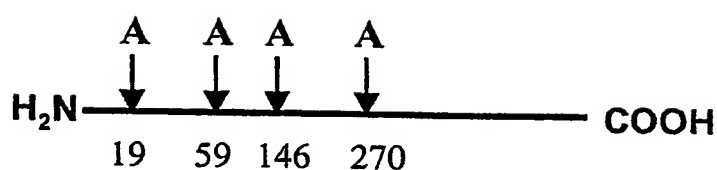
a-h, i-o, r-u (independently selected) = 0 or 1;

p, q = 0; v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 38N

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 39A

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CHO, BHK, 293 cells, Vero expressed Cerezyme  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 39B

CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. Sialidase
2. CMP-SA-M-6-P (1:2 mol eq),  
ST3Gal3
3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = mannose-6-phosphate

FIG. 39C

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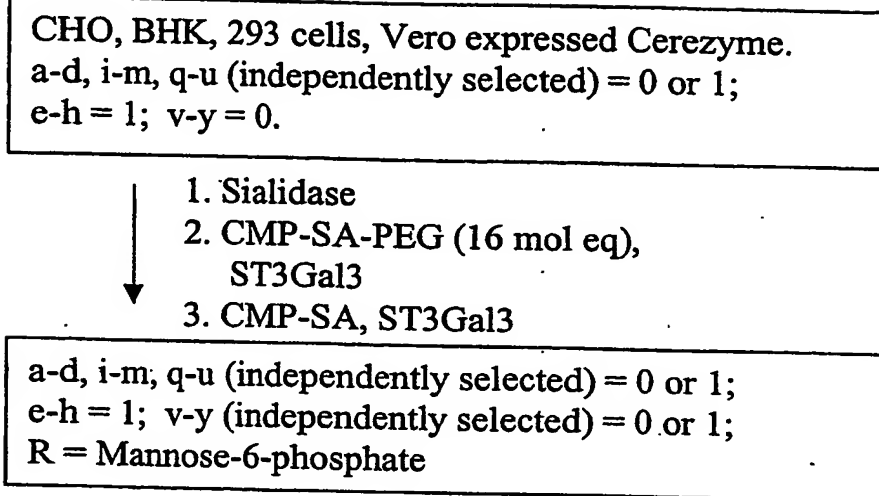


FIG. 39D

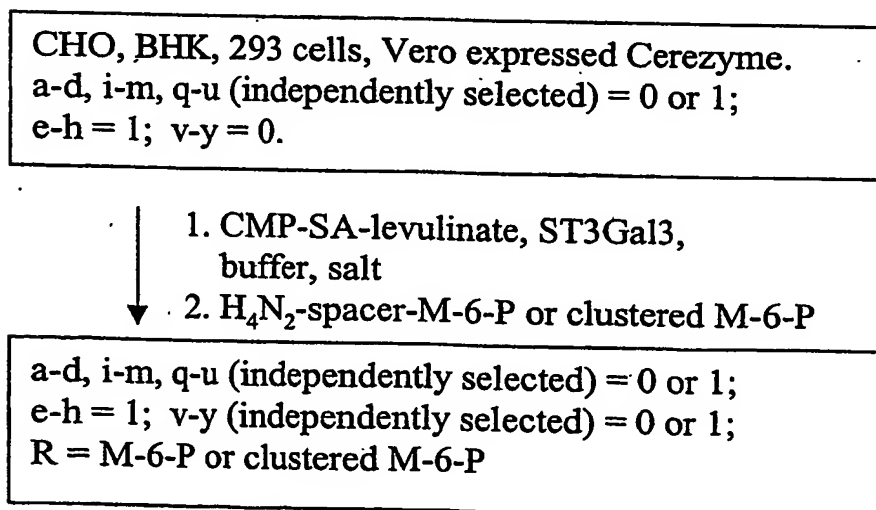


FIG. 39E

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CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

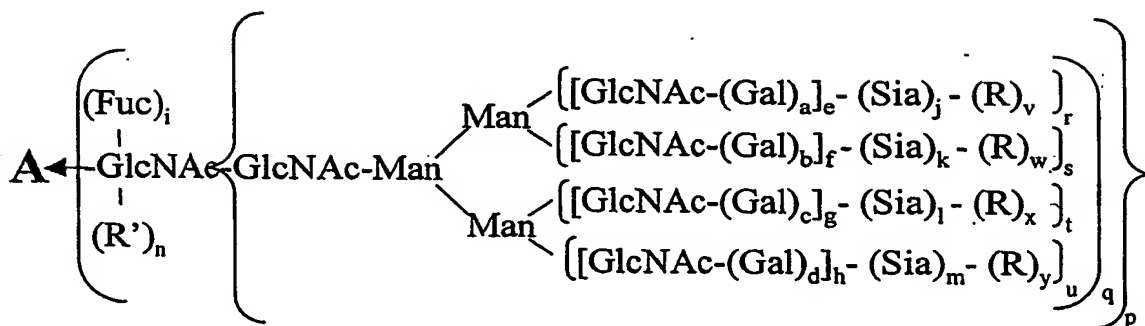
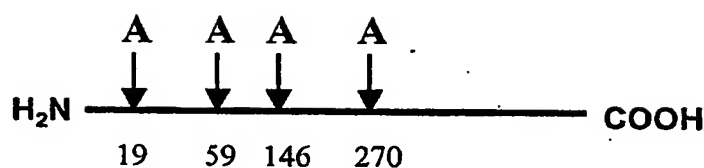


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 39F

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a-d, i, n, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 39G

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Insect cell expressed Cerezyme.  
 a-d, f, h, j-m, s, u, v-y = 0;  
 e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;  
 j-m = 0;  
 v-y (independently selected) = 1,  
 when e-h (independently selected) is 1;  
 R = PEG.

FIG. 39H

Yeast expressed Cerezyme.  
 a-m = 0; q-y (independently selected) = 0 to 1;  
 p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;  
 R' = -Gal-Sia-PEG.

FIG. 39I



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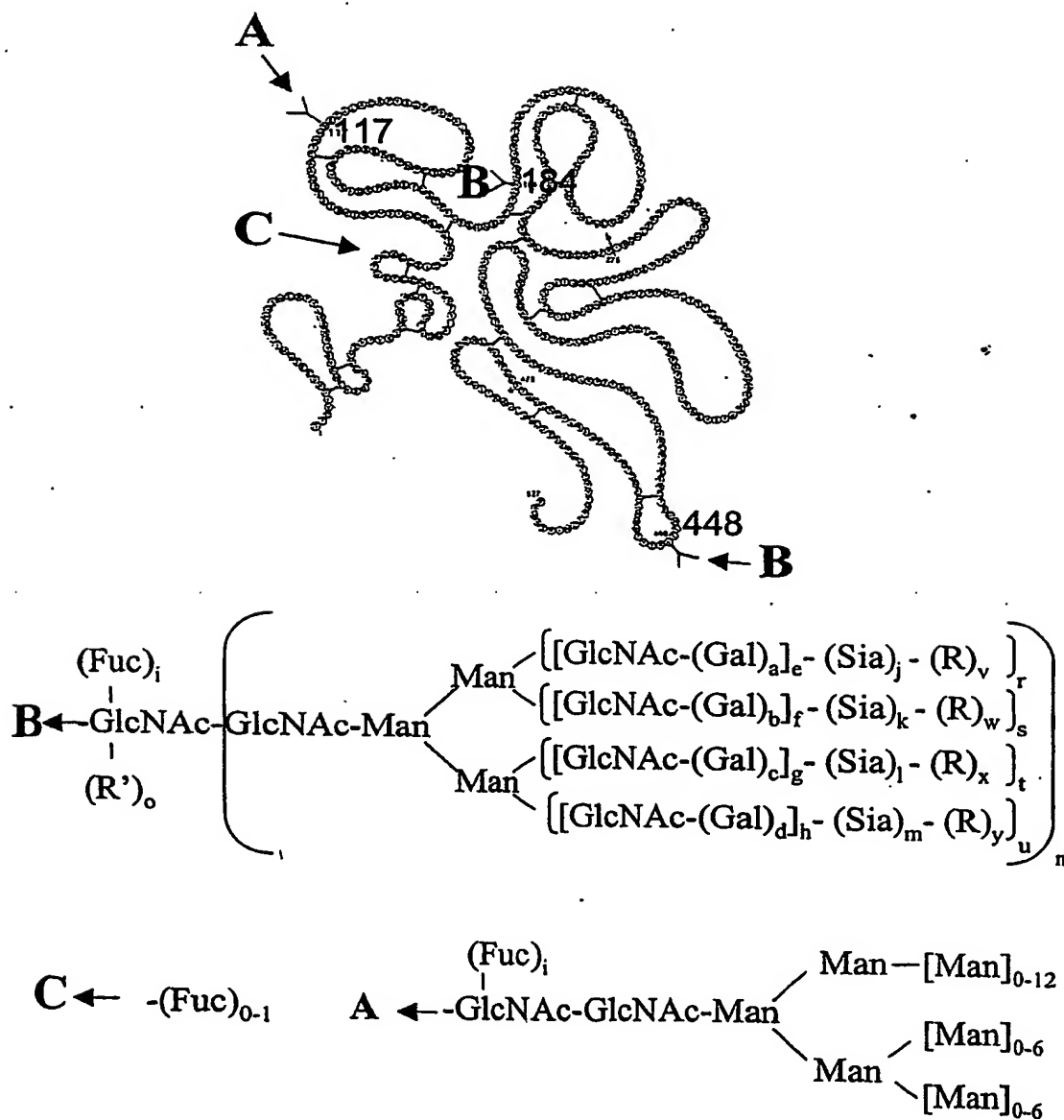
CHO, BHK, 293 cells, Vero expressed Cerezyme.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP,  
ST3Gal3
  2. ST3Gal3, desialylated transferrin.
  3. CMP-SA, ST3Gal3

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0; v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 39J

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40A

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CHO, BHK, 293 cells, Vero expressed tPA  
 a-g, n = 1; h = 1 to 3;  
 j-m, i, (independently selected) = 0 or 1;  
 r-u (independently selected) = 0 to 1; o, v-y = 0.

1. Mannosidase(s), sialidase
2. GNT1,2 (4 and/or 5) UDP-GlcNAc
3. Gal transferase, UDP-Gal
4. CMP-SA-PEG, ST3Gal3

A = B; a-g, n = 1; h = 1 to 3;  
 i, r-u (independently selected) = 0 or 1;  
 o = 0; j-m, v-y (independently selected) = 0 or 1;  
 R = PEG

FIG. 40B

Insect or fungi cell expressed tPA  
 A = B; a-d, f, h, j-o, s, u, v-y = 0;  
 e, g, i, n, r, t (independently selected) = 0 or 1.

1. GNT's 1&2, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

A = B; b, d, f, h, k, m, o, s, u, w, y = 0;  
 a, c, e, g, i, r, t (independently selected) = 0 or 1;  
 n = 1; j, l, v, x (independently selected) = 0 or 1;  
 R = PEG.

FIG. 40C

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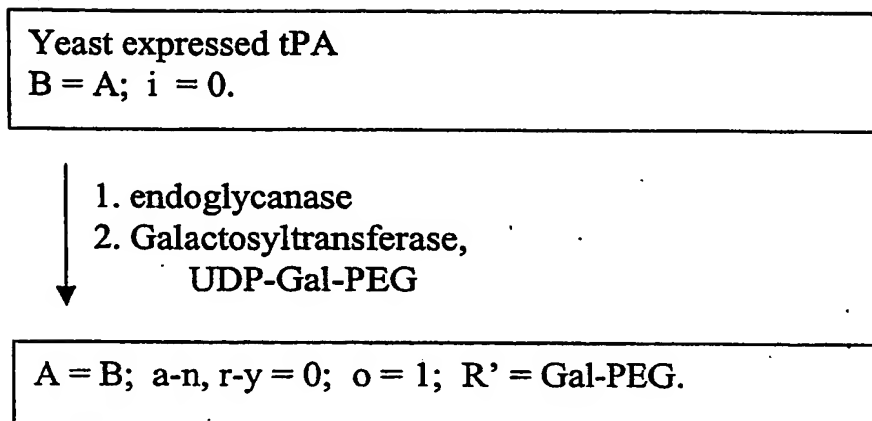


FIG. 40D

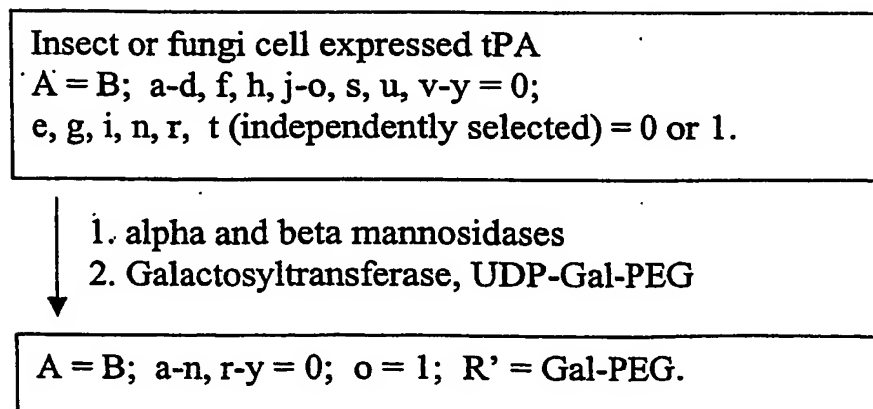


FIG. 40E

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Insect or fungi cell expressed tPA

A = B; a-d, f, h, j-o, s, u, v-y = 0;

e, g, i, n, r, t (independently selected) = 0 or 1.



1. GNT's 1&2, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

A = B; b, d, f, h, j-o, s, u, w, y = 0;

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;

n = 1; R = PEG.

FIG. 40F

Insect or fungi cell expressed tPA

A = B; a-d, f, h, j-o, s, u, v-y = 0;

e, g, i, n, r, t (independently selected) = 0 or 1.



1. GNT's 1 & 2, UDP-GlcNAc

2. Galactosidase (synthetic enzyme),  
PEG-Gal-F.

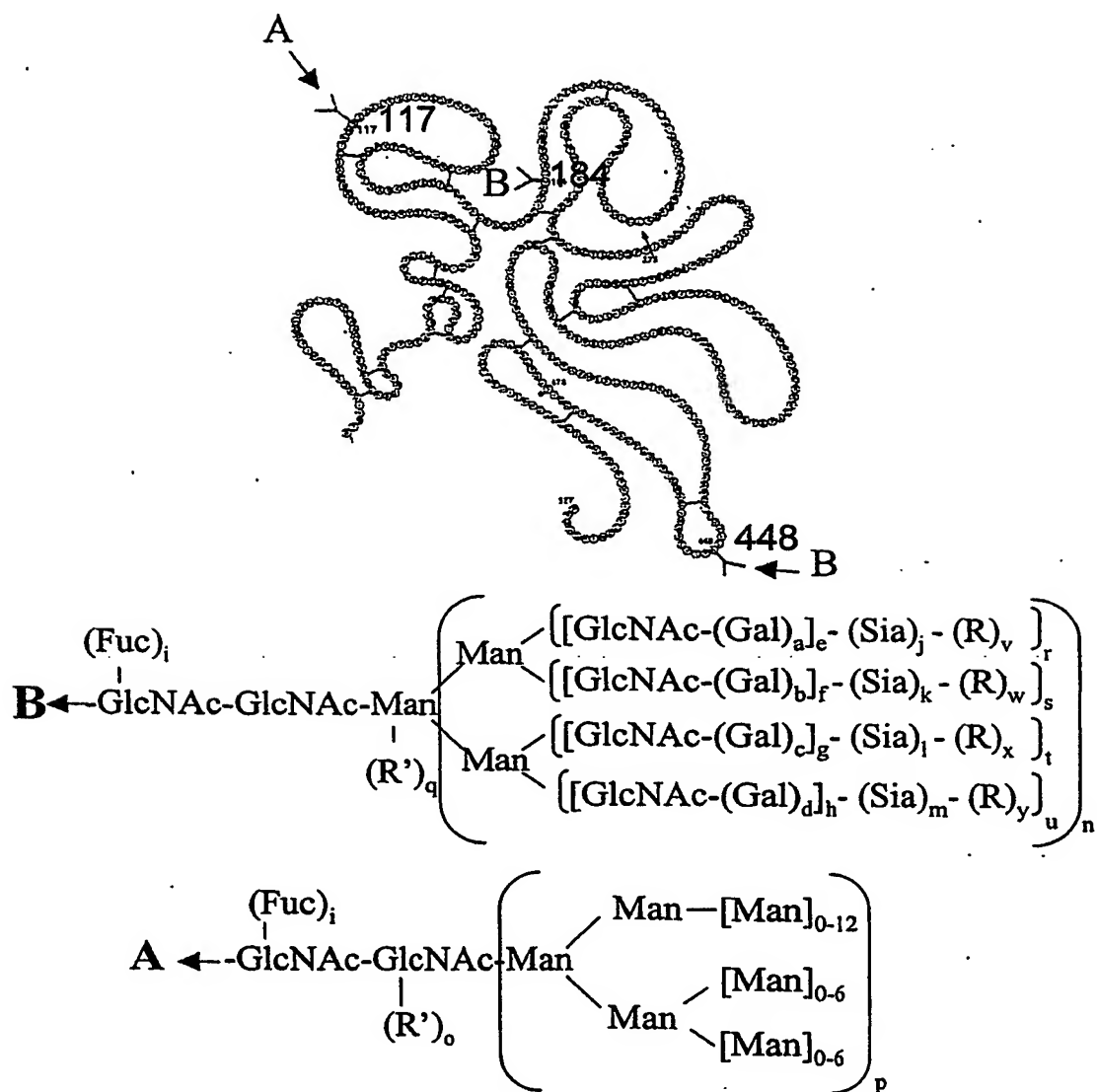
A = B; b, d, f, h, j-o, s, u, w, y = 0;

a, c, e, g, i, r, t, v, x (independently selected) = 0 or 1;

n = 1; R = PEG.

FIG. 40G

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer; R' = sugar, glycoconjugate.

FIG. 40H

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NSO expressed tPA

A = B; a-m, r-u (independently selected) = 0 or 1;  
n = 1; o, p, q, v-y = 0

- ↓
1. sialidase, alpha-galactosidase
  2. CMP-SA-levulinate, ST3Gal3,
  3. H<sub>4</sub>N<sub>2</sub>-PEG

A = B; a-m, r-y (independently selected) = 0 or 1;  
n = 1; o, p, q = 0;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 40I

CHO, BHK, 293 cells, Vero expressed tPA

a-g, n, p = 1; h = 1 to 3;  
j-m, i, (independently selected) = 0 or 1;  
r-u (independently selected) = 0 to 1; q, o, v-y = 0.

- ↓
1. alpha and beta Mannosidases
  2. CMP-SA, ST3Gal3
  3. Galactosyltransferase, UDP-Gal-PEG

a-g, n = 1; h = 1 to 3;  
i, r-u (independently selected) = 0 or 1; o = 1;  
q, p, v-y = 0; j-m (independently selected) = 0 or 1;  
R' = Gal-PEG

FIG. 40J

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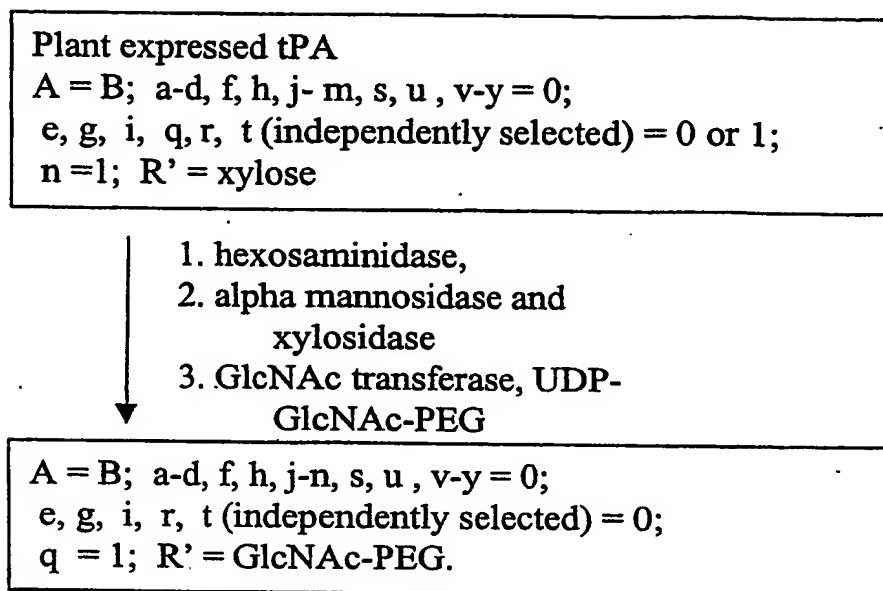
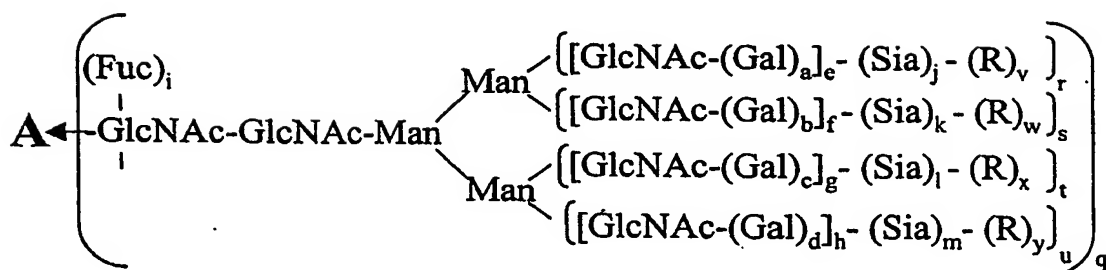
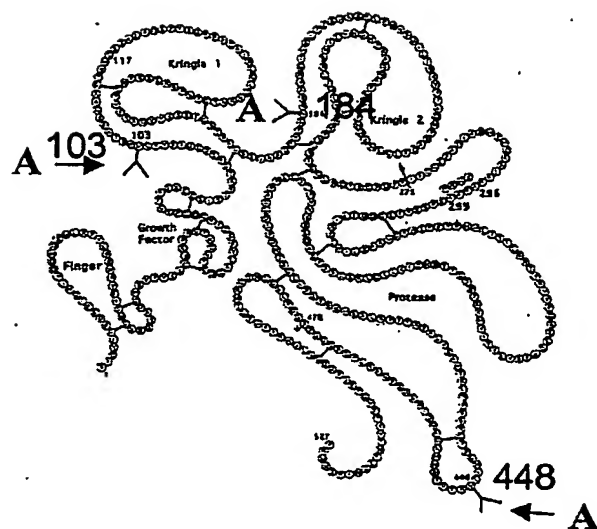


FIG. 40K



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40L

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
 a-d, i-m, q-u (independently selected) = 0 or 1;  
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
 e-h = 1; v-y (independently selected) = 1,  
 when j-m (independently selected) is 1;  
 R = PEG.

FIG. 40M

CHO, BHK, 293 cells, Vero expressed TNK tPA  
 a-d, i-m, q-u (independently selected) = 0 or 1;  
 e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
 e-h = 1; v-y (independently selected) = 0 or 1;  
 R = PEG.

FIG. 40N

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NSO expressed TNK tPA

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-PEG, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;

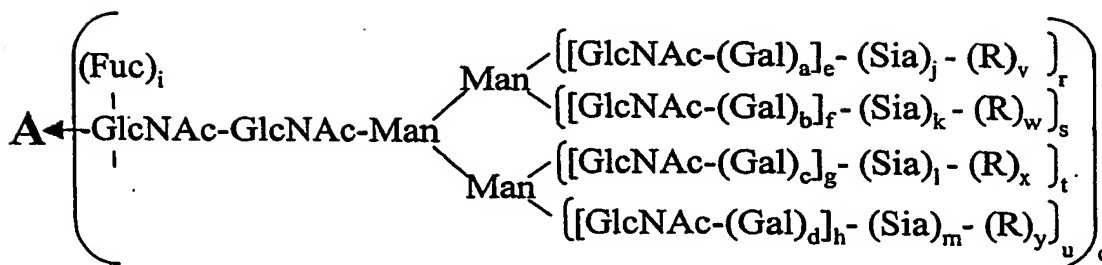
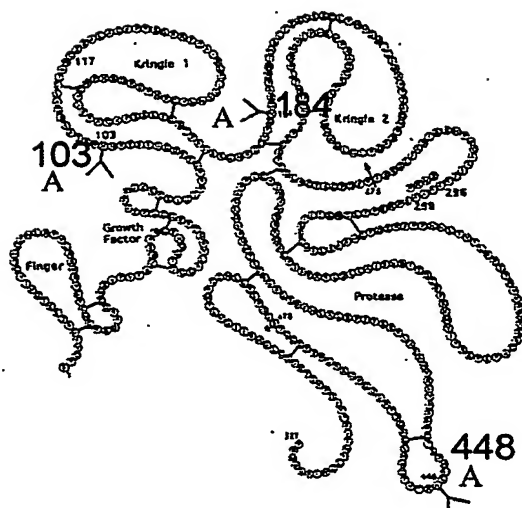
e-h = 1; v-y (independently selected) = 1,

when j-m (independently selected) is 1;

R = PEG.

FIG. 400

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 40P

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40Q

CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 40R

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CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

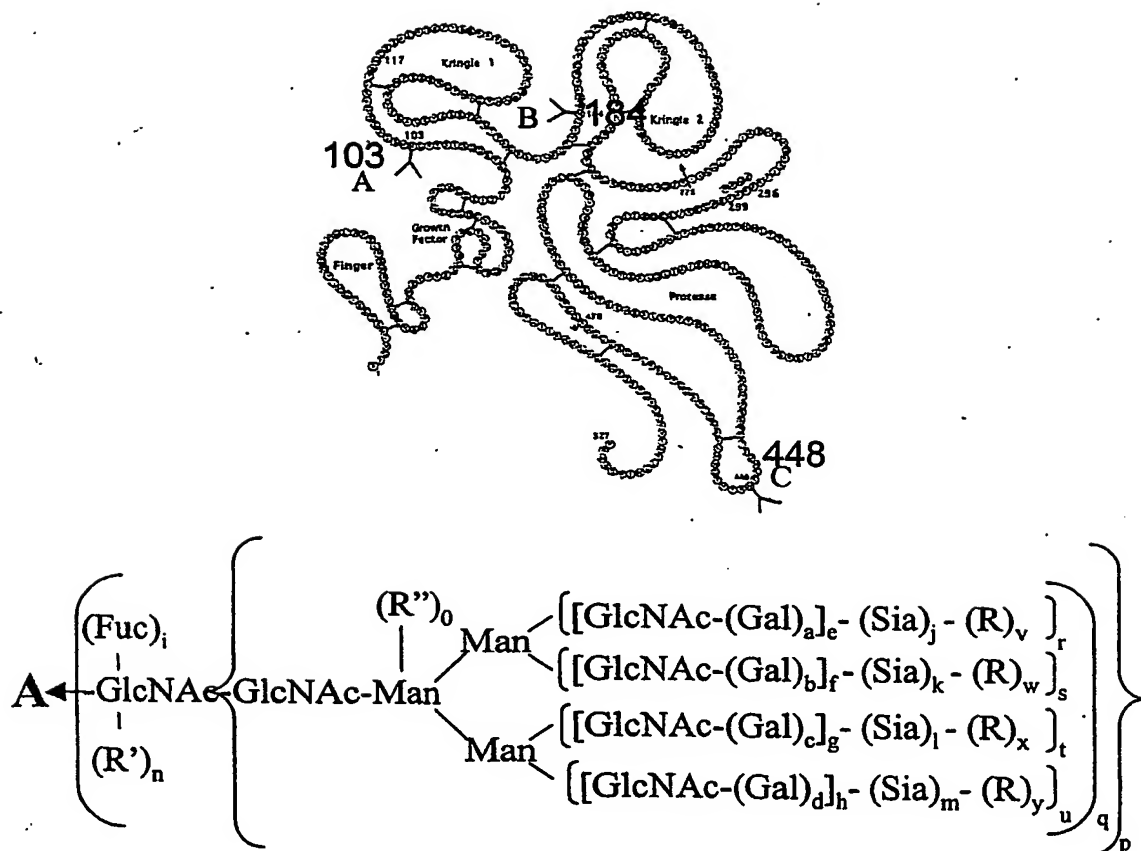


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 40S

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a-d, i, n-y (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

R'' = glycosyl residue.

FIG. 40T

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Insect cell expressed TNK tPA

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;

j-m = 0; v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 40U

Yeast expressed TNK tPA

a-m = 0; q-y (independently selected) = 0 to 1; p = 1;

R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal-PEG

a-m, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-PEG.

FIG. 40V



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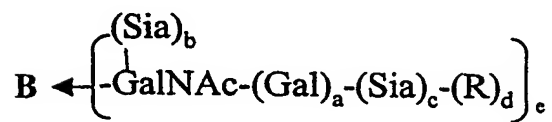
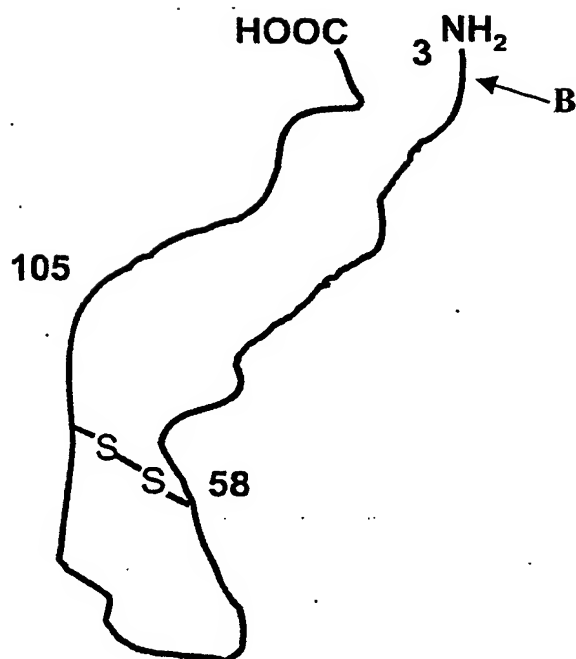
CHO, BHK, 293 cells, Vero expressed TNK tPA  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, anti-TNF  
IG chimera produced in CHO.

a-m, r-u (independently selected) = 0 or 1; p, q = 1;  
n = 0; v-y (independently selected) = 0 or 1;  
R = linker-anti-TNF IG chimera protein.

FIG. 40W

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a-c, e (independently selected) = 0 or 1;  
 d = 0;  
 R = modifying group, mannose, oligo-  
 mannose.

FIG. 41A

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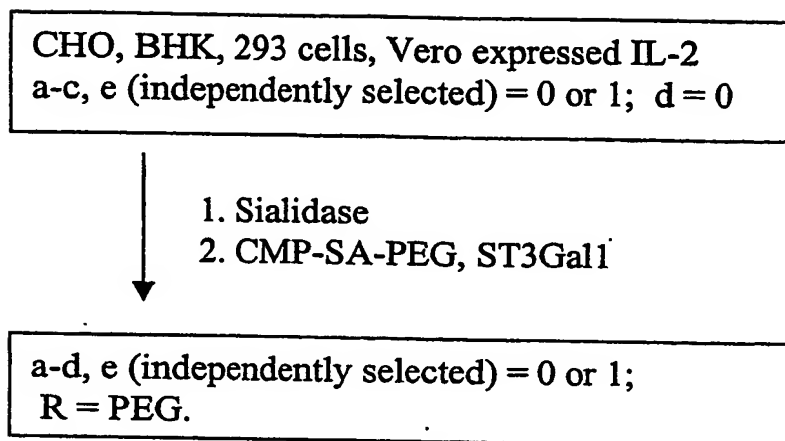


FIG. 41B

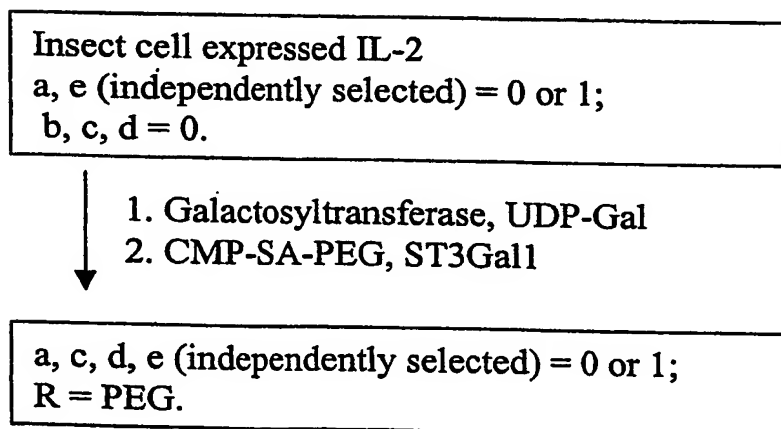


FIG. 41C

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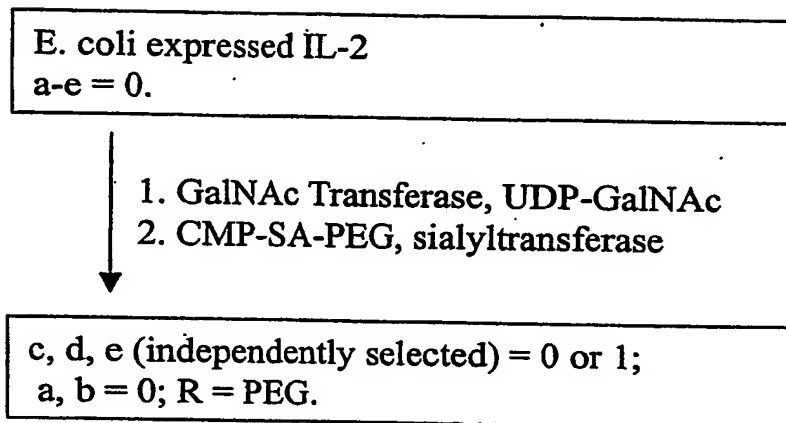


FIG. 41D

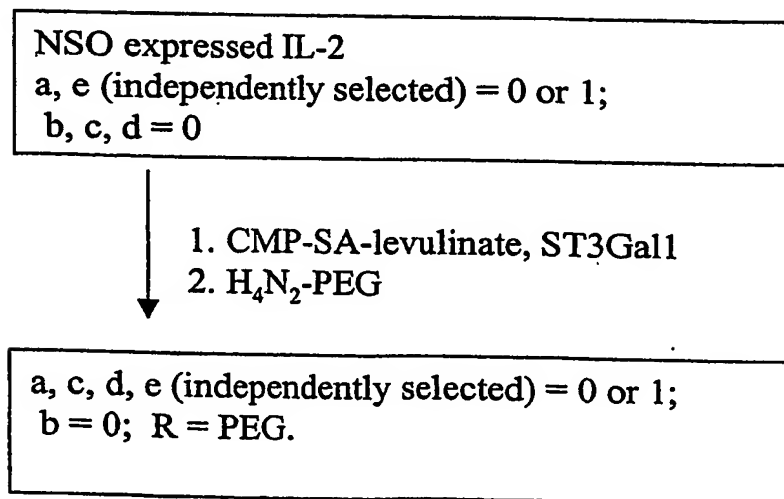


FIG. 41E

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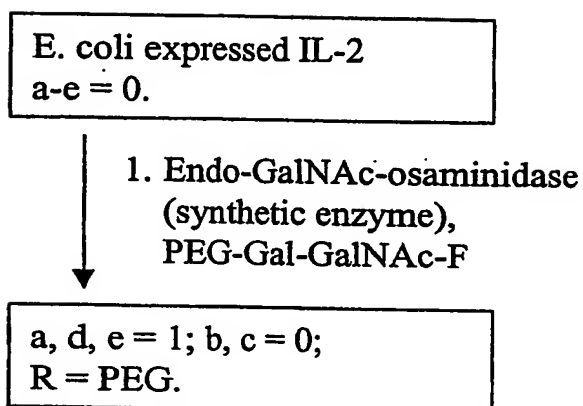


FIG. 41F

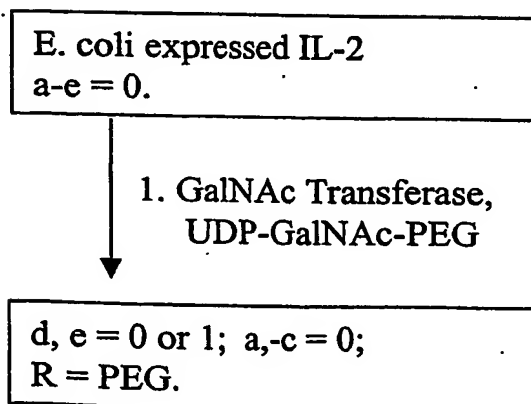
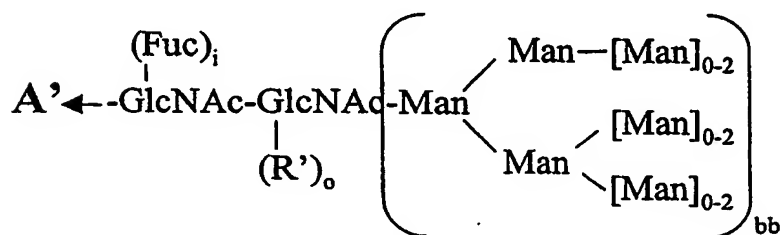
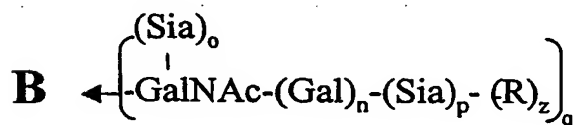
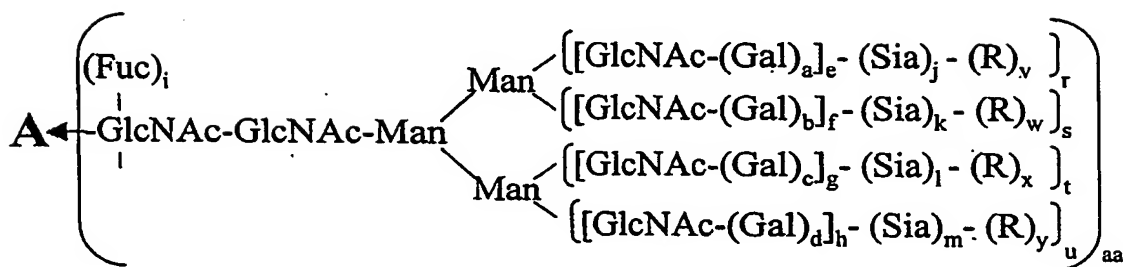


FIG. 41G

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2 peptides  
 A and A' - N-linked sites  
 B - O-linked sites



Alternate structure  
 for some N-linked  
 structures of A.

a-d, i, n-u (independently selected) = 0 or 1.  
 aa, bb (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 20.  
 v-z = 0; R = polymer, glycoconjugate.

FIG. 42A

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CHO, BHK, 293s cells, Vero, MDCK, HEKC expressed  
Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n, q-u (independently selected) = 0 or 1;

o, p, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42B

CHO, BHK, 293S cells, Vero, MDCK, 293S, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) = 0 or 1;

v-z = 0.



1. Sialidase

2. CMP-SA-PEG, ST3Gal3

3. ST3Gal1, CMP-SA

e-h = 1 to 4;

aa, bb, a-d, i, n, p-u (independently selected) = 0 or 1;

o, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42C

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CHO, BHK, 293s cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG, ST3Gal3

e-h = 1 to 4;

aa, bb, a-d, i, n-u (independently selected) = 0 or 1;

z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42D

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected) 0 or 1;

v-z = 0.



1. CMP-SA-PEG, ST3Gal1

e-h = 1 to 4;

aa, bb, a-d, i, n-u (independently selected) = 0 or 1;

z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42E



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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, a-d, j-m, i, n-u (independently selected)=0 or 1;

v-z = 0.



1. CMP-SA-PEG,  $\alpha$ 2,8-ST

e-h = 1 to 4;

aa, bb, a-d, i, n-y (independently selected) = 0 or 1;

z = 0; j-m (independently selected) = 0 to 2;

v-y (independently selected) = 1,

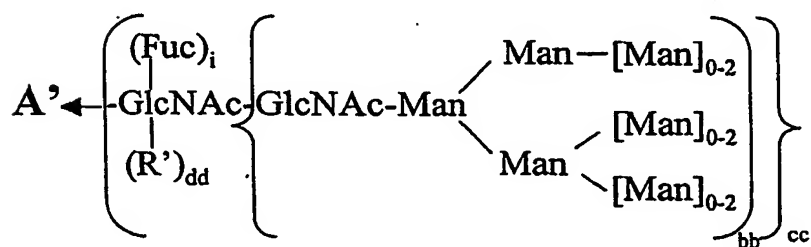
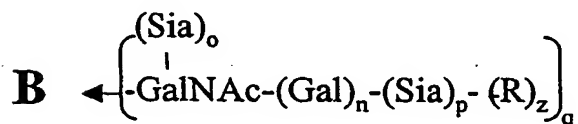
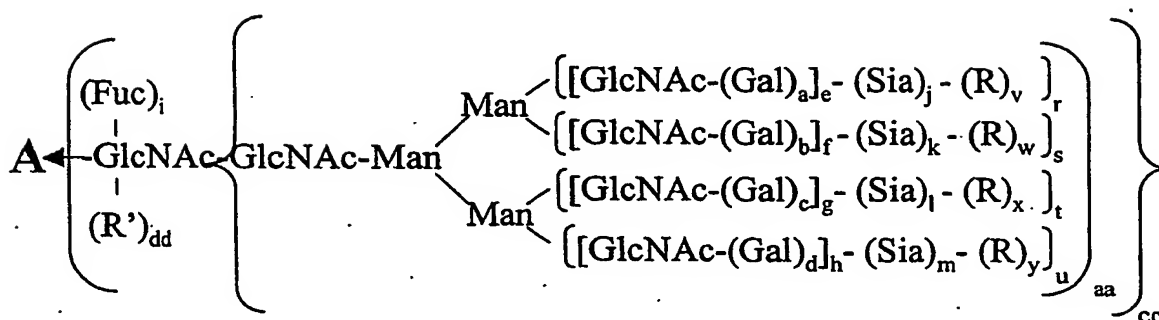
when j-m (independently selected) is 2;

R = PEG.

FIG. 42F

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2 peptides

**A or A'** - N-linked sites**B** - O-linked sites

Alternate structure  
for some N-linked  
structures of A.

a-d, i, n-u, (independently selected) = 0 or 1.

aa, bb, cc, dd (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 20.

v-z = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 42G

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓  
1. CMP-SA-levulinate, ST3Gal3,  
2. H<sub>4</sub>N<sub>2</sub>-PEG

e-h = 1 to 4;

aa, bb, cc, a-d, i, n-u (independently selected) = 0 or 1;

dd, z = 0; j-m, v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 42H

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓  
1. endo-H  
2. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42I

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. ST3Gal3, CMP-SA
  2. endo-H
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, bb, dd, a-d, i, j-u (independently selected) = 0 or 1;

cc, v-z = 0; R' = -Gal-PEG.

FIG. 42J

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

- ↓
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. galactosyltransferase, UDP-Gal-PEG

e-h = 1 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0; R = PEG.

FIG. 42K

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CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases

2. GNT-1, 2, 4 & 5; UDP-GlcNAc

↓ 3. galactosyltransferase, UDP-Gal

4. ST3Gal3, CMP-SA

e-h = 1 to 4;

aa, bb, cc, a-d, i, j-q (independently selected) = 0 or 1;

dd, v-z = 0.

FIG. 42L

CHO, BHK, 293S cells, Vero, MDCK, HEKC  
expressed Factor VIII.

e-h = 1 to 4;

aa, bb, cc, a-d, j-m, i, n-u (independently selected) = 0 or 1;

dd, v-z = 0.

1. mannosidases

↓ 2. GNT-1, UDP-GlcNAc-PEG

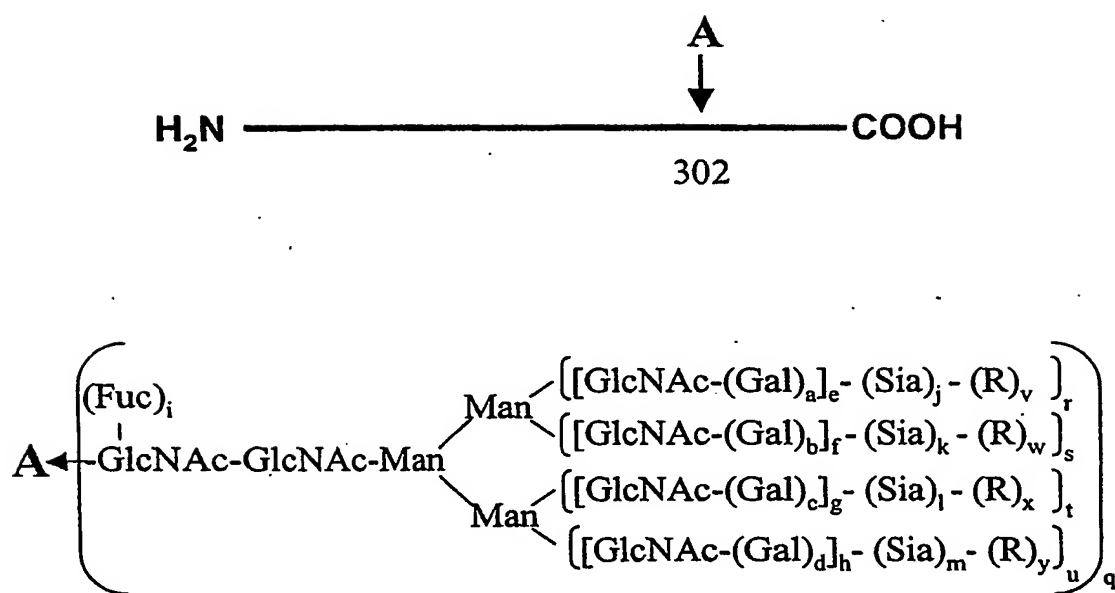
e-h = 0 to 4;

aa, a-d, i, j-y (independently selected) = 0 or 1;

bb, cc, dd, z = 0.

FIG. 42M

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer.

FIG. 43A

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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 43B

CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq),  
ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 43C

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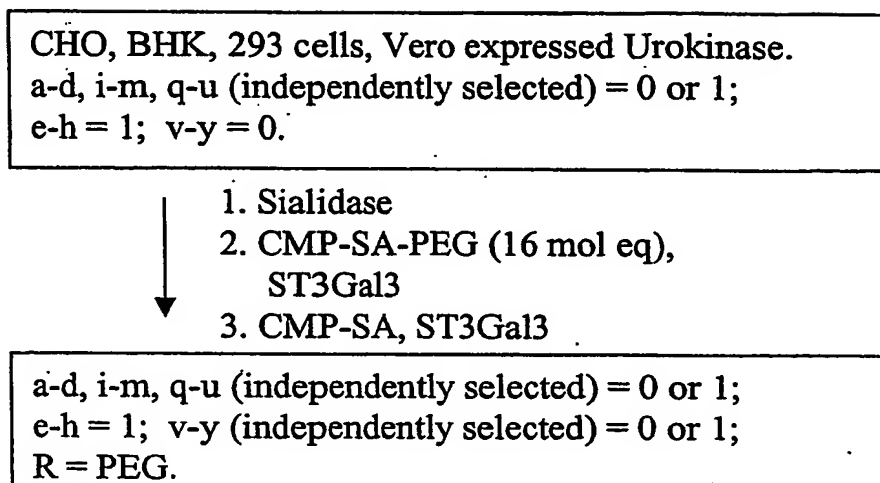


FIG. 43D

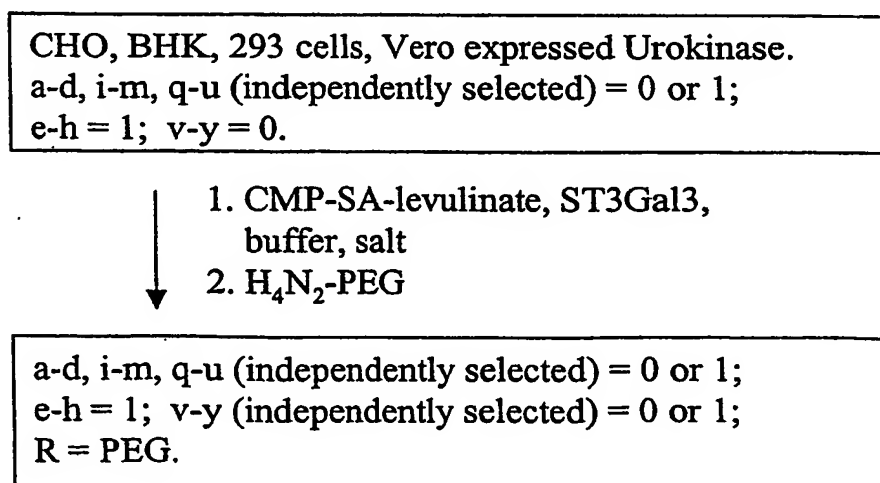


FIG. 43E



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CHO, BHK, 293 cells, Vero expressed Urokinase.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

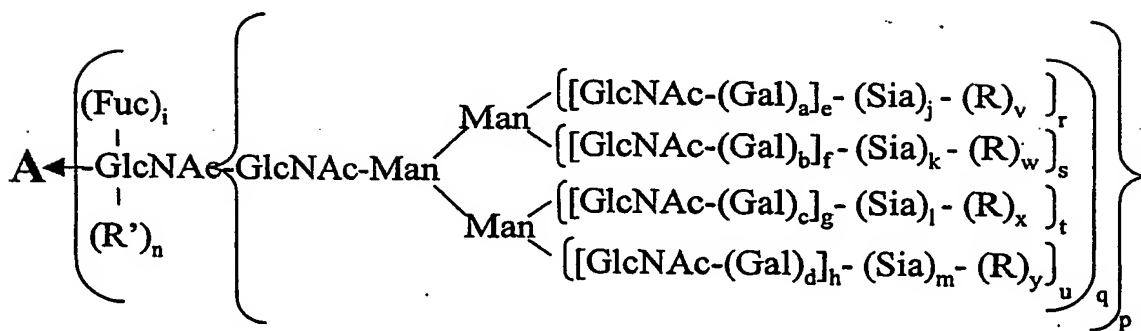


1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 43F

$\text{H}_2\text{N}$  —————  $\text{COOH}$   
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**FIG. 43G**

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Insect cell expressed Urokinase.

a-d, f, h, j-n, s, u, v-y = 0;  
e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc
2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1;  
j-n = 0; v-y (independently selected) = 1,  
when e-h (independently selected) is 1;  
R = PEG.

FIG. 43H

Yeast expressed Urokinase.

a-n = 0;  
q-y (independently selected) = 0 to 1;  
p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase
2. Galactosyltransferase, UDP-Gal
3. CMP-SA-PEG, ST3Gal3

a-m, p-y = 0; n (independently selected) = 0 or 1;  
R' = -Gal-Sia-PEG.

FIG. 43I

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CHO, BHK, 293 cells, Vero expressed Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated Urokinase produced in CHO.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;

p = 1; n = 0;

v-y (independently selected) = 0 or 1;

R = linker-Urokinase.

FIG. 43J

Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0; n = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

- ↓
1. sulfohydrolase
  2. CMP-SA-PEG, sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;

n = 0; e-h = 1; Sia = Sia;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.

v-y (independently selected) = 0 or 1;

R = PEG.

FIG. 43K

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Isolated Urokinase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; n = 0; v-y = 0;

Sia (independently selected) = Sia or SO<sub>4</sub>;

Gal (independently selected) = Gal or GalNAc;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc.



1. sulfohydrolase, hexosaminidase

2. UDP-Gal-PEG, galactosyltransferase

a-d, i, q-u (independently selected) = 0 or 1;

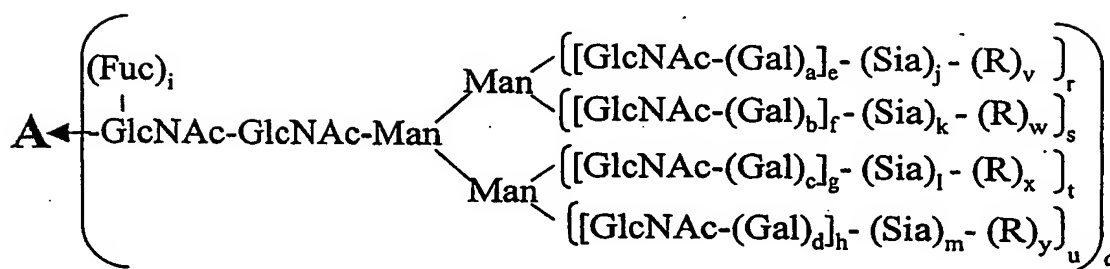
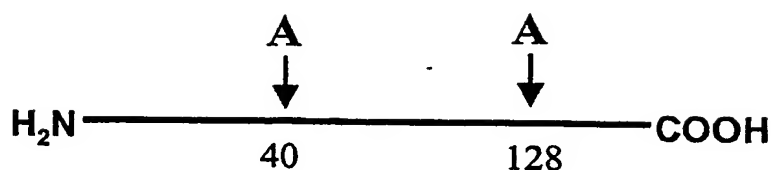
e-h = 1; j-n = 0; Gal (independently selected) = Gal;

GlcNAc (independently selected) = GlcNAc or GlcNAc-Fuc;

v-y (independently selected) = 0 or 1; R = PEG.

FIG. 43L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = polymer, glycoconjugate.

FIG. 44A

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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq),  
ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = PEG.

FIG. 44B

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (1.2 mol eq), ST3Gal3
  3. CMP-SA (16 mol eq), ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44C

194/498

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. Sialidase
  2. CMP-SA-PEG (16 mol eq), ST3Gal3
  3. CMP-SA, ST3Gal3

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44D

CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-levulinate, ST3Gal3,  
buffer, salt
  2. H<sub>4</sub>N<sub>2</sub>-PEG

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 0 or 1;  
R = PEG.

FIG. 44E



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CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.



1. CMP-SA,  $\alpha$ 2,8-ST

a-d, i, q-u (independently selected) = 0 or 1;  
e-h = 1;  
j-m (independently selected) = 0-20;  
v-y (independently selected) = 0.

FIG. 44F

**FIG. 44G**

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Insect cell expressed DNase I.

a-d, f, h, j-n, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.



1. GNT's 1,2,4,5, UDP-GlcNAc

2. Galactosyltransferase, UDP-Gal-PEG

a-i, q-u (independently selected) = 0 or 1; j-n = 0;

v-y (independently selected) = 1,

when e-h (independently selected) is 1;

R = PEG.

FIG. 44H

Yeast expressed DNase I.

a-n = 0;

q-y (independently selected) = 0 to 1;

p = 1; R (branched or linear) = Man, oligomannose.



1. Endoglycanase

2. Galactosyltransferase, UDP-Gal

3. CMP-SA-PEG, ST3Gal3

a-n, p-y = 0; n (independently selected) = 0 or 1;

R' = -Gal-Sia-PEG.

FIG. 44I

198/498

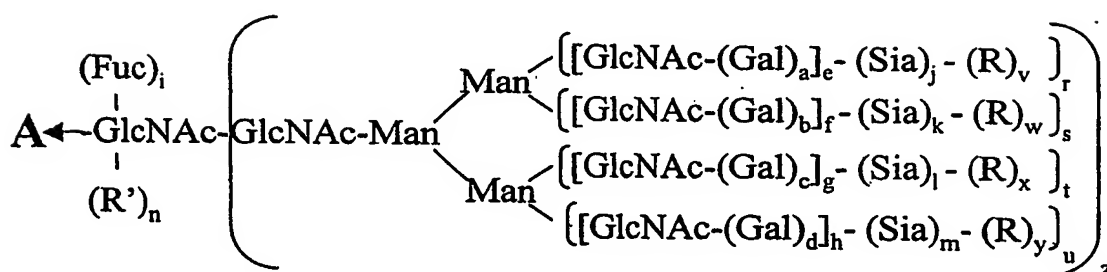
CHO, BHK, 293 cells, Vero expressed DNase I.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; n, v-y = 0.

- ↓
1. CMP-SA-linker-SA-CMP, ST3Gal3
  2. ST3Gal1, desialylated alpha-1-Proteinase inhibitor.
  3. CMP-SA, ST3Gal3, ST3Gal1

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker- alpha-1-Proteinase inhibitor.

FIG. 44J

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 45A

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CHO, BHK, 293 cells, Vero expressed Insulin.  
a-m, r-u (independently selected) = 0 or 1;  
n = 0; v-y = 0; z = 1.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
n = 0; R = PEG; z = 1.

FIG. 45B

Insect cell expressed Insulin.  
a-h, j-n, s-y = 0;  
i, r (independently selected) = 0 or 1; z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;  
e, g, i, r, t, v, x (independently selected) = 0 or 1;  
v, x (independently selected) = 1,  
when e, g (independently selected) is 1;  
z = 1; R = PEG.

FIG. 45C

201/498

Yeast expressed Insulin.

a-n = 0; r-y (independently selected) = 0 to 1;  
z = 1;

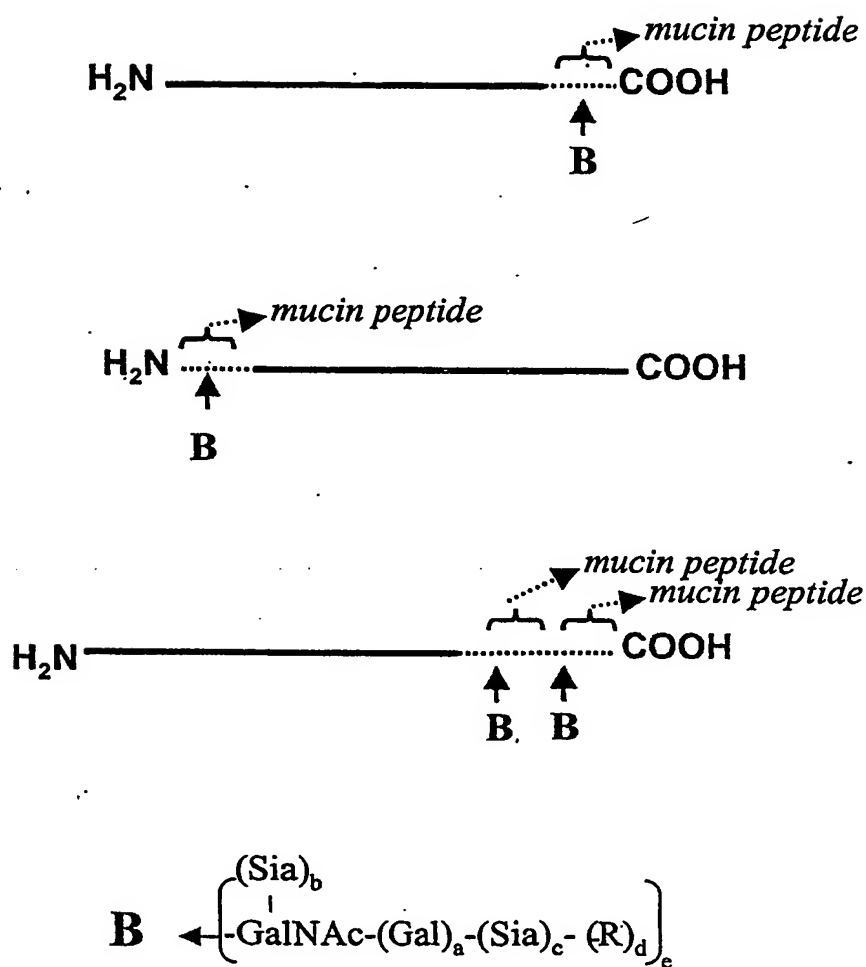
R (branched or linear) = Man, oligomannose or  
polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 45D

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer

FIG. 45E



203/498

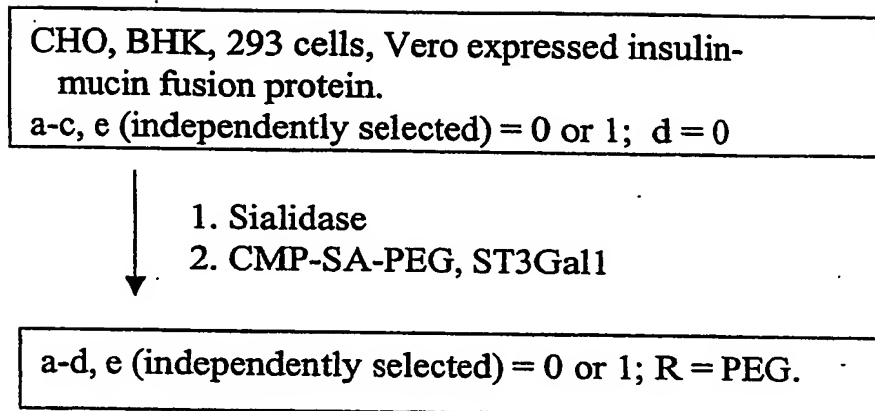


FIG. 45F

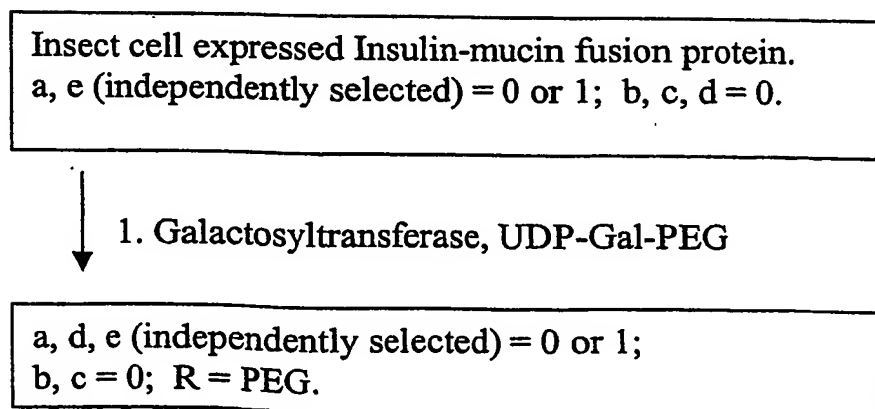


FIG. 45G

204/498

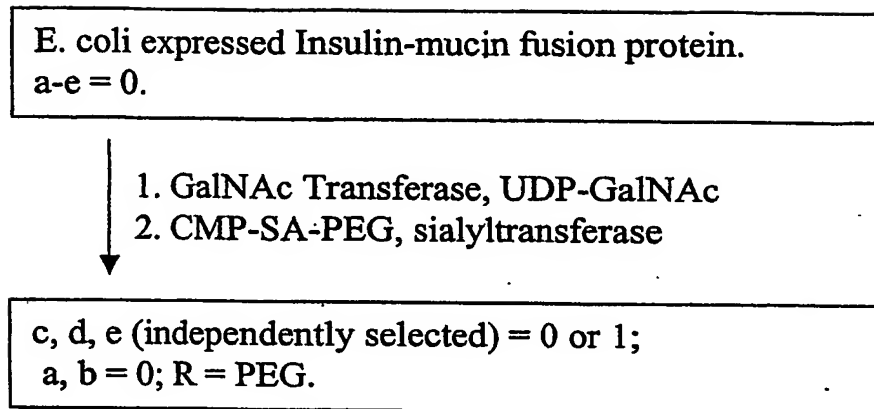
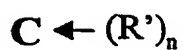
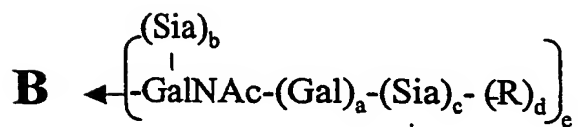
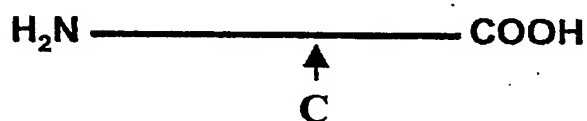
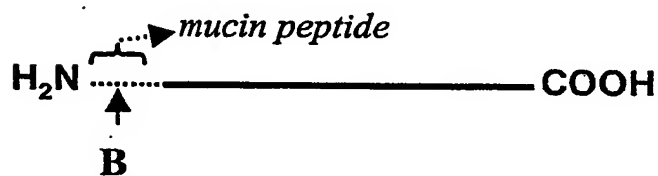


FIG. 45H

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = modifying group, mannose,  
oligo-mannose.

FIG. 45I

206/498

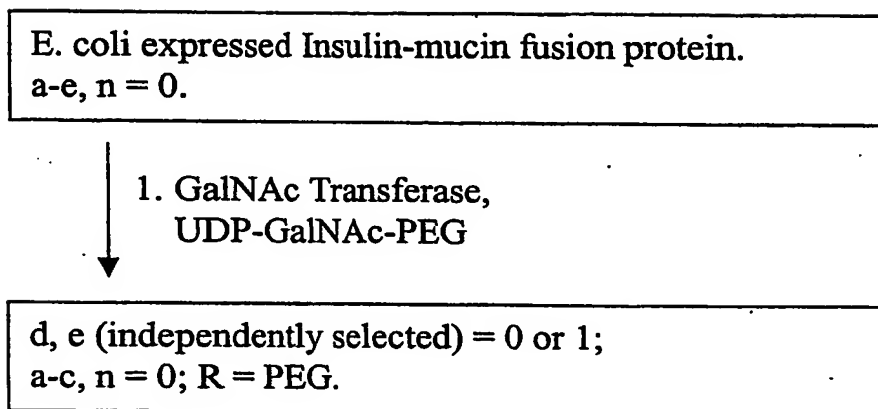


FIG. 45J

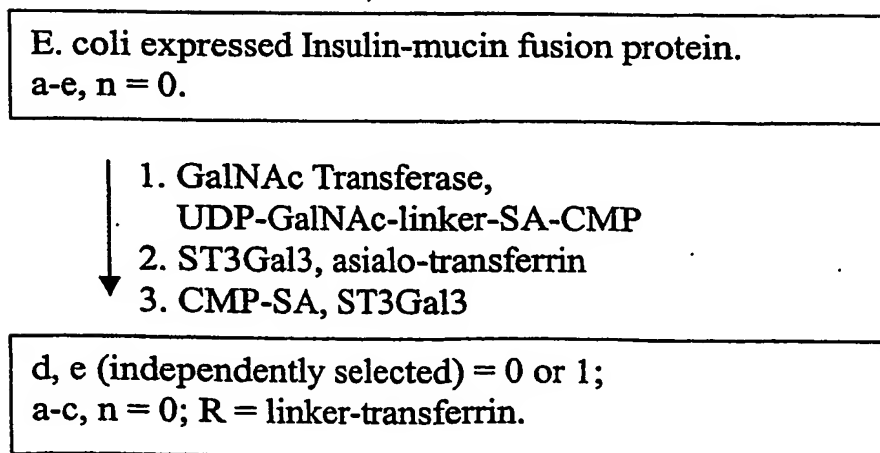


FIG. 45K

207/498

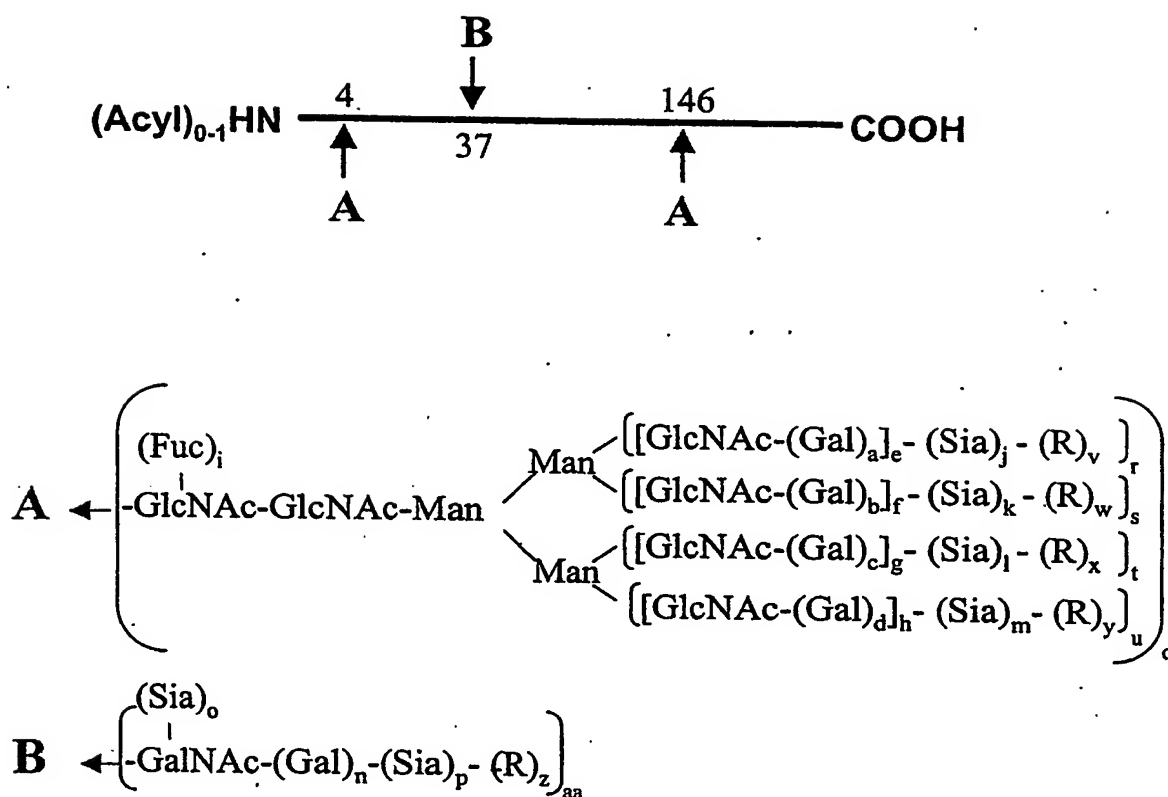
E. coli expressed Insulin (N)—no mucin peptide.  
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  3. CMP-SA, ST3Gal3

a-e = 0; n = 1;  
R' = linker-transferrin.

FIG. 45L

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a-d, i, n-u, aa (independently selected) = 0 or 1.  
 e-h (independently selected) = 0 to 6.  
 j-m (independently selected) = 0 to 100.  
 v-y = 0; R = polymer, glycoconjugate.

FIG. 46A

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CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. Sialidase
  2. CMP-SA-linker-lipid-A,  
ST3Gal3

a-d, i-m, q-u, aa (independently selected) = 0 or 1;  
o, p, z = 0; n, e-h = 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = linker-lipid-A.

FIG. 46B

CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-linker-tetanus toxin, ST3Gal1
  3. CMP-SA, ST3Gal3

a-d, i-m, p-u, z, aa (independently selected) = 0 or 1;  
o, v-y = 0; n, e-h = 1; R = tetanus toxin.

FIG. 46C

210/498

NSO expressed M-antigen.

a-d, i-n, o-u, aa (independently selected) = 0 or 1;

e-h = 1; v-z = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1.  $\alpha$ -galactosidase
  2. CMP-SA, ST3Gal3
  2. CMP-SA-KLH, ST3Gal1

a-d, i-n, p-u, z, aa (independently selected) = 0 or 1;

e-h = 1; o, v-y = 0;

z = 1, when p = 1;

R = KLH.

FIG. 46D

Yeast expressed M-antigen.

a-p, z = 0; q-y, aa (independently selected) = 0 to 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

- ↓
1.  $\alpha$ 1,2-mannosidase
  2. GNT 1,
- UDP-GlcNAc-linker-diphtheria toxin.

e, q, l, m, r, t, u, v, aa (independently selected) = 0 or 1;

a-d, f-h, j, k, n-p, s, w-z = 0;

Sia = Man; R = linker-diphtheria toxin.

FIG. 46E



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CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-m, o-u, aa (independently selected) = 0 or 1;  
n, e-h = 1; v-z = 0.



1. CMP-SA-levulinate, ST3Gal3,
2. H<sub>4</sub>N<sub>2</sub>-linker-DNA

a-d, i-m, o-y, aa (independently selected) = 0 or 1;  
z = 0; n, e-h = 1; R = linker-DNA.

FIG. 46F

CHO, BHK, 293 cells, Vero expressed M-antigen.  
a-d, i-n, o-u, aa (independently selected) = 0 or 1;  
e-h = 1; v-z = 0.

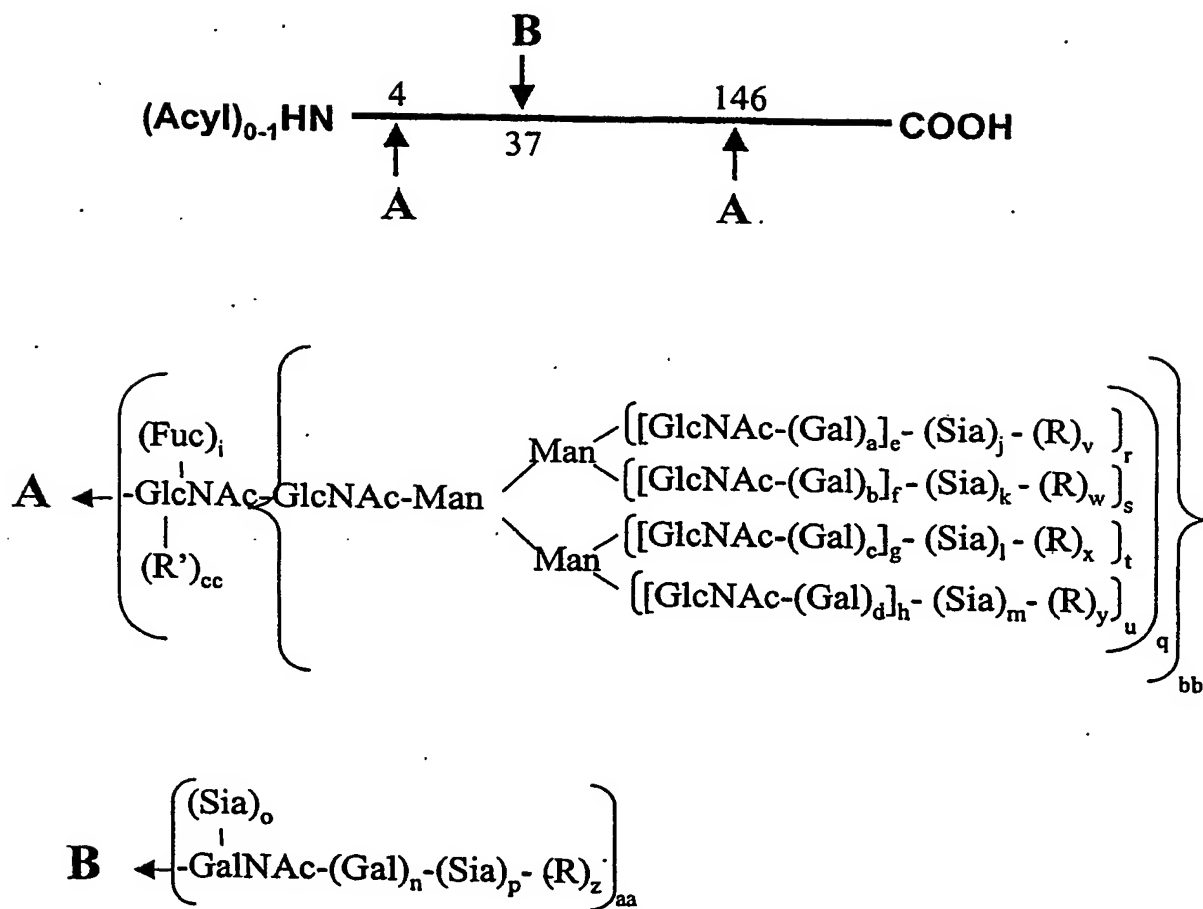


1. CMP-SA, poly- $\alpha$ 2,8-ST

a-d, i, n-u, aa (independently selected) = 0 or 1;  
e-h = 1; j-m (independently selected) = 0-100;  
v-z (independently selected) = 0;

FIG. 46G

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a-d, i, n, q-u, aa, bb, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-p (independently selected) = 0 to 100.

Cc, v-y = 0;

R = modifying group, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 46H

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Insect cell expressed M-antigen.

a-d, f, h, j-m, o, p, s, u, v-z, cc = 0;

bb = 1;

e, g, i, n, q, r, t, aa (independently selected) = 0 or 1.



1. GNT-2, UDP-GlcNAc-linker-  
Neisseria protein

a, c, e, g, i, n, q, r, t, v, x, aa (independently selected) =  
0 or 1;

b, d, f, h, j-p, s, u, w, y, z, cc = 0;

bb = 1; R = -linker-Neisseria protein.

FIG. 46I

Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1;

bb = 1; R (branched or linear) = Man, oligomannose;

GalNAc = Man.



1. Endoglycanase

2. Galactosyltransferase,

UDP-Gal-linker-Neisseria protein

a-p, r-z, bb = 0;

q, aa, cc (independently selected) = 0 or 1;

R' = -Gal-linker-Neisseria protein.

FIG. 46J

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Yeast expressed M-antigen.

a-p, z, cc = 0;

q-y, aa (independently selected) = 0 to 1; bb = 1;

R (branched or linear) = Man, oligomannose;

GalNAc = Man.

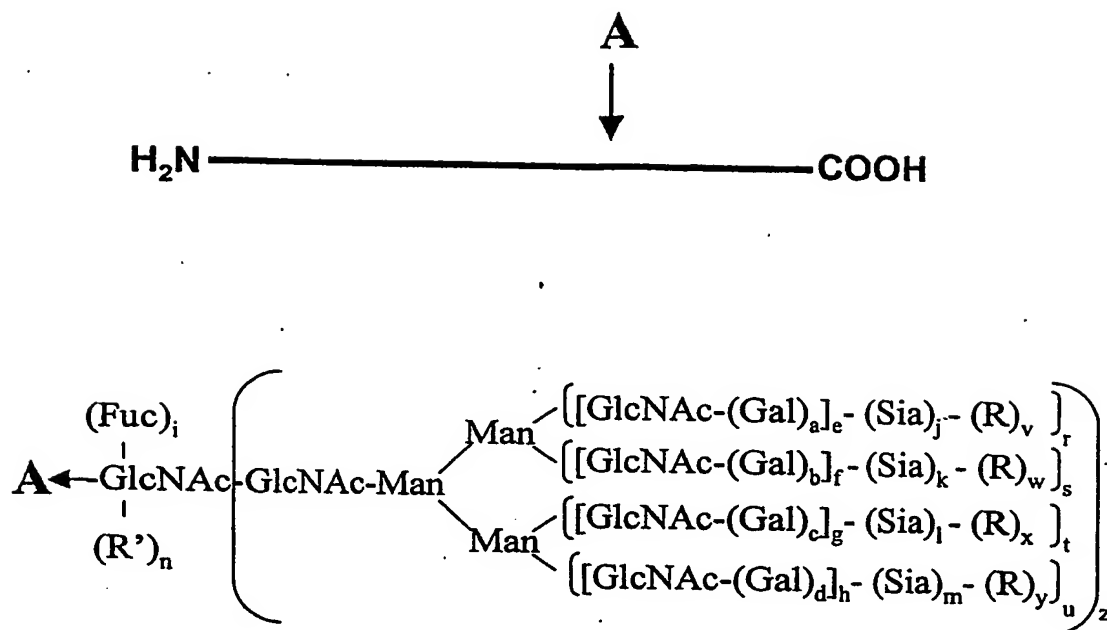
- 
1. mannosidases
  2. GNT 1 & 2, UDP-GlcNAc
  3. UDP-Gal, Galactosyltransferase,
  4. CMP-SA, sialyltransferase

a, c, e, g, j, l, q, r, t, aa (independently selected) = 0 or 1;

b, d, f, h, k, m-p, s, u-z, cc = 0; bb = 1.

FIG. 46K

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a-d, i, r-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group,  
glycoconjugate.

FIG. 47A

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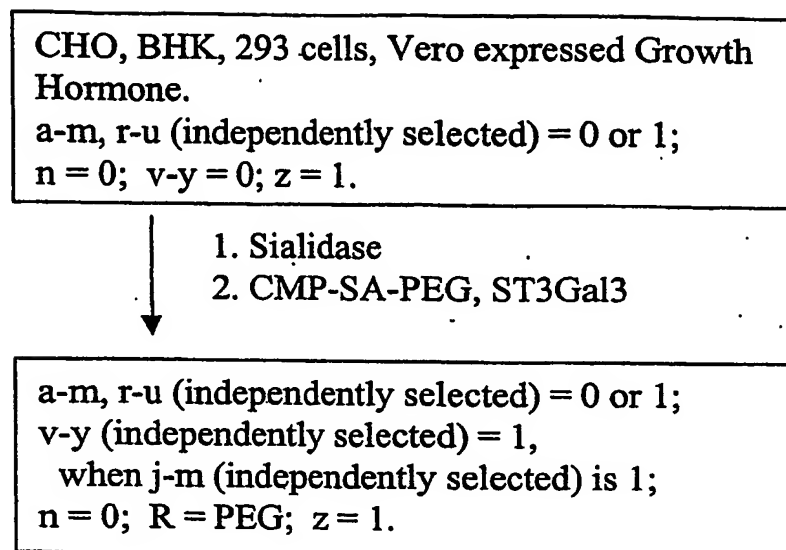


FIG. 47B

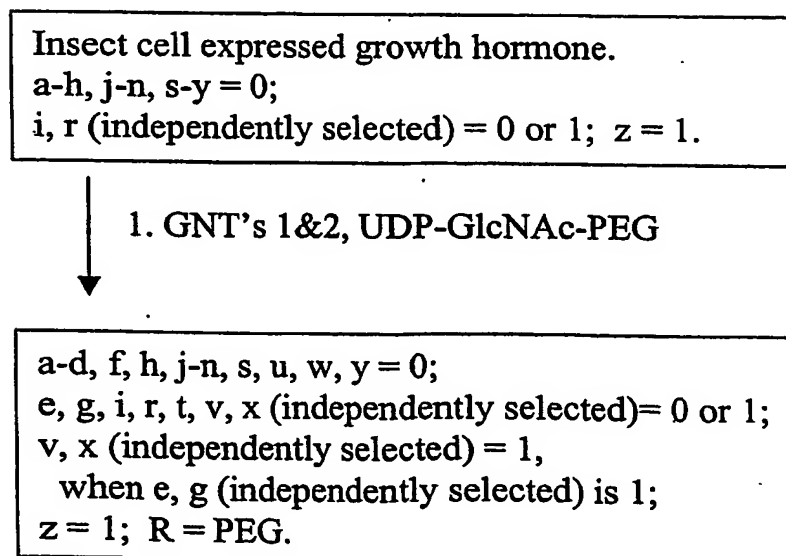


FIG. 47C

217/498

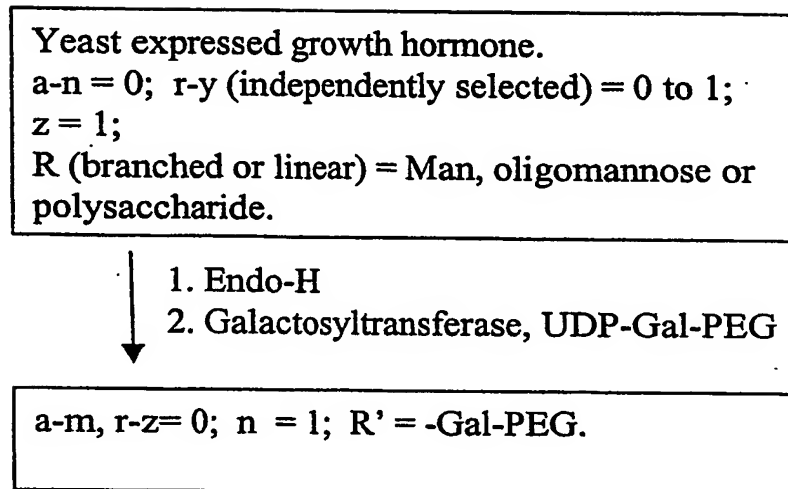
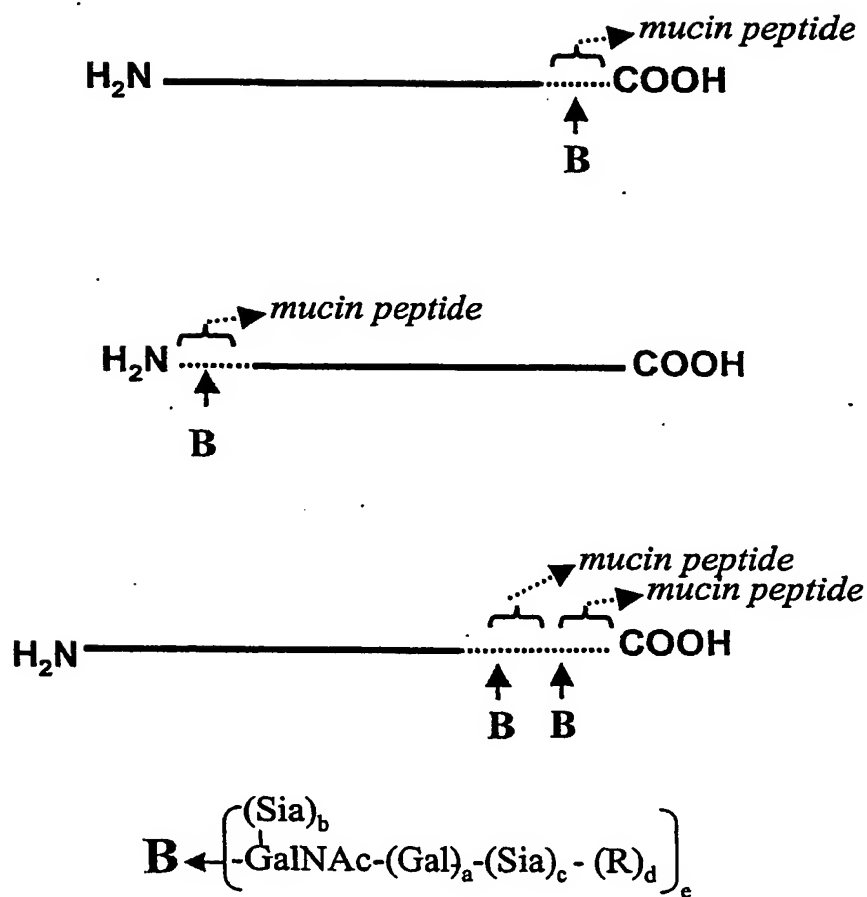


FIG. 47D

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a-c, e (independently selected) = 0 or 1;

d = 0;

R = modifying group, mannose, oligo-mannose.

FIG. 47E



219/498

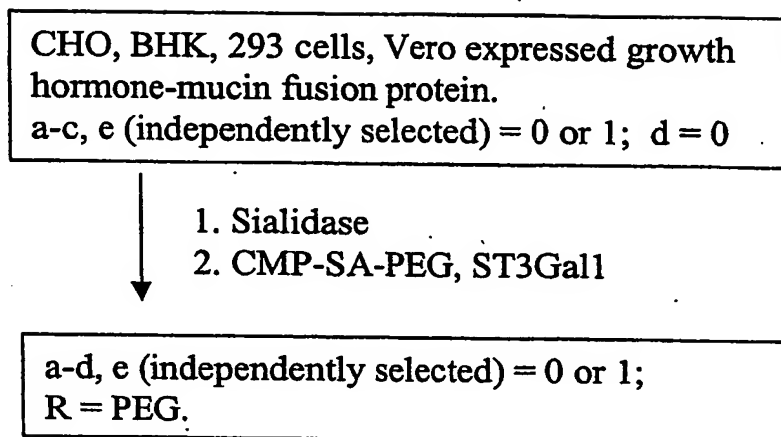


FIG. 47F

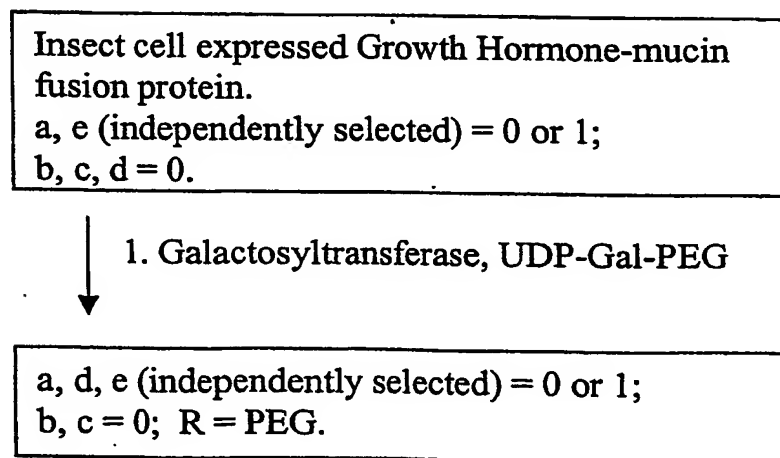


FIG. 47G

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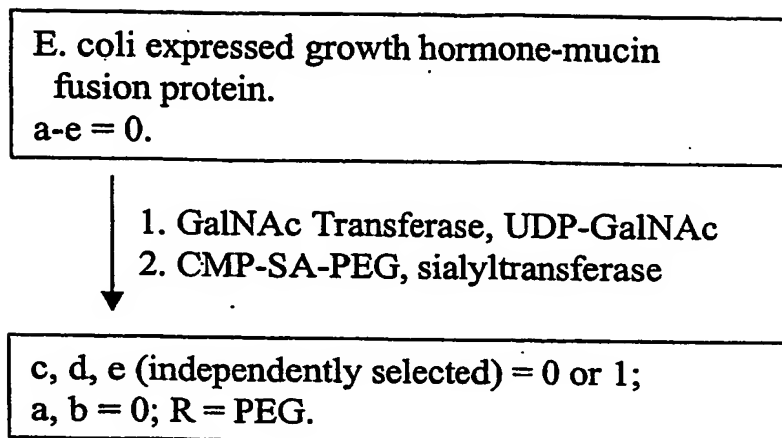


FIG. 47H

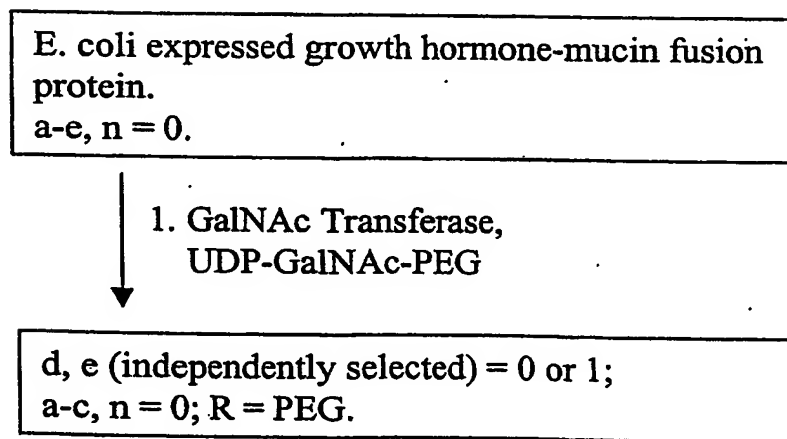


FIG. 47I

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E. coli expressed growth hormone-mucin fusion protein.

a-e, n = 0.

- ↓
1. GalNAc Transferase,  
UDP-GalNAc-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  - ↓ 3. CMP-SA, ST3Gal3

d, e (independently selected) = 0 or 1;  
a-c, n = 0; R = linker-transferrin.

FIG. 47J

E. coli expressed growth hormone  
(N)—no mucin peptide.

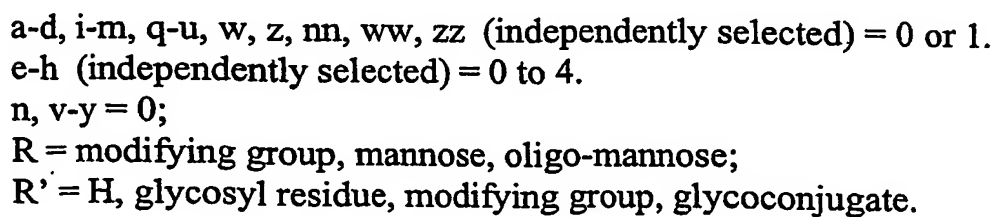
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  - ↓ 3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 47K

1



**FIG. 48A**

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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. CMP-SA, ST3Gal1
  2. galactosyltransferase, UPD-Gal
  3. CMP-SA-PEG, ST3Gal3

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48B

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓
1. sialidase
  2. CMP-SA-PEG, ST3Gal1

a-i, p-u, z, aa (independently selected) = 0 or 1;  
n = 1; o, j-m, v-y = 0; R = PEG.

FIG. 48C

224/498

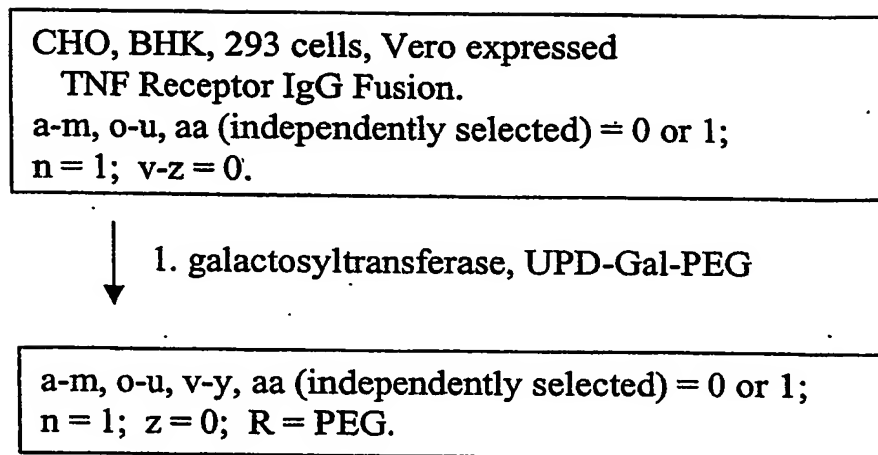


FIG. 48D

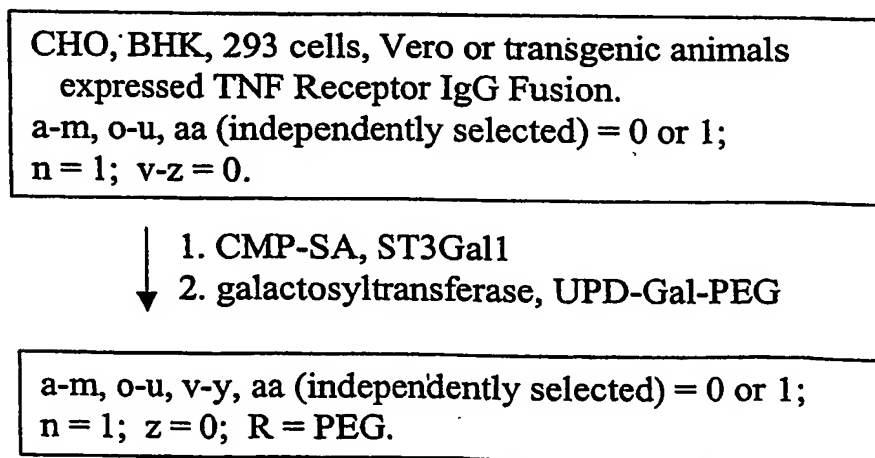


FIG. 48E

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CHO, BHK, 293 cells, Vero or transgenic animals  
expressed TNF Receptor IgG Fusion.

a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. CMP-SA-levulinate, ST3Gal1  
2. H<sub>4</sub>N<sub>2</sub>-PEG

a-m, o-u, v-y, aa (independently selected) = 0 or 1;  
n = 1; z = 0; R = PEG.

FIG. 48F

CHO, BHK, 293 cells, Vero expressed  
TNF Receptor IgG Fusion.

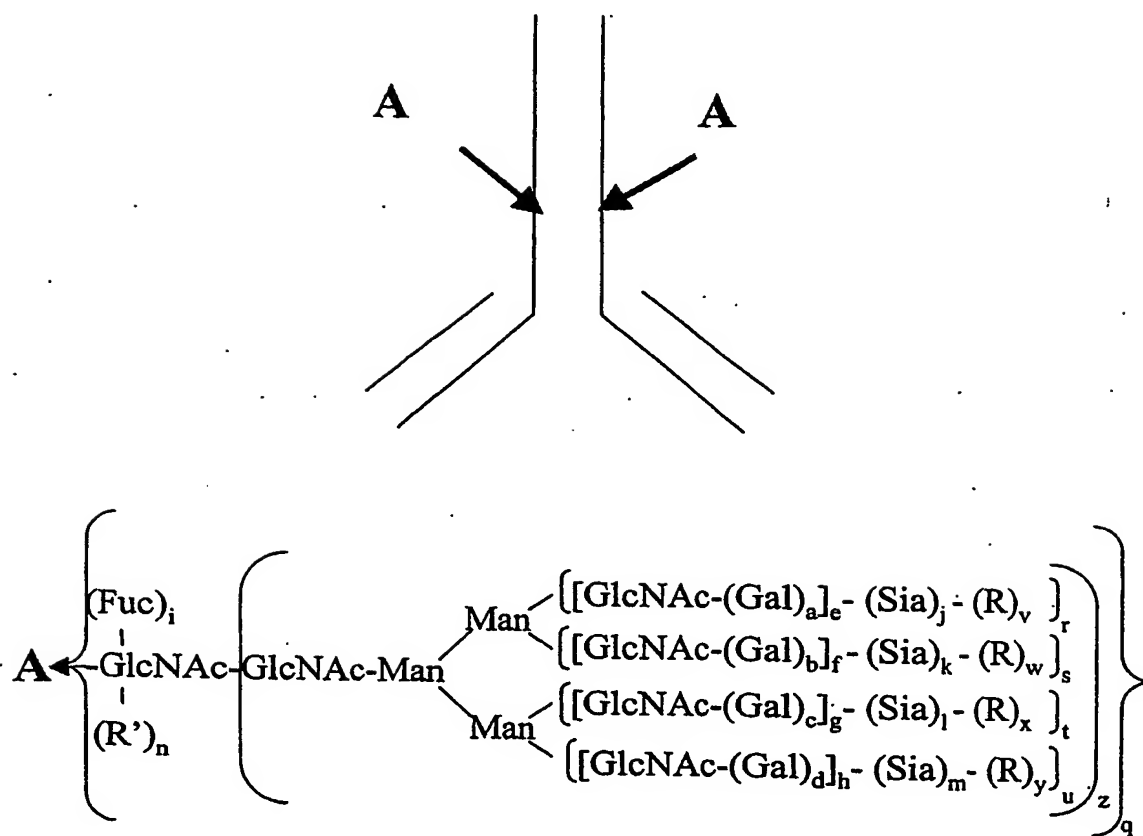
a-m, o-u, aa (independently selected) = 0 or 1;  
n = 1; v-z = 0.

- ↓  
1. CMP-SA-PEG,  $\alpha$ 2,8-ST

a-i, o, q-u, v-z, aa (independently selected) = 0 or 1;  
n = 1; j-m, p (independently selected) = 0 to 2;  
v-z (independently selected) = 1,  
when j-m, p (independently selected) is 2;  
R = PEG.

FIG. 48G

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a-d, i, l, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-k (independently selected) = 0 or 1.

M = 0 to 20.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 49A



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CHO, BHK, 293 cells, Vero expressed Herceptin.

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.



1. galactosyltransferase, UPD-Gal  
 2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
 e, g, r, t = 1; R = toxin;  
 f, h, k, m, n, s, u-y = 0; q, z = 1;  
 v-y (independently selected) = 51,  
 when j, l (independently selected) is 1.

FIG. 49B

CHO, BHK, 293 cells, Vero or fungal expressed Herceptin.

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.



1. galactosyltransferase,  
 UPD-Gal-Toxin

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when a, c (independently selected) is 1;  
 R = toxin.

FIG. 49C

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Fungi expressed Herceptin.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

1. Endo-H

2. Galactosyltransferase, UDP-Gal

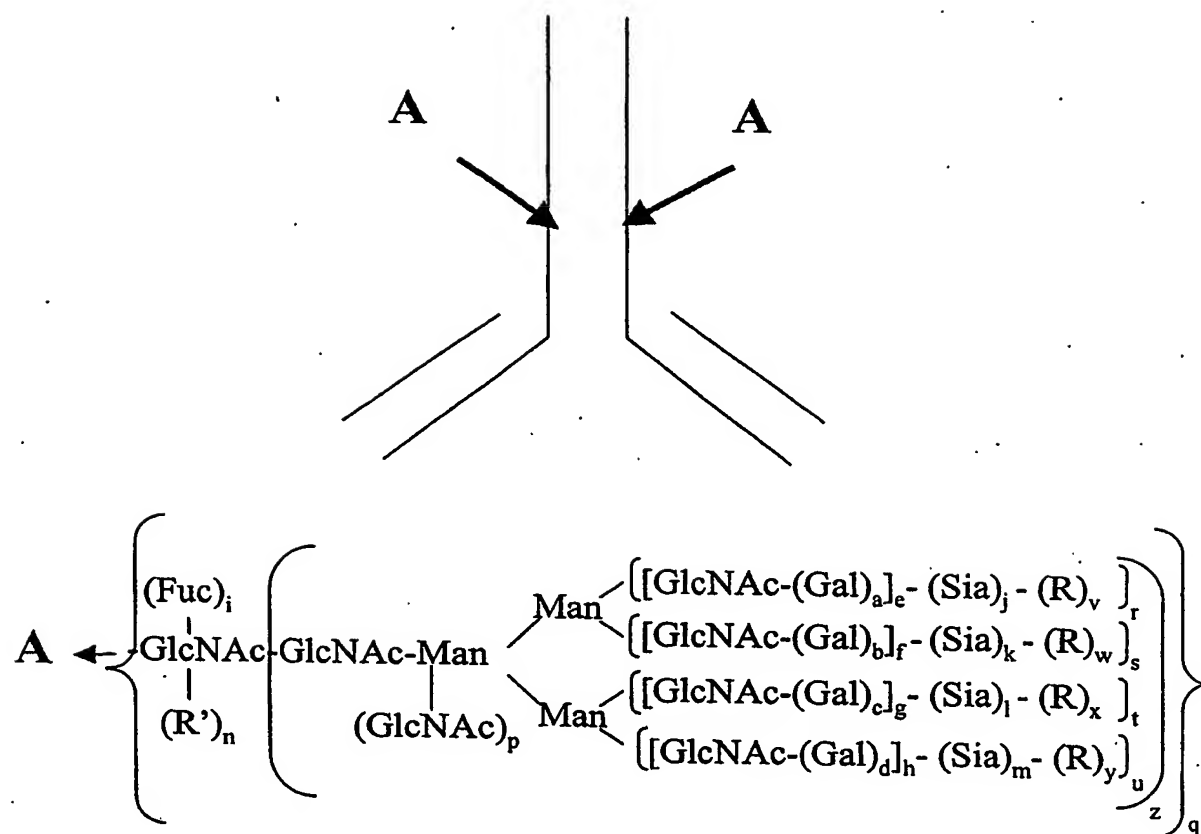
↓ 3.. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 49D

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a-d, i, p-u, (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1;

R = polymer, toxin, radioisotope-complex, drug, mannose, oligo-mannose.

R' = H, glycosyl residue, modifying group, glycoconjugate.

FIG. 50A

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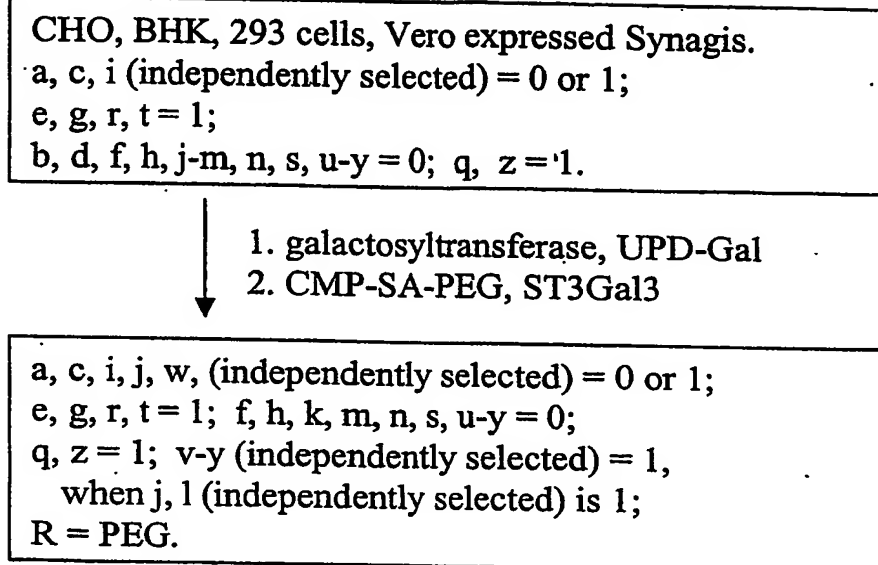


FIG. 50B

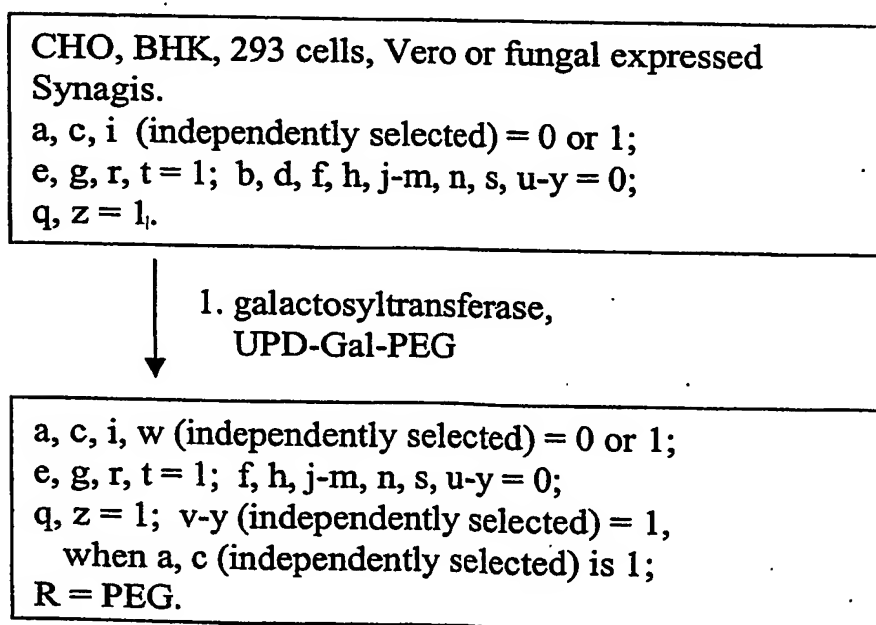


FIG. 50C

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Fungi expressed Synagis.

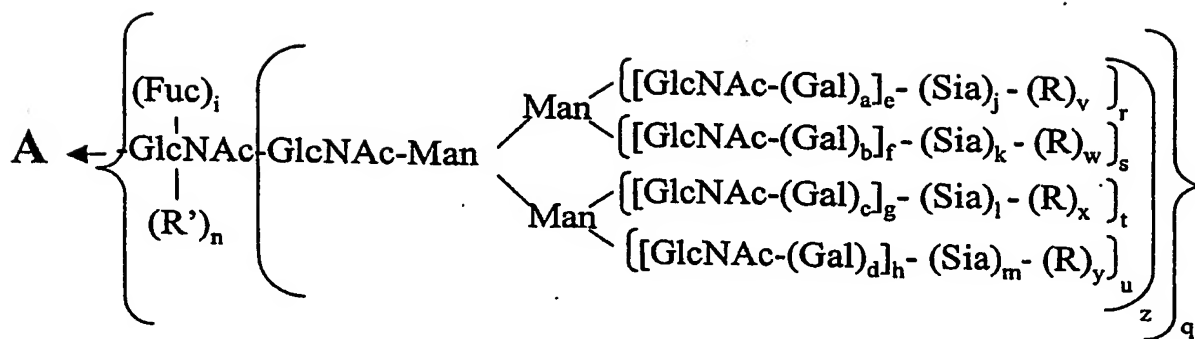
e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-PEG, ST3Gal3

a-m, r-z= 0; q, n = 1; R' = -Gal-Sia-PEG.

FIG. 50D



**R' = H, glycosyl residue, modifying group, glycoconjugate.**

**FIG. 51A**

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CHO, BHK, 293 cells, Vero expressed Remicade.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.

- ↓
1. galactosyltransferase, UPD-Gal
  2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when j, l (independently selected) is 1;  
 R = PEG.

FIG. 51B

CHO, BHK, 293 cells, Vero or fungal expressed Remicade.  
 a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
 q, z = 1.

- ↓
1. galactosyltransferase,  
UPD-Gal-PEG

a, c, i (independently selected) = 0 or 1;  
 e, g, r, t = 1; f, h, j-m, n, s, u-y = 0;  
 q, z = 1; v-y (independently selected) = 1,  
 when a, c (independently selected) is 1;  
 R = PEG.

FIG. 51C

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Fungi expressed Remicade.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - 3.. CMP-SA-radioisotope complex, ST3Gal3

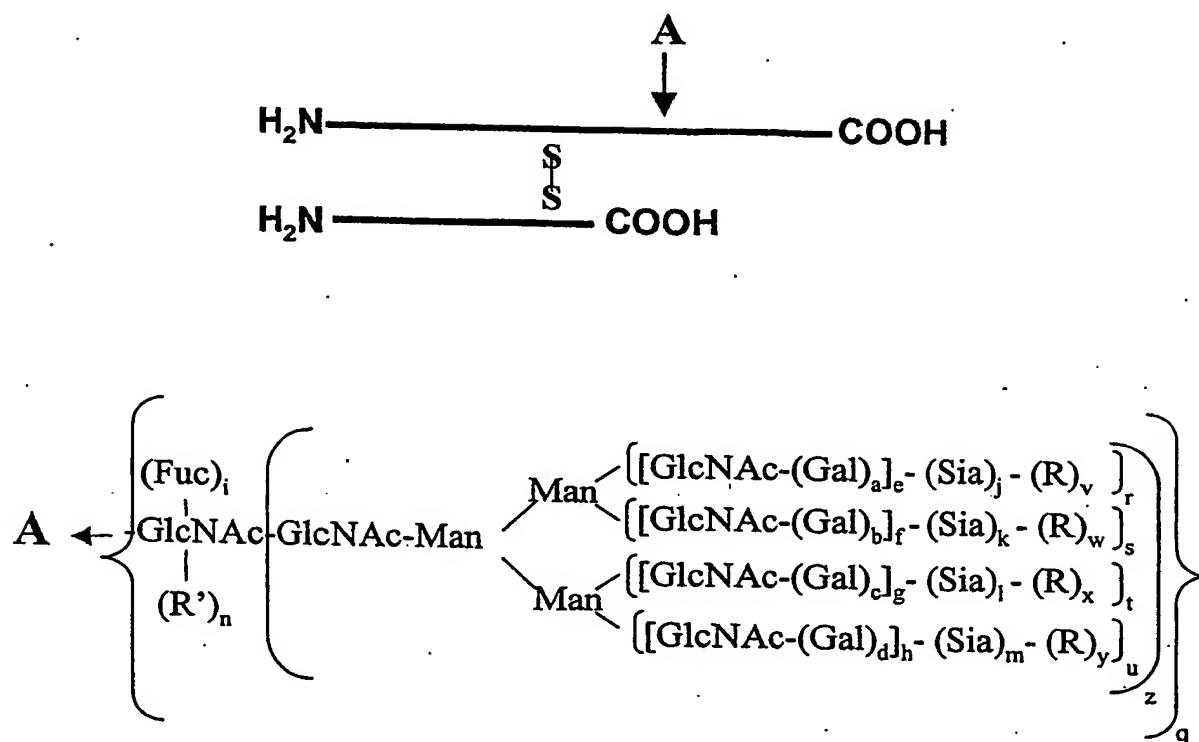
a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 51D



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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

$j$ -m (independently selected) = 0 or 1.

$$n, v-y=0; z=0 \text{ or } 1;$$

R = modifying group, mannose, oligo-mannose;

R' = H, glycosyl residue, modifying group, glycoconjugate.

**FIG. 52A**

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CHO, BHK, 293 cells, Vero expressed Reopro.  
a-m, r-u (independently selected) = 0 or 1;  
n = 0; v-y = 0; z = 1.

- ↓
1. Sialidase
  2. CMP-SA-PEG, ST3Gal3

a-m, r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
n = 0; R = PEG; z = 1.

FIG. 52B

Insect cell expressed Reopro.  
a-h, j-n, s-y = 0; i, r (independently selected) = 0 or 1;  
z = 1.

- ↓
1. GNT's 1&2, UDP-GlcNAc-PEG

a-d, f, h, j-n, s, u, w, y = 0;  
e, g, i, r, t, v, x (independently selected) = 0 or 1;  
v, x (independently selected) = 1,  
when e, g (independently selected) is 1;  
z = 1; R = PEG.

FIG. 52C

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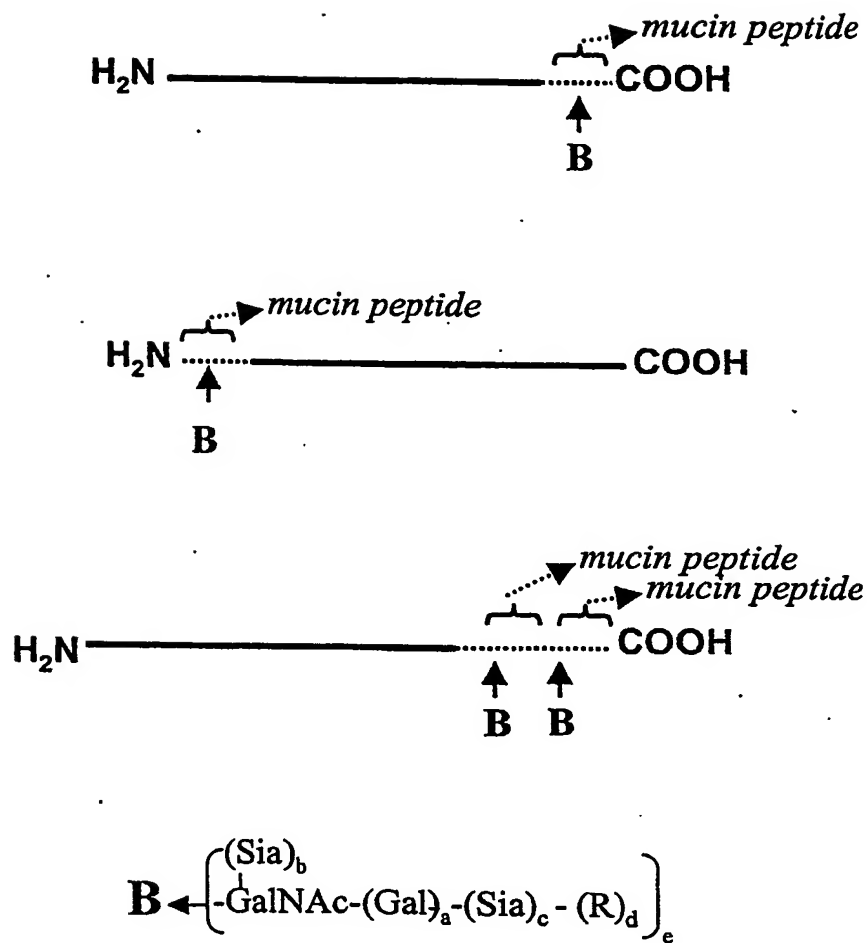
Yeast expressed Reopro.  
a-n = 0; r-y (independently selected) = 0 to 1;  
z = 1;  
R (branched or linear) = Man, oligomannose or  
polysaccharide.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal-PEG

a-m, r-z= 0; n = 1; R' = -Gal-PEG.

FIG. 52D

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**a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer**

**FIG. 52E**

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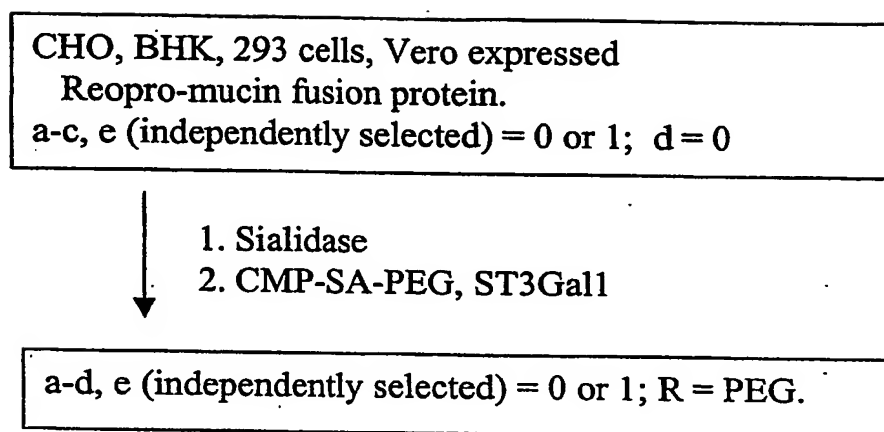


FIG. 52F

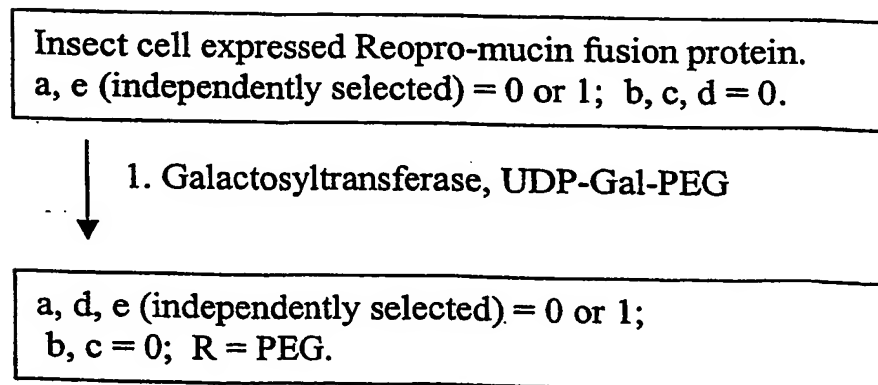


FIG. 52G

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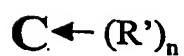
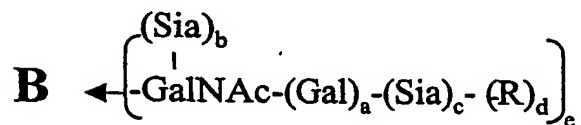
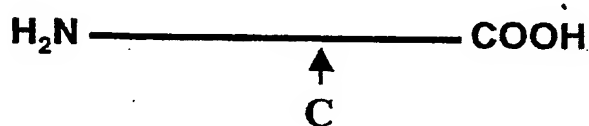
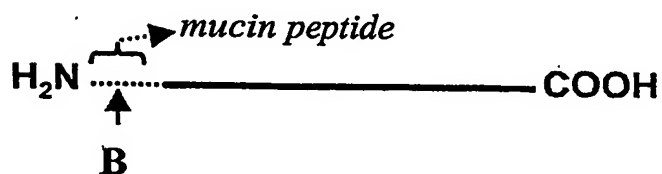
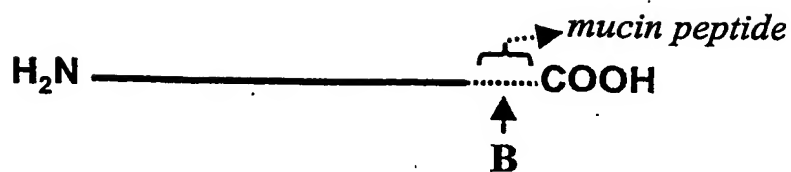
E. coli expressed Reopro-mucin fusion protein.  
a-e = 0.

- ↓
1. GalNAc Transferase, UDP-GalNAc
  2. CMP-SA-PEG, sialyltransferase

c, d, e (independently selected) = 0 or 1;  
a, b = 0; R = PEG.

FIG. 52H

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a-c, e (independently selected) = 0 or 1;  
d = 0; R = polymer, linker.

FIG. 52I

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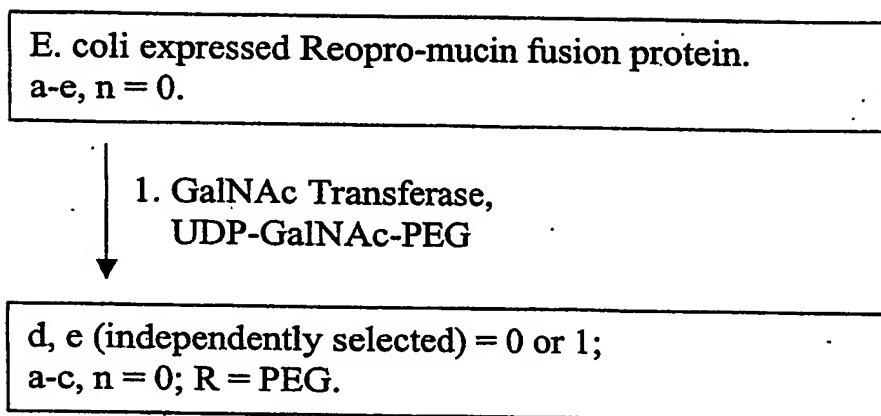


FIG. 52J

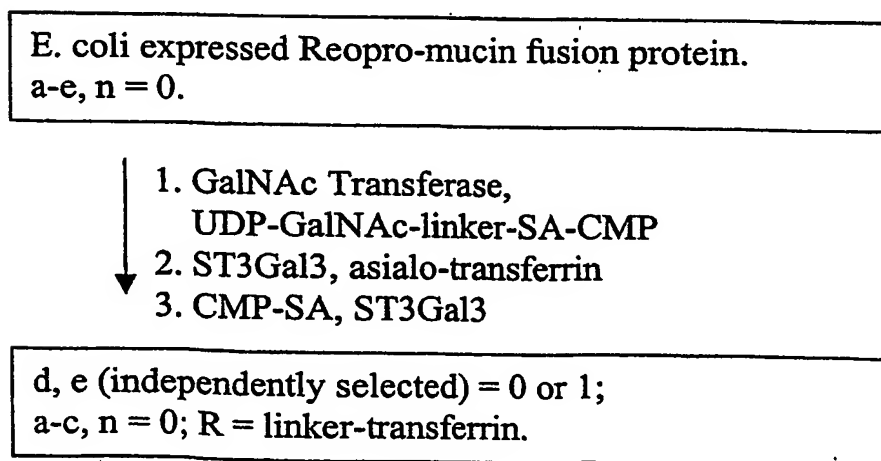


FIG. 52K



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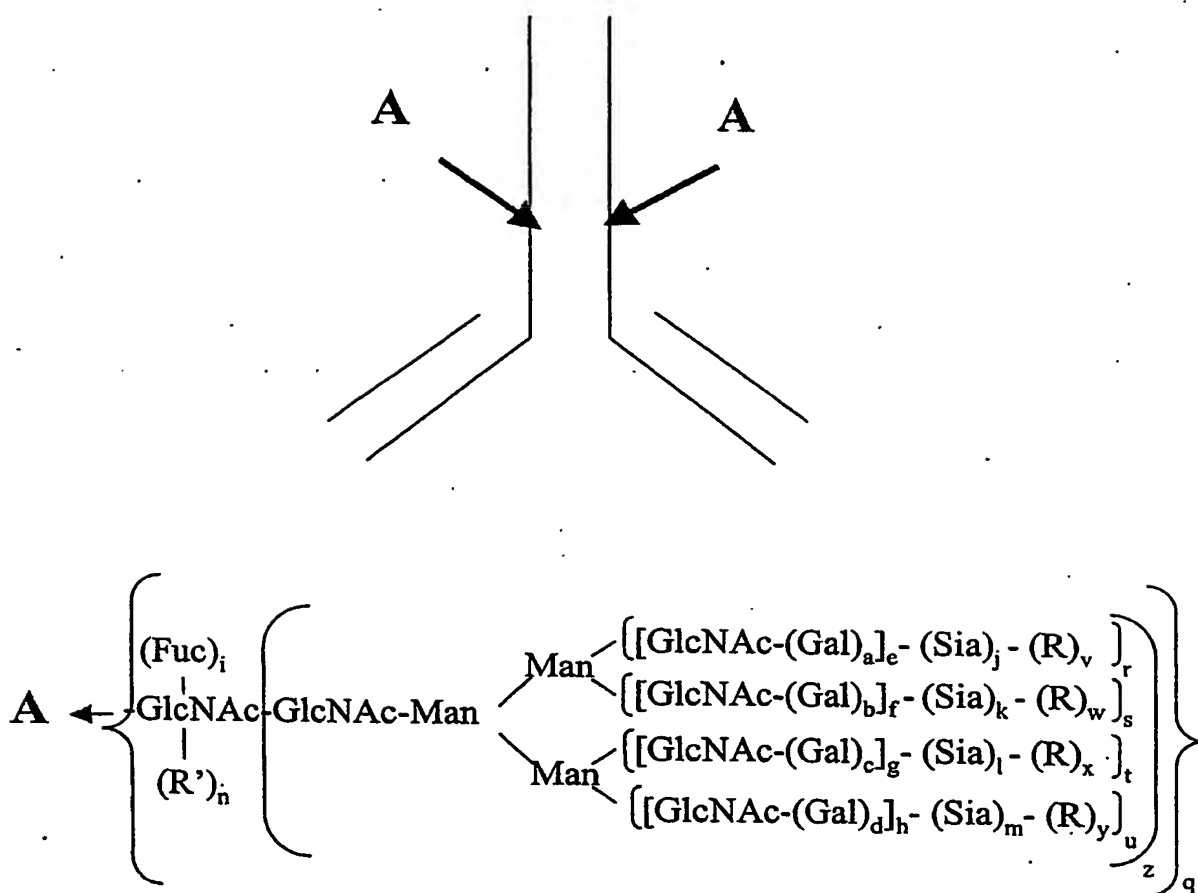
E. coli expressed Reopro(N)—no mucin peptide.  
a-e, n = 0.

- ↓
1. NHS-CO-linker-SA-CMP
  2. ST3Gal3, asialo-transferrin
  3. CMP-SA, ST3Gal3

a-e = 0; n = 1; R' = linker-transferrin.

FIG. 52L

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 or 1.

n, v-y = 0; z = 0 or 1; R = polymer, toxin, radioisotope-complex, drug, glycoconjugate.

R' = H, sugar, glycoconjugate.

z

FIG. 53A

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase, UPD-Gal
2. CMP-SA-toxin, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1;  
f, h, k, m, n, s, u-y = 0; q, z = 1;  
v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = toxin.

FIG. 53B

CHO, BHK, 293 cells, Vero or fungal expressed  
Rituxan.

a, c, e, g, i, r, t (independently selected) = 0 or 1;  
b, d, f, h, j-m, n, s, u-y = 0; q, z = 1.



1. galactosyltransferase,  
UPD-Gal-drug

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, j-m, n, s, u-y = 0; q, z = 1;  
v-y (independently selected) = 1,  
when a, c (independently selected) is 1;  
R = toxin.

FIG. 53C

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Fungi expressed Rituxan.

e, g, i, r, t (independently selected) = 0 or 1;

a-d, f, h, j-m, n, s, u-y = 0; q, z = 1.

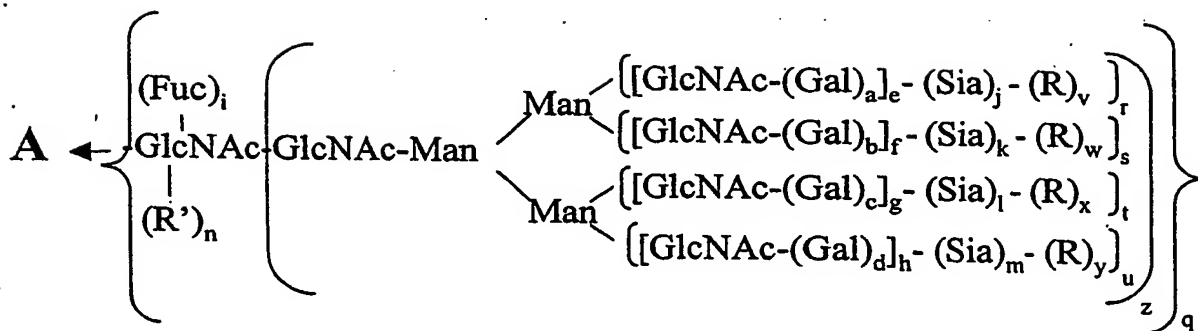
- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal
  - ↓ 3. CMP-SA-radioisotope complex, ST3Gal3

a-m, r-z = 0; q, n = 1;

R' = -Gal-Sia-radioisotope complex.

FIG. 53D

A diagram illustrating the setup for observing interference. Two slits are shown, each with an arrow pointing towards a central point labeled 'A'.



**R' = H, glycosyl residue, modifying group, glycoconjugate.**

**FIG. 53E**

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CHO, BHK, 293 cells, Vero or transgenic animal  
expressed Rituxan.

a, c, i (independently selected) = 0 or 1;  
e, g, r, t = 1; b, d, f, h, j-m, n, s, u-y = 0;  
q, z = 1.



1. galactosyltransferase, UDP-Gal
2. CMP-SA-PEG, ST3Gal3

a, c, i, j, l (independently selected) = 0 or 1;  
e, g, r, t = 1; f, h, k, m, n, s, u-y = 0;  
q, z = 1; v-y (independently selected) = 1,  
when j, l (independently selected) is 1;  
R = PEG.

FIG. 53F

Fungi, yeast or CHO expressed Rituxan.

e, g, i, r, t, v, x (independently selected) = 0 or 1;  
a-d, f, h, j-m, n, s, u, w, y = 0; q, z = 1;

R (independently selected) = mannose, oligomannose,  
polymannose.

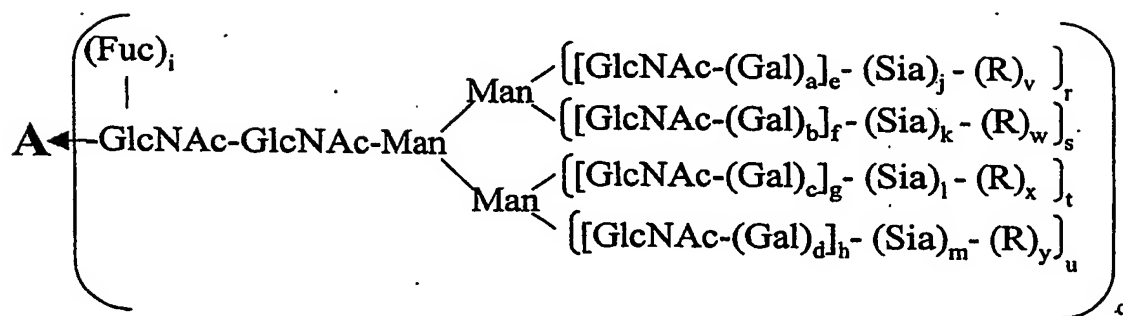
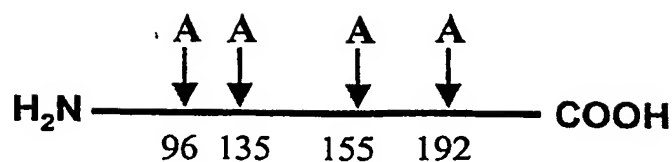


1. mannosidases (alpha and beta)
2. GNT-I,II, UDP-GlcNAc
3. Galactosyltransferase, UDP-Gal-radioisotope

a-m, r-z = 0; q, n = 1;  
R' = -Gal-radioisotope complex.

FIG. 53G

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a-d, i, q-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0; R = mannose, polymer.

FIG. 54A

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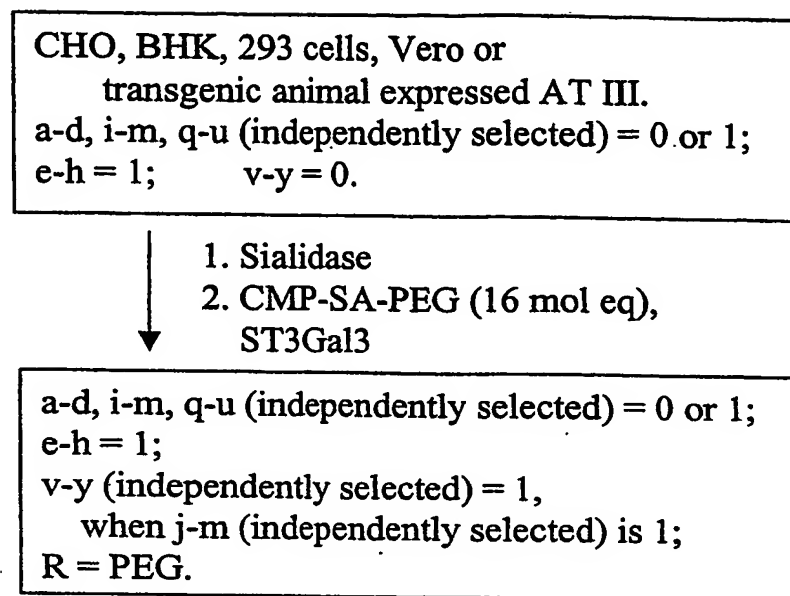


FIG. 54B

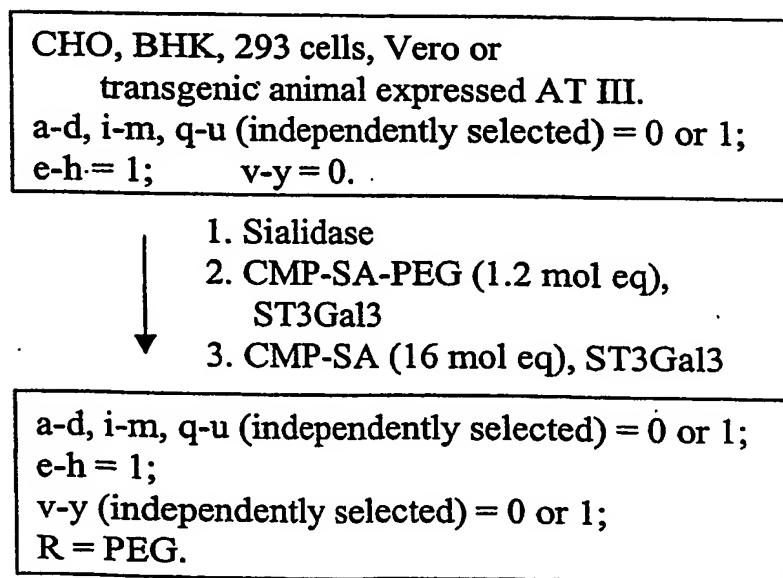


FIG. 54C



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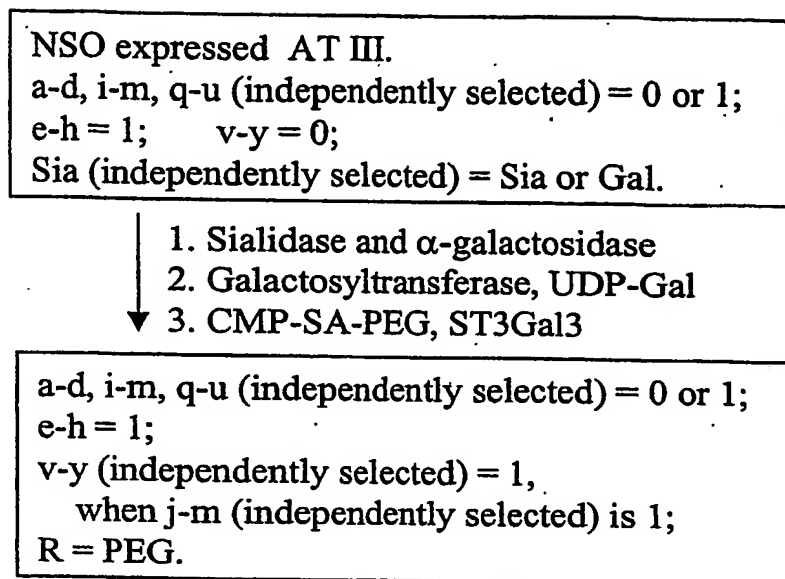


FIG. 54D

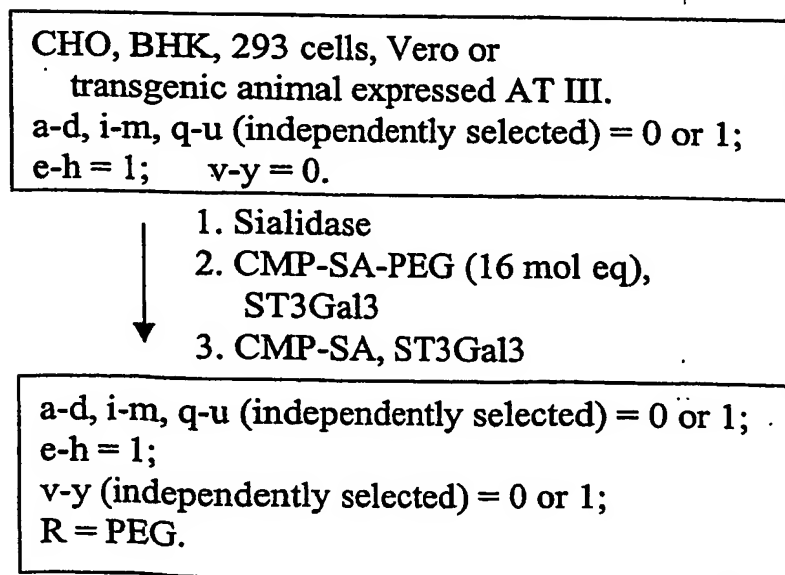


FIG. 54E

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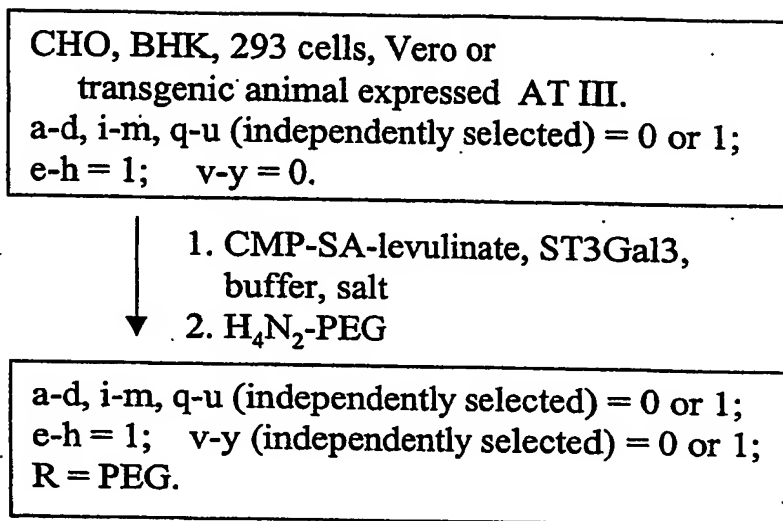


FIG. 54F

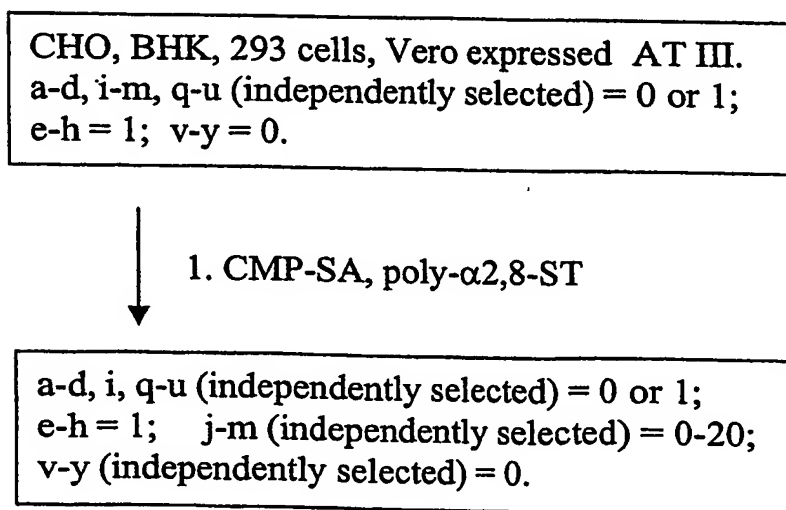
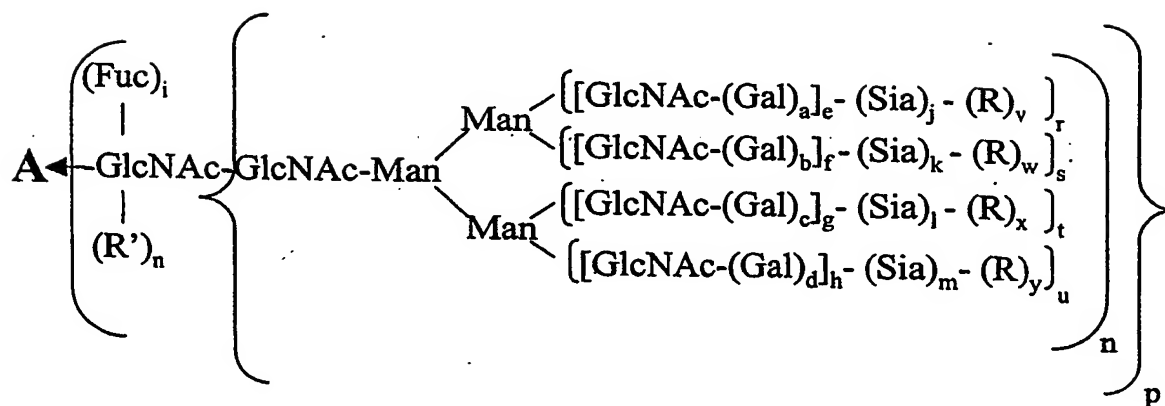
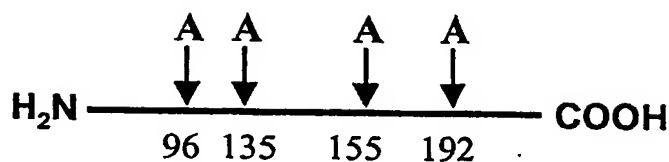


FIG. 54G

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a-d, i, p-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100.

R = polymer, linker, mannose.

R' = H, sugar, glycoconjugate.

FIG. 54H

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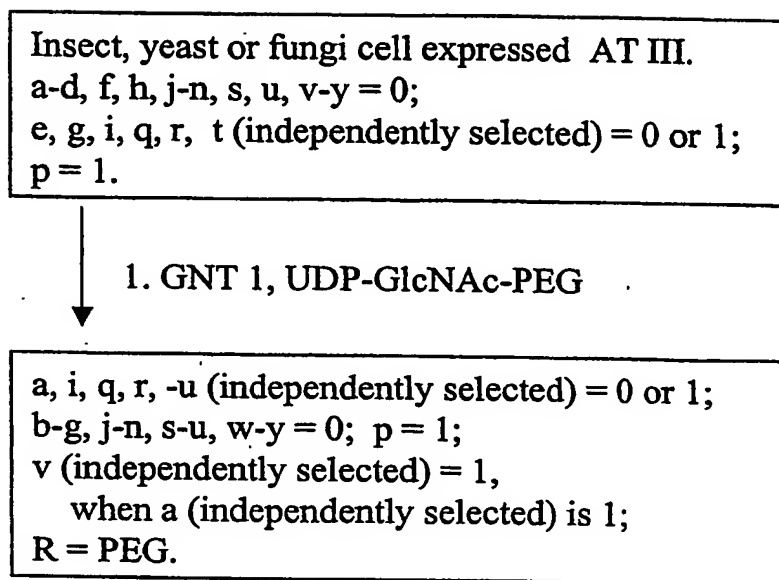


FIG. 54I

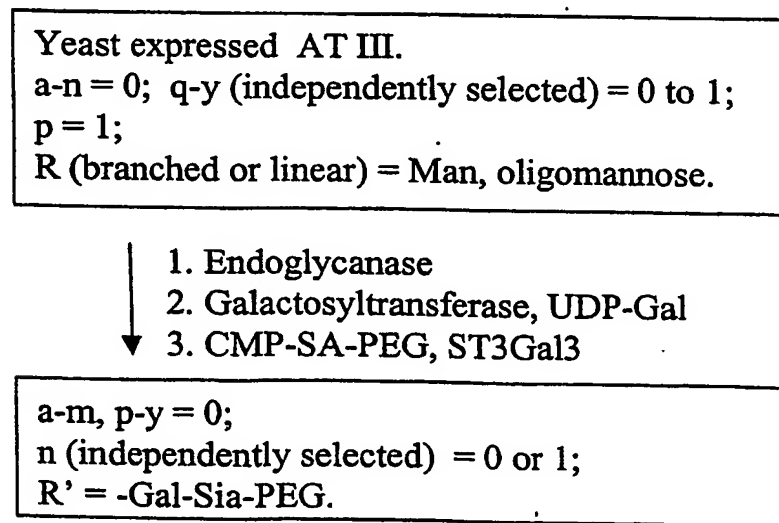


FIG. 54J

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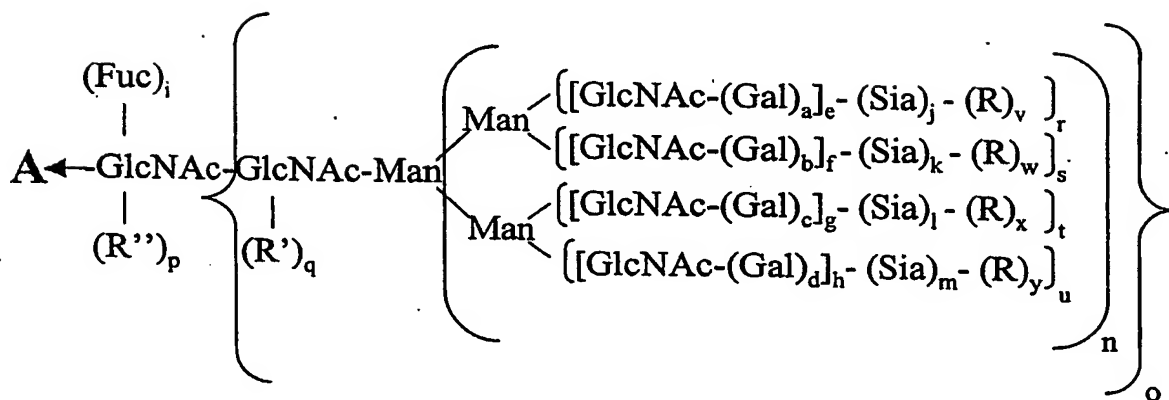
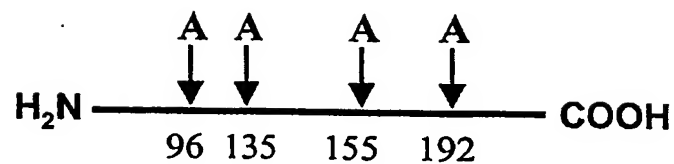
CHO, BHK, 293 cells, Vero expressed AT III.  
a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y = 0.

- ↓
1. CMP-SA-linker-Gal-UDP,  
ST3Gal3
  2. Galactosyltransferase, transferrin  
treated with endoglycanase

a-m, q-u (independently selected) = 0 or 1;  
p = 1; n = 0;  
v-y (independently selected) = 0 or 1;  
R = linker-transferrin.

FIG. 54K

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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

R = polymer.

R', R'' (independently selected) = sugar, glycoconjugate.

FIG. 54L

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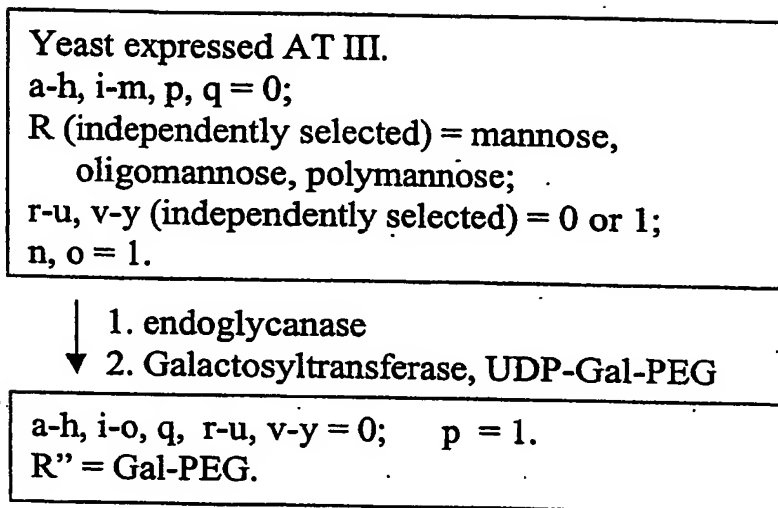


FIG. 54M

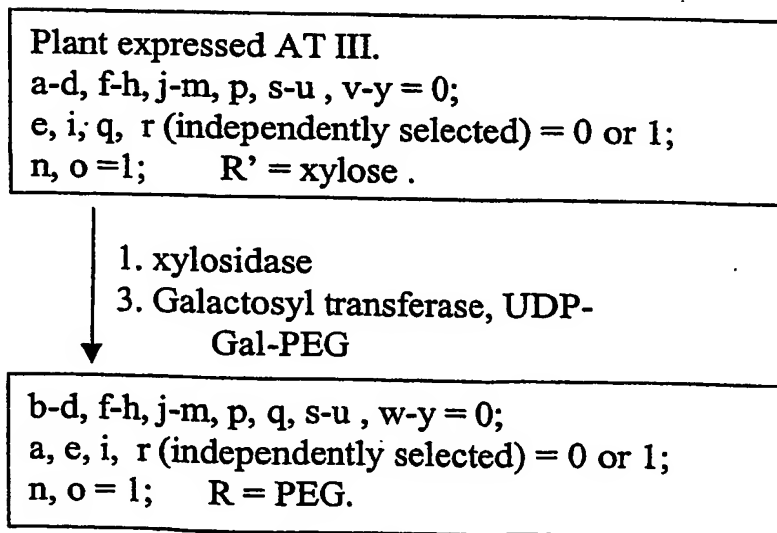


FIG. 54N

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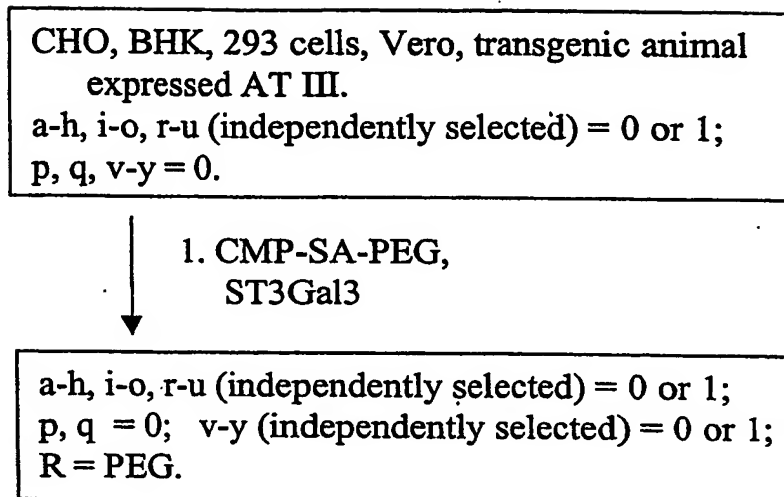
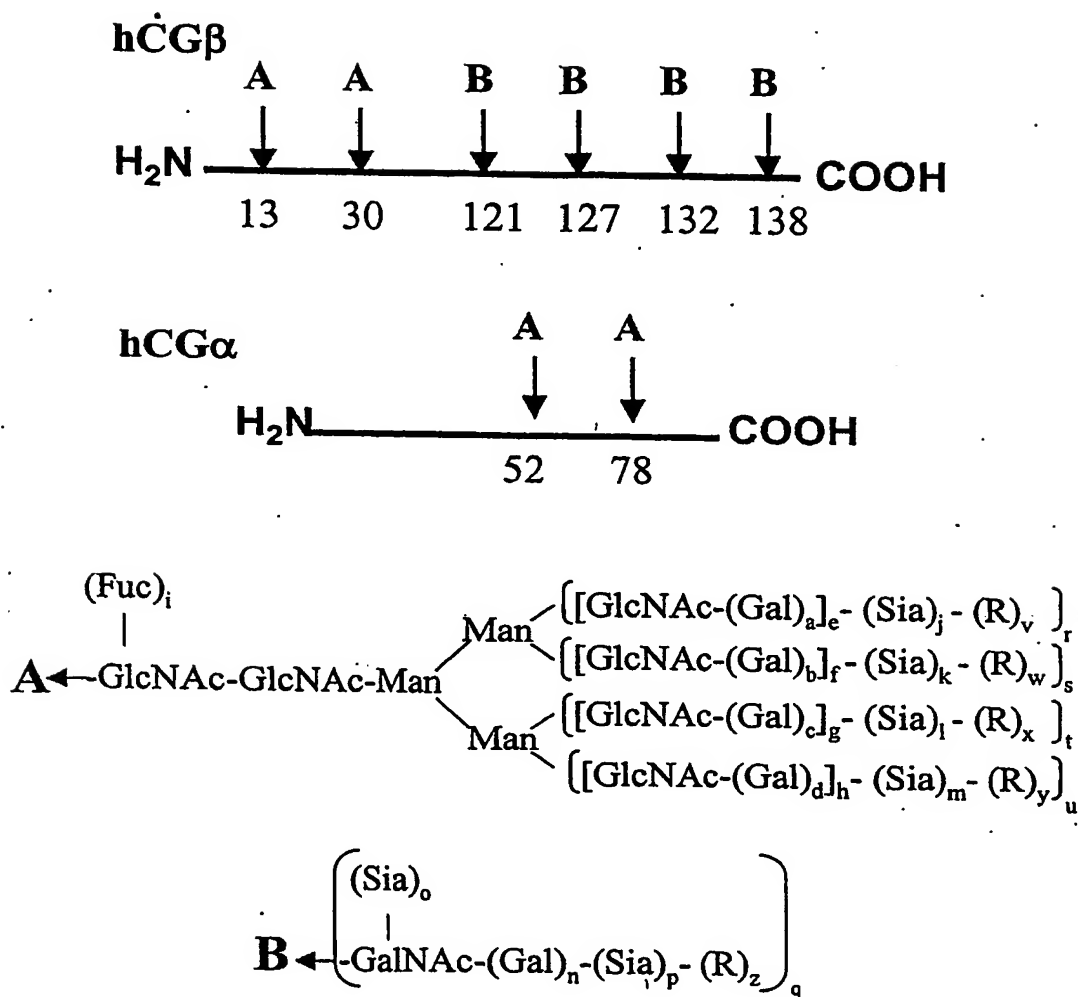


FIG. 540



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a-d, i, n-u (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 4.

j-m (independently selected) = 0 to 20.

v-z = 0; R = polymer

FIG. 55A

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CHO, BHK, 293 cells, insect cell, Vero  
expressed hCG  
a-g, n, q = 1; h = 1 to 3; j-m, i, o, p  
(independently selected) = 0 or 1; r-u  
(independently selected) = 0 to 1; v-z = 0

- ↓ 1. Sialidase  
2. CMP-SA-PEG, ST3Gal3

a-g, n, q = 1; h = 1 to 3; i, o, p (independently  
selected) = 0 or 1; r-u (independently selected)  
= 0 or 1; j-m, v-y (independently selected) = 0  
or 1; R = PEG; z = 0.

FIG. 55B

Insect cell, yeast, fungi expressed hCG  
a-d, f, h, j-m, o, p, s, u, v-z = 0;  
e, g, i, n, q, r, t (independently selected)  
= 0 or 1.

- ↓ 1. GNT's 1&2, UDP-GlcNAc  
2. Galactosyltransferase, UDP-Gal  
2. CMP-SA-PEG, ST3Gal3

b, d, f, h, k, m, o, p, s, u, w, y, z = 0;  
a, c, e, g, i, n, q, r, t (independently selected)  
= 0 or 1;  
j, l, v, x (independently selected) = 0 or 1;  
R = PEG.

FIG. 55C

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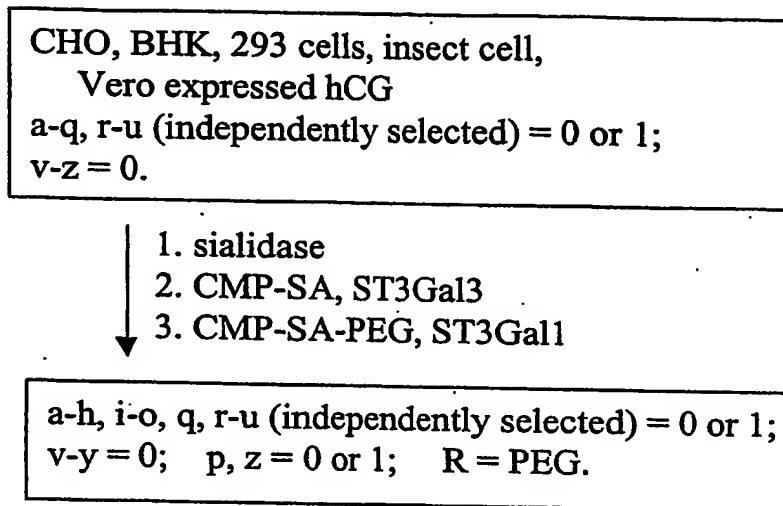


FIG. 55D

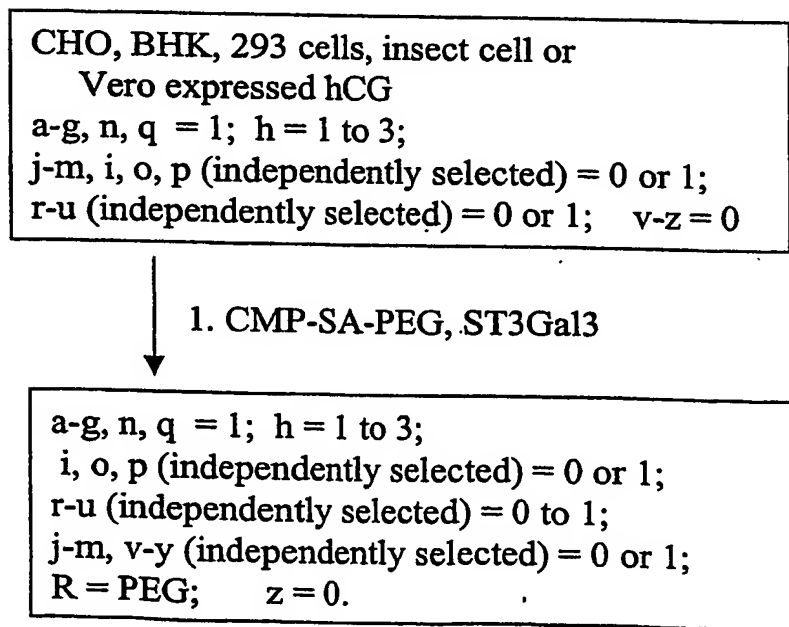


FIG. 55E

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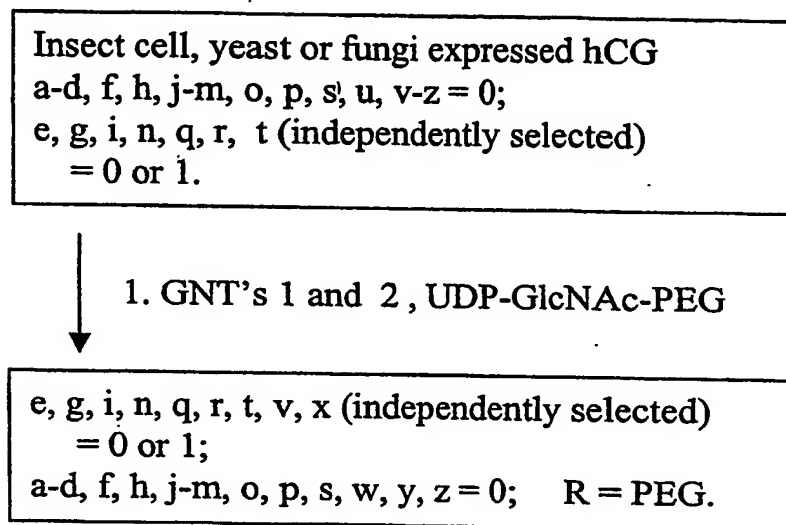


FIG. 55F

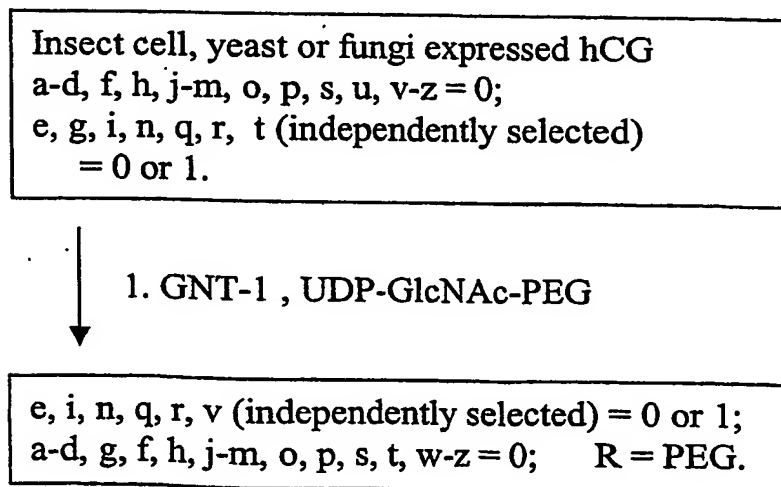


FIG. 55G

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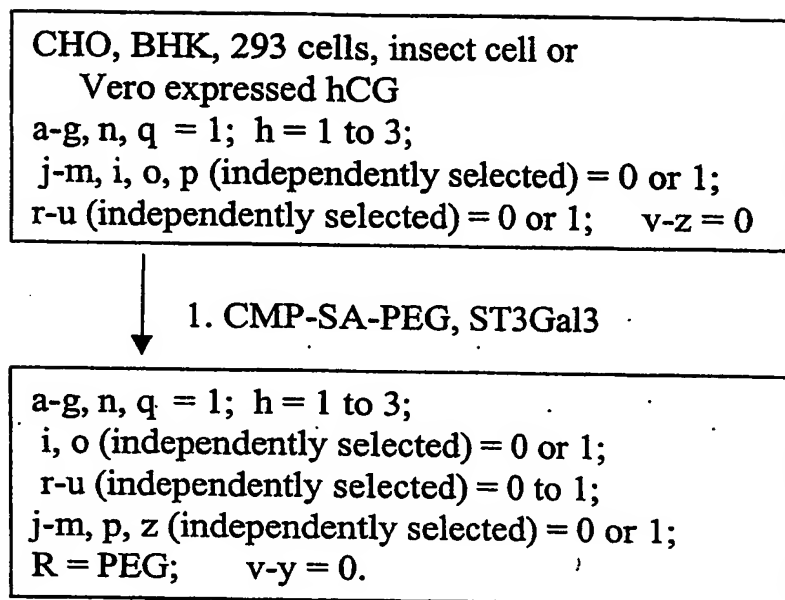


FIG. 55H

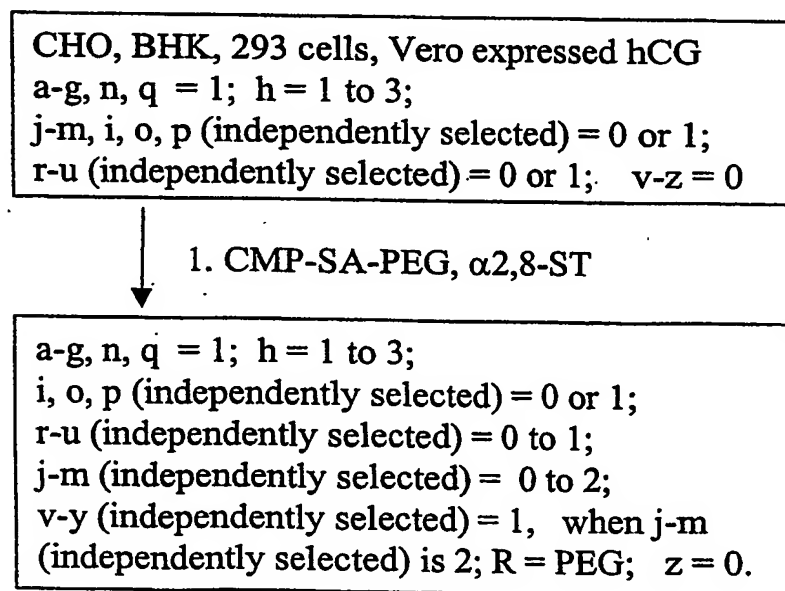


FIG. 55I

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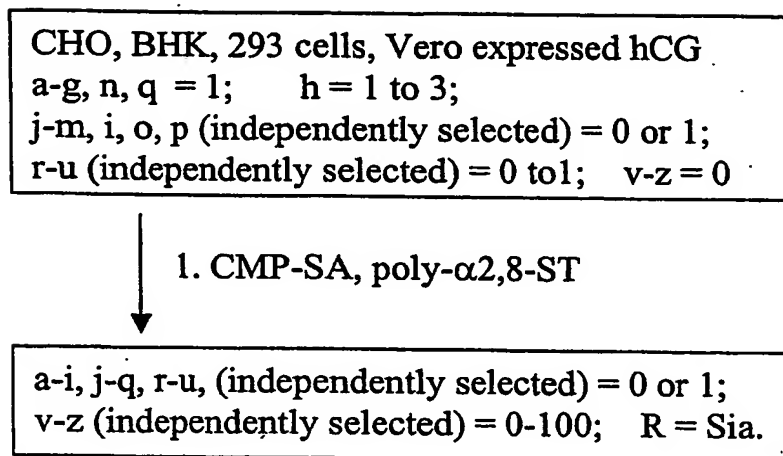
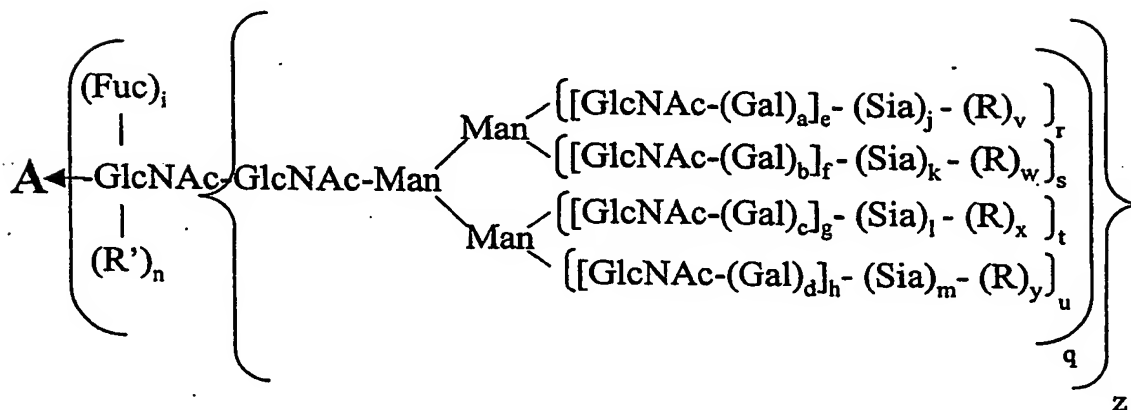
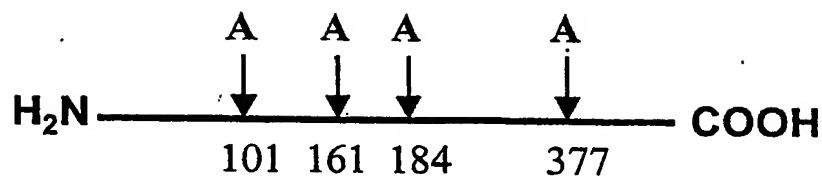


FIG. 55J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 56A

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CHO, BHK, 293 cells, insect cells, Vero expressed and secreted alpha-galactosidase  
 a-h, i-m, q-u (independently selected) = 0 or 1;  
 z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Endo-H
  2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
 n, v-y = 0; z = 1; and when z = 0 and q = 1,  
 then n (independently selected) = 0 or 1;  
 R' = Gal-PEG-transferrin.

FIG. 56B

CHO, BHK, 293 cells, Insect cells,  
 Vero expressed and secreted alpha-galactosidase  
 a-h, i-m, q-u (independently selected) = 0 or 1; z = 1; n, v-y = 0; and when a-n = 0, then r-u (independently selected) = 0 or 1; v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-linker-Mannose-6-phosphate  
ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1;  
 n = 0; z = 1; R = mannose-6-phosphate; and when a-n = 0, then r-u (independently selected) = 0 or 1;  
 v-y (independently selected) = 0-100;  
 R = mannose or mannose with mannose-6-phosphate.

FIG. 56C



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NSO expressed alpha-galactosidase.

a-d, i-m, q-u (independently selected) = 0 or 1;

e-h = 1; v-y = 0;

Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  3. CMP-SA-linker-mannose-6-phosphate  
sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
v-y (independently selected) = 1, when j-m (independently  
selected) is 1; R = mannose-6 phosphate

FIG. 56D

CHO, BHK, 293 cells, Insect cells, Vero expressed and  
secreted alpha-galactosidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;

n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;

R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0; z  
= 1; R = PEG; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y = 0-100; R = mannose or mannose  
with mannose-6-phosphate.

FIG. 56E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate;  
v-y (independently selected) = 0 or 1;  
R = mannose-linker-ApoE.

FIG. 56F

CHO, BHK, 293 cells, Insect cells, Vero, yeast,  
fungi expressed alpha-galactosidase.  
a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;  
r-u (independently selected) = 0 or 1;  
j-m (independently selected) = 0-100;  
Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;  
R' = galactose-linker-alpha2-macroglobulin.

FIG. 56G

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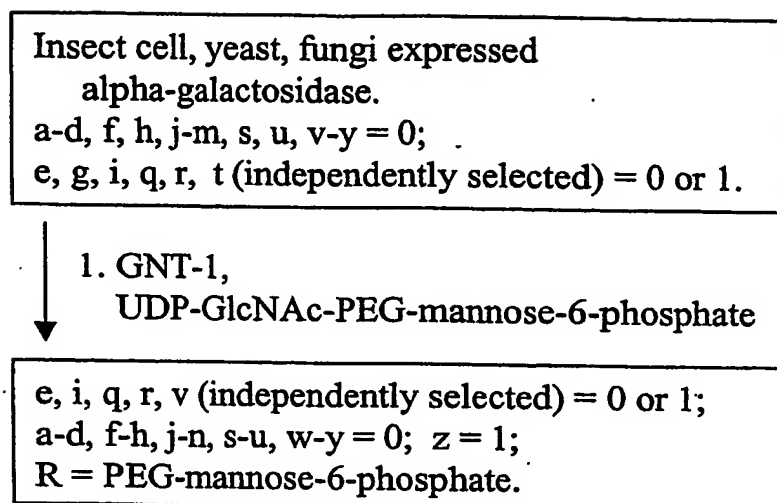


FIG. 56H

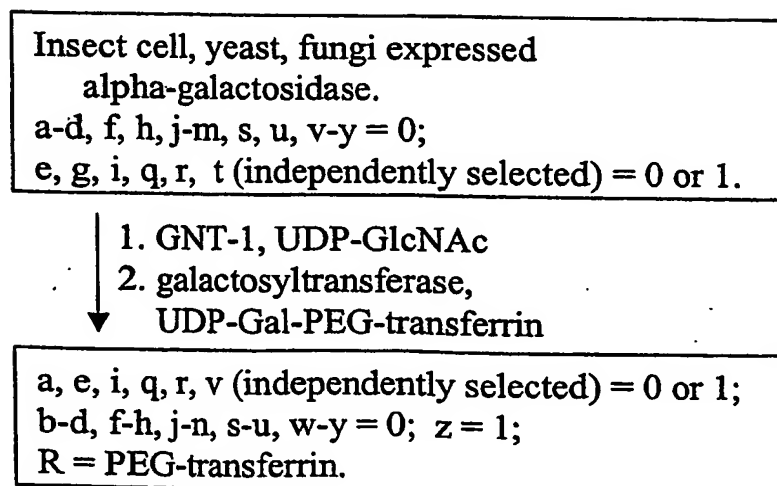


FIG. 56I

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Insect cell, yeast, fungi expressed  
alpha-galactosidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

- ↓
1. GNT-1 and 2, UDP-GlcNAc
  2. galactosyltransferase, UDP-Gal
  3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

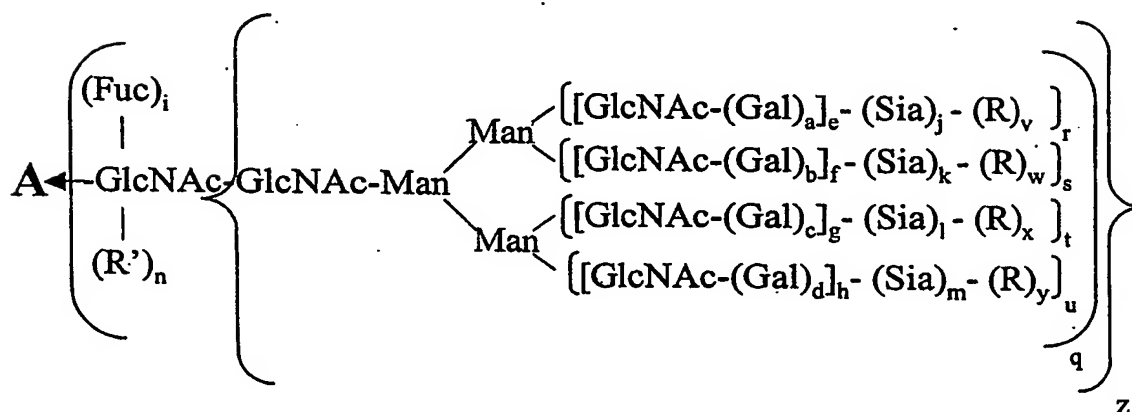
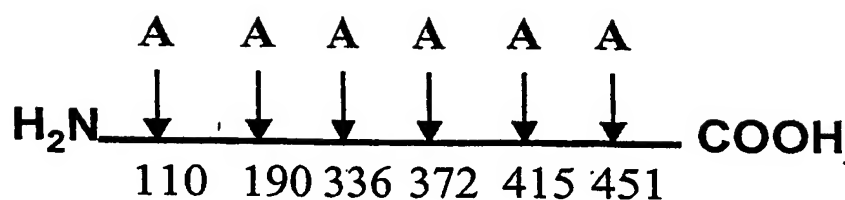
a, c, e, g, i, j, l, q, r, t, v, x (independently  
selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0;

z = 1; R = PEG-melanotransferrin.

FIG. 56J

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a-d, i, n, q-u, z (independently selected) = 0 or 1.

e-h (independently selected) = 0 to 6.

j-m (independently selected) = 0 to 100.

v-y = 0 to 100;

R = mannose, mannose-6-phosphate and mannose, polymer.

FIG. 57A

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CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Endo-H  
↓  
2. Galactosyltransferase, UDP-Gal-PEG-transferrin

a-h, i-m, q-u (independently selected) = 0 or 1;  
n, v-y = 0; z = 1; and when z = 0 and q = 1, then n  
(independently selected) = 0 or 1; R' = Gal-PEG-transferrin.

FIG. 57B

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase  
a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓  
1. Sialidase  
↓  
2. CMP-SA-linker-Mannose-6-phosphate ST3Gal3

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = mannose-6-phosphate; and when a-n = 0,  
then r-u (independently selected) = 0 or 1;  
v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57C

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NSO expressed alpha-iduronidase.

a-d, i-m, q-u (independently selected) = 0 or 1; e-h = 1;  
v-y = 0; Sia (independently selected) = Sia or Gal.

- ↓
1. Sialidase and  $\alpha$ -galactosidase
  2. Galactosyltransferase, UDP-Gal
  - ↓ 3. CMP-SA-linker-mannose-6-phosphate sialyltransferase

a-d, i-m, q-u (independently selected) = 0 or 1;  
e-h = 1; v-y (independently selected) = 1,  
when j-m (independently selected) is 1;  
R = mannose-6 phosphate

FIG. 57D

CHO, BHK, 293 cells, Insect cells, Vero expressed  
and secreted alpha-iduronidase

a-h, i-m, q-u (independently selected) = 0 or 1; z = 1;  
n, v-y = 0; and when a-n = 0, then r-u (independently  
selected) = 0 or 1; v-y (independently selected) = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

- ↓
1. Sialidase
  2. CMP-SA-PEG, sialyltransferase

a-h, i-m, q-u, v-y (independently selected) = 0 or 1; n = 0;  
z = 1; R = PEG; and when a-n = 0, then r-u  
(independently selected) = 0 or 1; v-y = 0-100;  
R = mannose or mannose with mannose-6-phosphate.

FIG. 57E

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CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.

a-i, v-y = 0; q (independently selected) = 0 or 1; z = 1;

r-u (independently selected) = 0 or 1;

j-m (independently selected) = 0-100;

Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. mannosyltransferase,  
GDP-mannose-linker-ApoE

a-i = 0; q (independently selected) = 0 or 1; z = 1;

r-u (independently selected) = 0 or 1; j-m (independently  
selected) = 0-100;

Sia = mannose or mannose with mannose-6-phosphate;

v-y (independently selected) = 0 or 1;

R = mannose-linker-ApoE.

FIG. 57F

CHO, BHK, 293 cells, Insect cells, Vero, yeast, fungi  
expressed alpha-iduronidase.

a-i, v-y = 0; q (independently selected) = 0 or 1;

z = 1; r-u (independently selected) = 0 or 1;

j-m (independently selected) = 0-100;

Sia = mannose or mannose with mannose-6-phosphate.

↓ 1. endo-H  
2. galactosyltransferase,  
UDP-Gal-linker-alpha2-macroglobulin

a-m, r-z = 0; n, q (independently selected) = 0 or 1;

R' = galactose-linker-alpha2-macroglobulin.

FIG. 57G



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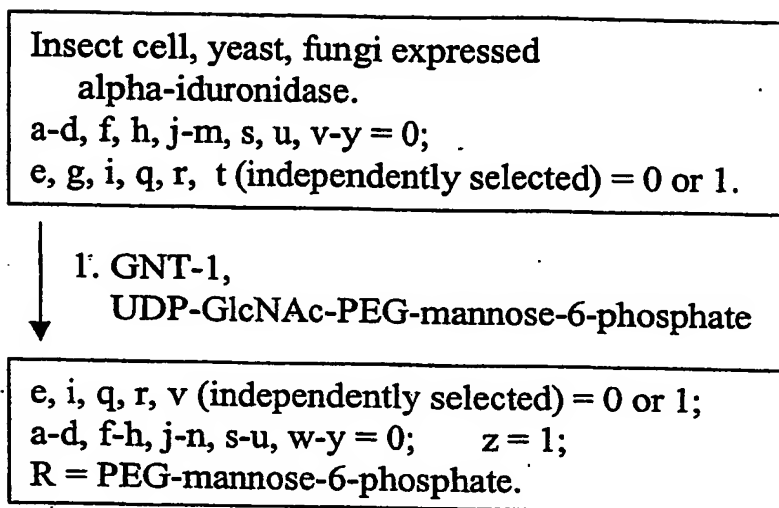


FIG. 57H

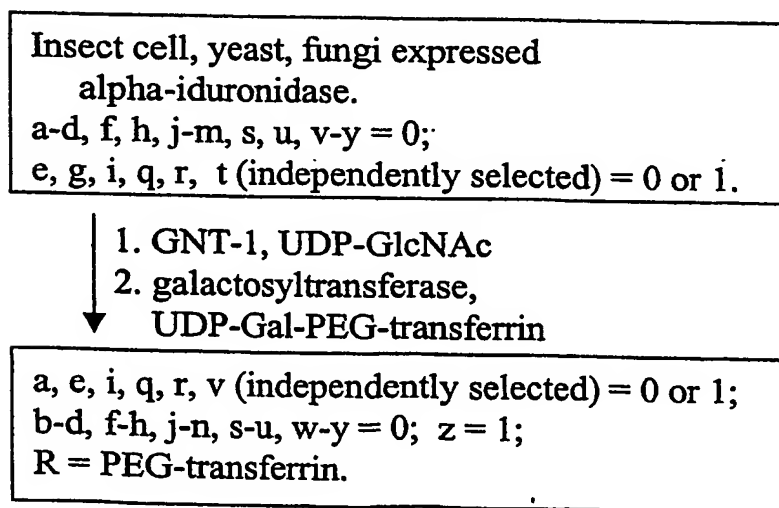


FIG. 57I

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Insect cell, yeast, fungi expressed  
alpha-iduronidase.

a-d, f, h, j-m, s, u, v-y = 0;

e, g, i, q, r, t (independently selected) = 0 or 1.

1. GNT-1 and 2, UDP-GlcNAc

2. galactosyltransferase, UDP-Gal

↓ 3. sialyltransferase,  
CMP-SA-PEG-melanotransferrin

a, c, e, g, i, j, l, q, r, t, v, x

(independently selected) = 0 or 1;

b, d, f, h, k, m, n, s, u, w, y = 0; z = 1;

R = PEG-melanotransferrin.

FIG. 57J

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FIG. 58A

ACCCCCCTGGGCCCCTGCCAGCTCCCTGCCCCAGAGCTTCCTGCTCAAT  
GCTTAGAGCAAGTGAGGAAGATCCAGGGCGATGGCGCAGCGCTCCAG  
GAGAAGCTGTGTGCCACCTACAAGCTGTGCCACCCCGAGGAGCTGGT  
GCTGCTCGGACACTCTCTGGGCATCCCCTGGGCTCCCCTGAGCAGCTG  
CCCCAGCCAGGCCCTGCAGCTGGCAGGCTGCTTGAGCCAACTCCATA  
GCGGCCTTTTCCTCTACCAGGGGCTCCTGCAGGCCCTGGAAGGGATCT  
CCCCCGAGTTGGGTCCCACCTTGGACACACTGCAGCTGGACGTCGCCG  
ACTTTGCCACCACCATCTGGCAGCAGATGGAAGAACTGGGAATGGCC  
CCTGCCCTGCAGCCCACCCAGGGTGCCATGCCGGCCTTCGCCTCTGCT  
TTCCAGCGCCGGGCAGGAGGGGTCTGGTTGCCTCCCATCTGCAGAG  
CTTCTGAGGTGTCGTACCGCGTTCTACGCCACCTTGCCCAGCCCTG  
A

FIG. 58B

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu  
Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys Leu Cys Ala Thr  
Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro  
Trp Ala Pro Leu Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser  
Gln Leu His Ser Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile  
Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe  
Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu Gln Pro  
Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val  
Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu Arg His  
Leu Ala Gln Pro

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FIG. 59A

GCGCCTCTTATGTACCCACAAAAATCTATTTTCAAAAAAGTTGCTCTA  
AGAATATAGTTATCAAGTTAAGTAAAAATGTCAATAGCCTTTTAATTTA  
ATTTTAAATTGTTTTATCATTCTTTGCAATAATAAAACATTAACTTTAT  
ACTTTTTAATTTAATGTATAGAATAGAGATATACATAGGATATGTAAA  
TAGATACACAGTGTATATGTGATTAAAAATATAATGGGAGATTCAATC  
AGAAAAAAGTTTCTAAAAAGGCTCTGGGGTAAAAGAGGAAGGAAAC  
AATAATGAAAAAAATGTGGTGAGAAAAACAGCTGAAAACCCATGTA  
AAGAGTGTATAAAGAAAGCAAAAAGAGAAGTAGAAAGTAACACAGG  
GGCATTGTGAAAATGTAAACGAGTATGTTCCCTATTTAAGGCTAGGC  
ACAAAGCAAGGTCTTCAGAGAACCTGGAGCCTAAGGTTTAGGCTCAC  
CCATTTCACACAGTCTAGCAGCATCTGCAACATCTACAATGGCCTTGA  
CCTTTGCTTTACTGGTGGCCCTCCTGGTGCTCAGCTGCAAGTCAAGCT  
GCTCTGTGGGCTGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGG  
AGGACCTTGATGCTCCTGGCACAGATGAGGAGAATCTCTCTTTTCTCC  
TGCTTGAAGGACAGACATGACTTTGGATTTCCTCCAGGAGGAGTTTGG  
CAACCAGTTCCAAAAGGCTGAAACCATCCCTGTCCTCCATGAGATGA  
TCCAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTT  
GGGATGAGACCCTCCTAGACAAATTCTACACTGAACTCTACCAGCAG  
CTGAATGACCTGGAAGCCTGTGTGATACAGGGGGTGGGGGTGACAGA  
GACTCCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGGAAATACT  
TCCAAAGAATCACTCTCTATCTGAAAGAGAAGAAATACAGCCCTTGT  
GCCTGGGAGGTTGTCAGAGCAGAAATCATGAGATCTTTTTTCTTTGTCA  
ACAAACTTGCAAGAAAGTTTAAGAAGTAAGGAATGAAAACCTGGTTCA  
ACATGGAAATGATTTTTCATTGATTTCGTATGCCAGCTCACCTTTTTATG  
ATCTGCCATTTCAAAGACTCATGTTTCTGCTATGACCATGACACGATT  
TAAATCTTTTCAAATGTTTTTAGGAGTATTAATCAACATTGTATTAG  
CTCTTAAGGCACTAGTCCCTTACAGAGGACCATGCTGACTGATCCATT  
ATCTATTTAAATATTTTTTAAAATATTATTTATTTAACTATTTATAAAC  
AACTTATTTTTGTTTCATATTATGTCATGTGCACCTTTGCACAGTGGTTA  
ATGTAATAAAATGTGTTCTTTGTATTTGGTAAATTTATTTTGTGTTGTT  
CATTGAACTTTTGCTATGGAACCTTTGTAAGTTTATTCTTTAAAATG  
AAATTCCAAGCCTAATTGTGCAACCTGATTACAGAATAACTGGTACA  
CTTCATTTGTCCATCAATATTATATTCAAGATATAAGTAAAAATAAAC  
TTTCTGTAAACCAAGTTGTATGTTGTACTCAAGATAACAGGGTGAACC  
TAACAAATACAATTCTGCTCTCTTGTGTATTTGATTTTTGTATGAAAA  
AACTAAAAATGGTAATCACTTAATTATCAGTTATGGTAAATGGT  
ATGAAGAGAAGAAGGAACG

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FIG. 59B

Met Ala Leu Thr Phe Ala Leu Leu Val Ala Leu Leu Val Leu Ser Cys Lys Ser  
Ser Cys Ser Val Gly Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr  
Leu Met Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala  
Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr  
Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr Thr Glu  
Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln Gly Val Gly Val  
Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe  
Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val  
Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu  
Arg Ser Lys Glu

FIG. 59C

ATGGCCCTCCTGTTCCCTCTACTGGCAGCCCTAGTGATGACCAGCTAT  
AGCCCTGTTGGATCTCTGGGCTGTGATCTGCCTCAGAACCATGGCCTA  
CTTAGCAGGAACACCTTGGTGCTTCTGCACCAAATGAGGAGAATCTCC  
CCTTTCTTGTGTCTCAAGGACAGAAGAGACTTCAGGTTCCCCCAGGAG  
ATGGTAAAAGGGAGCCAGTTGCAGAAGGCCCATGTCATGTCTGTCTCCT  
CCATGAGATGCTGCAGCAGATCTTCAGCCTCTTCCACACAGAGCGCTC  
CTCTGCTGCCTGGAACATGACCCTCCTAGACCAACTCCACACTGGACT  
TCATCAGCAACTGCAACACCTGGAGACCTGCTTGCTGCAGGTTAGTGG  
GAGAAGGAGAATCTGCTGGGGCAATTAGCAGCCCTGCACTGACCTTG  
AGGAGGTACTTCCAGGGAATCCGTGTCTACCTGAAAGAGAAGAAATA  
CAGCGACTGTGCCTGGGAAGTTGTCAGAATGGAAATCATGAAATCCT  
TGTTCTTATCAACAAACATGCAAGAAAGACTGAGAAGTAAAGATAGA  
GACCTGGGCTCATCTTGA

FIG. 59D

Met Ala Leu Leu Phe Pro Leu Leu Ala Ala Leu Val Met Thr Ser Tyr Ser Pro Val  
Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu Leu Ser Arg Asn Thr  
Leu Val Leu Leu His Gln Met Arg Arg Ile Ser Pro Phe Leu Cys Leu Lys Asp  
Arg Arg Asp Phe Arg Phe Pro Gln Glu Met Val Lys Gly Ser Gln Leu Gln Lys  
Ala His Val Met Ser Val Leu His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His  
Thr Glu Arg Ser Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr  
Gly Leu His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg Arg Tyr Phe  
Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser Asp Cys Ala Trp Glu Val  
Val Arg Met Glu Ile Met Lys Ser Leu Phe Leu Ser Thr Asn Met Gln Glu Arg  
Leu Arg Ser Lys Asp Arg Asp Leu Gly Ser Ser

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FIG. 60A

ATGACCAACAAGTGTCTCCTCCAAATTGCTCTCCTGTTGTGCTTCTCC  
ACTACAGCTCTTTCCATGAGCTACAACCTTGCTTGGATTCTACAAAGA  
AGCAGCAATTTTCAGTGTGAGAAGCTCCTGTGGCAATTGAATGGGAG  
GCTTGAATATTGCCTCAAGGACAGGATGAACTTTGACATCCCTGAGG  
AGATTAAGCAGCTGCAGCAGTTCCAGAAGGAGGACGCCGCATTGACC  
ATCTATGAGATGCTCCAGAACATCTTTGCTATTTTCAGACAAGATTCA  
TCTAGCACTGGCTGGAATGAGACTATTGTTGAGAACCTCCTGGCTAA  
TGTCTATCATCAGATAAACCATCTGAAGACAGTCCTGGAAGAAAAAC  
TGGAGAAAGAAGATTTTACCAGGGGAAAACATCATGAGCAGTCTGCAC  
CTGAAAAGATATTATGGGAGGATTCTGCATTACCTGAAGGCCAAGGA  
GTACAGTCACTGTGCCTGGACCATAGTCAGAGTGGAATCCTAAGGA  
ACTTTTACTTCATTAACAGACTTACAGGTTACCTCCGAAACTGAAGAT  
CTCCTAGCCTGTCCCTCTGGGACTGGACAATTGCTTCAAGCATTCTTC  
AACCAGCAGATGCTGTTTAAGTGACTGATGGCTAATGTACTGCAAAT  
GAAAGGACACTAGAAGATTTTGAAATTTTATTAAATTATGAGTTATT  
TTTATTTAT TTAAATTTTATTTTGGAAAATAAATTATTTTGGTGC

FIG. 60B

Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser Thr Thr Ala  
Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg Ser Ser Asn Phe Gln  
Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg Leu Glu Tyr Cys Leu Lys Asp  
Arg Met Asn Phe Asp Ile Pro Glu Glu Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu  
Asp Ala Ala Leu Thr Ile Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln  
Asp Ser Ser Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val  
Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu Lys Glu Asp  
Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys Arg Tyr Tyr Gly Arg Ile  
Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser His Cys Ala Trp Thr Ile Val Arg Val  
Glu Ile Leu Arg Asn Phe Tyr Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn

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FIG. 61A

ATGGTCTCCCAGGCCCTCAGGCTCCTCTGCCTTCTGCTTGGGCTTCAG  
GGCTGCCTGGCTGCAGTCTTCGTAACCCAGGAGGAAGCCCACGGCGT  
CCTGCACCGGCGCCGGCGCGCCAACGCGTTCCCTGGAGGAGCTGCGGC  
CGGGCTCCCTGGAGAGGGAGTGCAAGGAGGAGCAGTGCTCCTTCGA  
GGAGGCCCGGGAGATCTTCAAGGACGCGGAGAGGACGAAGCTGTTC  
TGGATTTCTTACAGTGATGGGGACCAGTGTGCCTCAAGTCCATGCCA  
GAATGGGGGCTCCTGCAAGGACCAGCTCCAGTCCTATATCTGCTTCT  
GCCTCCCTGCCTTCGAGGGGCCGGAAGTGTGAGACGCACAAGGATGAC  
CAGCTGATCTGTGTGAACGAGAACGGCGGGCTGTGAGCAGTACTGCAG  
TGACCACACGGGACCAAGCGCTCCTGTCGGTGCCACGAGGGGTACT  
CTCTGCTGGCAGACGGGGTGTCTGCACACCCACAGTTGAATATCCA  
TGTGGA AAAAATACCTATTCTAGAAAAAAGAAATGCCAGCAAACCCCA  
AGGCCGAATTGTGGGGGGGCAAGGTGTGCCCCAAAGGGGAGTGTCCA  
TGGCAGGTCCTGTTGTTGGTGAATGGAGCTCAGTTGTGTGGGGGGAC  
CCTGATCAACACCATCTGGGTGGTCTCCGCGGCCCACTGTTTCGACAA  
AATCAAGAACTGGAGGAACCTGATCGCGGTGCTGGGCGAGCACGAC  
CTCAGCGAGCACGACGGGGATGAGCAGAGCCGGCGGGTGGCGCAGG  
TCATCATCCCCAGCACGTACGTCCCGGGCACCAACCAACGACATC  
GCGCTGCTCCGCCTGCACCAGCCCGTGGTCCTCACTGACCATGTGGTG  
CCCCTCTGCCTGCCCCGAACGGACGTTCTCTGAGAGGACGCTGGCCTTC  
GTGCGCTTCTCATTGGTCAGCGGCTGGGGGCCAGCTGCTGGACCGTGG  
CGCCACGGCCCTGGAGCTCATGGTGCTCAACGTGCCCCGGCTGATGA  
CCCAGGACTGCCTGCAGCAGTCACGGAAGGTGGGAGACTCCCCAAAT  
ATCACGGAGTACATGTTCTGTGCCGGCTACTCGGATGGCAGCAAGGA  
CTCCTGCAAGGGGGACAGTGGAGGCCACATGCCACCCACTACCGGG  
GCACGTGGTACCTGACGGGCATCGTCAGCTGGGGGCCAGGGCTGCGCA  
ACCGTGGGCCACTTTGGGGTGTACACCAGGGTCTCCCAGTACATCGA  
GTGGCTGCAAAAGCTCATGCGCTCAGAGCCACGCCCAGGAGTCCTCC  
TGCGAGCCCCATTTCCC

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## FIG. 61B

Met Val Ser Gln Ala Leu Arg Leu Leu Cys Leu Leu Leu Gly Leu Gln Gly Cys  
Leu Ala Ala Val Phe Val Thr Gln Glu Glu Ala His Gly Val Leu His Arg Arg Arg  
Arg Ala Asn Ala Phe Leu Glu Glu Leu Arg Pro Gly Ser Leu Glu Arg Glu Cys  
Lys Glu Glu Gln Cys Ser Phe Glu Glu Ala Arg Glu Ile Phe Lys Asp Ala Glu Arg  
Thr Lys Leu Phe Trp Ile Ser Tyr Ser Asp Gly Asp Gln Cys Ala Ser Ser Pro Cys  
Gln Asn Gly Gly Ser Cys Lys Asp Gln Leu Gln Ser Tyr Ile Cys Phe Cys Leu Pro  
Ala Phe Glu Gly Arg Asn Cys Glu Thr His Lys Asp Asp Gln Leu Ile Cys Val  
Asn Glu Asn Gly Gly Cys Glu Gln Tyr Cys Ser Asp His Thr Gly Thr Lys Arg  
Ser Cys Arg Cys His Glu Gly Tyr Ser Leu Leu Ala Asp Gly Val Ser Cys Thr Pro  
Thr Val Glu Tyr Pro Cys Gly Lys Ile Pro Ile Leu Glu Lys Arg Asn Ala Ser Lys  
Pro Gln Gly Arg Ile Val Gly Gly Lys Val Cys Pro Lys Gly Glu Cys Pro Trp Gln  
Val Leu Leu Leu Val Asn Gly Ala Gln Leu Cys Gly Gly Thr Leu Ile Asn Thr Ile  
Trp Val Val Ser Ala Ala His Cys Phe Asp Lys Ile Lys Asn Trp Arg Asn Leu Ile  
Ala Val Leu Gly Glu His Asp Leu Ser Glu His Asp Gly Asp Glu Gln Ser Arg  
Arg Val Ala Gln Val Ile Ile Pro Ser Thr Tyr Val Pro Gly Thr Thr Asn His Asp  
Ile Ala Leu Leu Arg Leu His Gln Pro Val Val Leu Thr Asp His Val Val Pro Leu  
Cys Leu Pro Glu Arg Thr Phe Ser Glu Arg Thr Leu Ala Phe Val Arg Phe Ser  
Leu Val Ser Gly Trp Gly Gln Leu Leu Asp Arg Gly Ala Thr Ala Leu Glu Leu  
Met Val Leu Asn Val Pro Arg Leu Met Thr Gln Asp Cys Leu Gln Gln Ser Arg  
Lys Val Gly Asp Ser Pro Asn Ile Thr Glu Tyr Met Phe Cys Ala Gly Tyr Ser Asp  
Gly Ser Lys Asp Ser Cys Lys Gly Asp Ser Gly Gly Pro His Ala Thr His Tyr Arg  
Gly Thr Trp Tyr Leu Thr Gly Ile Val Ser Trp Gly Gln Gly Cys Ala Thr Val Gly  
His Phe Gly Val Tyr Thr Arg Val Ser Gln Tyr Ile Glu Trp Leu Gln Lys Leu Met  
Arg Ser Glu Pro Arg Pro Gly Val Leu Leu Arg Ala Pro Phe Pro



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FIG. 62A

ATGCAGCGCGTGAACATGATCATGGCAGAATCACCAAGCCTCATCAC  
CATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTACAGTTTTTCTT  
GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAA  
TTCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAAT  
GTATGGAAGAAAAGTGTAGTTTTTGAAGAACCACGAGAAGTTTTTGAA  
AACACTGAAAAGACAACCTGAATTTTGAAGCAGTATGTTGATGGAGA  
TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG  
ACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAAGA  
ACTGTGAATTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG  
CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT  
GAGGGATATCGACTTGCAGAAAACCAGAAAGTCCTGTGAACCAGCAGT  
GCCATTTCCATGTGGAAGAGTTTCTGTTTCACAACTTCTAAGCTCAC  
CCGTGCTGAGGCTGTTTTTCCTGATGTGGACTATGTAAATCCTACTGA  
AGCTGAAACCATTTTGGATAACATCACTCAAGGCACCCAATCATTTA  
ATGACTTCACTCGGGTTGTTGGTGGAGAAGATGCCAAACCAGGTCAA  
TTCCCTTGGCAGGTTGTTTTGAATGGTAAAGTTGATGCATTCTGTGGA  
GGCTCTATCGTTAATGAAAAATGGATTGTAAGTCTGCCCACTGTGTT  
GAAACTGGTGTTAAAATTACAGTTGTCTGCAGGTGAACATAATATTGA  
GGAGACAGAACATACAGAGCAAAAGCGAAATGTGATTCGAGCAATT  
ATTCCTCACCACAAC TACAATGCAGCTATTAATAAGTACAACCATGA  
CATTGCCCTTCTGGAAC TGGACGAACCCTTAGTGCTAAACAGCTACG  
TTACACCTATTTGCATTGCTGACAAGGAATACACGAACATCTTCCTCA  
AATTTGGATCTGGCTATGTAAAGTGGCTGGGCAAGAGTCTTCCACAAA  
GGGAGATCAGCTTTAGTTCTTCAGTACCTTAGAGTTCCACTTGTTGAC  
CGAGCCACATGTCTTCGATCTACAAAGTTCACCATCTATAACAACAT  
GTTCTGTGCTGGCTTCCATGAAGGAGGTAGAGATTCATGTCAAGGAG  
ATAGTGGGGGACCCCATGTTACTGAAGTGGAAAGGGACCAGTTTCTTA  
ACTGGAATTATTAGCTGGGGTGAAGAGTGTGCAATGAAAGGCAAATA  
TGGAATATATACCAAGGTATCCCGGTATGTCAACTGGATTAAGGAAA  
AAACAAAGCTCACTTAATGAAAGATGGATTTC CAAGGTTAATTCATT  
GGAATTGAAAATTAACAG

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## FIG. 62B

Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Ser Leu Ile Thr Ile Cys Leu  
Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala  
Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe  
Val Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu Glu  
Pro Arg Glu Val Phe Glu Asn Thr Glu Lys Thr Thr Glu Phe Trp Lys Gln Tyr  
Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys  
Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn  
Cys Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe Cys  
Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu  
Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser  
Val Ser Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp Tyr  
Val Asn Pro Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln Gly Thr Gln Ser  
Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe  
Pro Trp Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Gly Ser Ile Val  
Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly Val Lys Ile Thr  
Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu His Thr Glu Gln Lys Arg Asn  
Val Ile Arg Ala Ile Ile Pro His His Asn Tyr Asn Ala Ala Ile Asn Lys Tyr Asn  
His Asp Ile Ala Leu Leu Glu Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr  
Pro Ile Cys Ile Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly  
Tyr Val Ser Gly Trp Ala Arg Val Phe His Lys Gly Arg Ser Ala Leu Val Leu Gln  
Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg Ser Thr Lys Phe  
Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His Glu Gly Gly Arg Asp Ser  
Cys Gln Gly Asp Ser Gly Gly Pro His Val Thr Glu Val Glu Gly Thr Ser Phe Leu  
Thr Gly Ile Ile Ser Trp Gly Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr  
Thr Lys Val Ser Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr

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FIG. 63A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCCA  
GAATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCC  
AATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCC  
ACTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAG  
AGTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATG  
GGGGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTG  
TTATTATCACAAATCTTAAATGTTTTACCAAGTGCTGTCTTGATGACT  
GCTGATTTTCTGGAATGGAAAATTAAGTTGTTTAGTGTTTATGGCTTT  
GTGAGATAAACTCTCCTTTTCCTTACCATACCACTTTGACACGCTTC  
AAGGATATACTGCAGCTTTACTGCCTTCCTCCTTATCCTACAGTACAA  
TCAGCAGTCTAGTTCTTTTCATTTGGAATGAATACAGCATTAAGCTTG  
TTCCACTGCAAATAAAGCCTTTTAAATCATC

FIG. 63B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

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FIG. 63C

ATGAAGACACTCCAGTTTTTCTTCCTTTTCTGTTGCTGGAAAGCAATC  
TGCTGCAATAGCTGTGAGCTGACCAACATCACCATTGCAATAGAGAA  
AGAAGAATGTCGTTTCTGCATAAGCATCAACACCACTTGGTGTGCTG  
GCTACTGCTACACCAGGGATCTGGTGTATAAGGACCCAGCCAGGCC  
AAAATCCAGAAAACATGTACCTTCAAGGAACTGGTATATGAAACAGT  
GAGAGTGCCCGGCTGTGCTCACCATGCAGATTCCTTGTATACATACCC  
AGTGGCCACCCAGTGTCACTGTGGCAAGTGTGACAGCGACAGCACTG  
ATTGTACTGTGCGAGGCCTGGGGCCCAGCTACTGCTCCTTTGGTGAAA  
TGAAAGAATAA

FIG. 63D

Met Lys Thr Leu Gln Phe Phe Phe Leu Phe Cys Cys Trp Lys Ala Ile Cys Cys  
Asn Ser Cys Glu Leu Thr Asn Ile Thr Ile Ala Ile Glu Lys Glu Glu Cys Arg Phe  
Cys Ile Ser Ile Asn Thr Thr Trp Cys Ala Gly Tyr Cys Tyr Thr Arg Asp Leu Val  
Tyr Lys Asp Pro Ala Arg Pro Lys Ile Gln Lys Thr Cys Thr Phe Lys Glu Leu Val  
Tyr Glu Thr Val Arg Val Pro Gly Cys Ala His His Ala Asp Ser Leu Tyr Thr Tyr  
Pro Val Ala Thr Gln Cys His Cys Gly Lys Cys Asp Ser Asp Ser Thr Asp Cys  
Thr Val Arg Gly Leu Gly Pro Ser Tyr Cys Ser Phe Gly Glu Met Lys Glu

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FIG. 64A

CCCGGAGCCGGACCGGGGCCACCGCGCCCGCTCTGCTCCGACACCGC  
GCCCCCTGGACAGCCGCCCTCTCCTCCAGGCCCGTGGGGCTGGCCCT  
GCACCGCCGAGCTTCCCGGGATGAGGGCCCCCGGTGTGGTCACCCGG  
CGCGCCCCAGGTCGCTGAGGGACCCCGGCCAGGCGCGGAGATGGGG  
GTGCACGAATGTCCTGCCTGGCTGTGGCTTCTCCTGTCCCTGCTGTCG  
CTCCCTCTGGGCCTCCAGTCCTGGGCGCCCCACCACGCCTCATCTGT  
GACAGCCGAGTCCTGGAGAGGTACCTCTTGGAGGCCAAGGAGGCCG  
AGAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAAT  
ATCACTGTCCCAGACACCAAAGTTAATTTCTATGCCTGGAAGAGGAT  
GGAGGTCGGGCAGCAGGCCGTAGAAGTCTGGCAGGGGCCTGGCCCTG  
CTGTCGGAAGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCC  
CAGCCGTGGGAGCCCCCTGCAGCTGCATGTGGATAAAGCCGTCAGTGG  
CCTTCGCAGCCTCACCCTCTGCTTCGGGCTCTGCGAGCCCAGAAGG  
AAGCCATCTCCCCTCCAGATGCGGCCTCAGCTGCTCCACTCCGAACA  
ATCACTGCTGACACTTTCCGCAAACCTCTTCCGAGTCTACTCCAATTT  
CTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTGCAGGACAG  
GGGACAGATGACCAGGTGTGTCCACCTGGGCATATCCACCACCTCCC  
TCACCAACATTGCTTGTGCCACACCCTCCCCCGCCACTCCTGAACCCC  
GTCGAGGGGGCTCTCAGCTCAGCGCCAGCCTGTCCCATGGACACTCCA  
GTGCCAGCAATGACATCTCAGGGGCCAGAGGAACTGTCCAGAGAGC  
AACTCTGAGATCTAAGGATGTCACAGGGGCCAACTTGAGGGGCCAGAG  
CAGGAAGCATTGAGAGAGCAGCTTTAAACTCAGGGACAGAGCCATG  
CTGGGAAGACGCCTGAGCTCACTCGGCACCCTGCAAAATTTGATGCC  
AGGACACGCTTTGGAGGCGATTTACCTGTTTTTCGCACCTACCATCAGG  
GACAGGATGACCTGGAGAACTTAGGTGGCAAGCTGTGACTTCTCCAG  
GTCTCACGGGCATGGGCACTCCCTTGGTGGCAAGAGCCCCCTTGACA  
CCGGGGTGGTGGGAACCATGAAGACAGGATGGGGGGCTGGCCTCTGG  
CTCTCATGGGGTCCAAGTTTTGTGTATTCTTCAACCTCATTGACAAGA  
ACTGAAACCACCAAAAAAAAAAAAAA

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FIG. 64B

Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu Leu Ser  
Leu Pro Leu Gly Leu Pro Val Leu Gly Ala Pro Pro Arg Leu Ile Cys Asp Ser  
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr  
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys  
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val  
Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu  
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser  
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Arg Ala Gln Lys Glu Ala Ile  
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe  
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr  
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg

FIG. 65

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala  
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn  
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly  
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg  
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val  
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly  
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr  
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly  
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp

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FIG. 66A

ATGTGGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCAT  
CTCTGCACCCGCCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGC  
ATGTGAATGCCATCCAGGAGGCCCCGGCGTCTCCTGAACCTGAGTAGA  
GACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAAAT  
GTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGT  
ACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCCTTG  
ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGA  
AACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGA  
ACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG  
TCCAGGAGTGA

FIG. 66B

Met Trp Leu Gln Ser Leu Leu Leu Leu Gly Thr Val Ala Cys Ser Ile Ser Ala Pro  
Ala Arg Ser Pro Ser Pro Ser Thr Gln Pro Trp Glu His Val Asn Ala Ile Gln Glu  
Ala Arg Arg Leu Leu Asn Leu Ser Arg Asp Thr Ala Ala Glu Met Asn Glu Thr  
Val Glu Val Ile Ser Glu Met Phe Asp Leu Gln Glu Pro Thr Cys Leu Gln Thr Arg  
Leu Glu Leu Tyr Lys Gln Gly Leu Arg Gly Ser Leu Thr Lys Leu Lys Gly Pro  
Leu Thr Met Met Ala Ser His Tyr Lys Gln His Cys Pro Pro Thr Pro Glu Thr Ser  
Cys Ala Thr Gln Ile Ile Thr Phe Glu Ser Phe Lys Glu Asn Leu Lys Asp Phe Leu  
Leu Val Ile Pro Phe Asp Cys Trp Glu Pro Val Gln Glu

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FIG. 67A

ATGAAATATACAAGTTATATCTTGGCTTTTCAGCTCTGCATCGTTTTG  
GGTTCTCTTGGCTGTTACTGCCAGGACCCATATGTAAAAGAAGCAGA  
AAACCTTAAGAAATATTTTAATGCAGGTCATTCAGATGTAGCGGATA  
ATGGAACTCTTTTCTTAGGCATTTTGAAGAATTGGAAAGAGGAGAGT  
GACAGAAAAATAATGCAGAGCCAAATTGTCCTCTTTTACTTCAAAC  
TTTTAAAAACTTTAAAGATGACCAGAGCATCCAAAAGAGTGTGGAGA  
CCATCAAGGAAGACATGAATGTCAAGTTTTTCAATAGCAACAAAAAG  
AAACGAGATGACTTCGAAAAGCTGACTAATTATTCGGTAACTGACTT  
GAATGTCCAACGCAAAGCAATACATGAATCATCCAAGTGATGGCTG  
AACTGTCGCCAGCAGCTAAAACAGGGAAGCGAAAAAGGAGTCAGAT  
GCTGTTTCGAGGTCGAAGAGCATCCCAGTAA

FIG. 67B

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu Gly Ser Leu  
Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu Asn Leu Lys Lys Tyr  
Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn Gly Thr Leu Phe Leu Gly Ile  
Leu Lys Asn Trp Lys Glu Glu Ser Asp Arg Lys Ile Met Gln Ser Gln Ile Val Ser  
Phe Tyr Phe Lys Leu Phe Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val  
Glu Thr Ile Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys  
Arg Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val Gln  
Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser Pro Ala Ala Lys  
Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg Gly Arg Arg Ala Ser Gln



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FIG. 68A

CTGGGACAGTGAATCGACAATGCCGTCTTCTGTCTCGTGGGGCATCCT  
CCTGCTGGCAGGCCTGTGCTGCCTGGTCCCTGTCTCCCTGGCTGAGGA  
TCCCCAGGGAGATGCTGCCCAGAAGACAGATACATCCCACCATGATC  
AGGATCACCCAACCTTCAACAAGATCACCCCCAACCTGGCTGAGTTC  
GCCTTCAGCCTATACCGCCAGCTGGCACACCAGTCCAACAGCACCAA  
TATCTTCTTCTCCCCAGTGAGCATCGCTACAGCCTTTGCAATGCTCTC  
CCTGGGGACCAAGGCTGACACTCACGATGAAATCCTGGAGGGCCTGA  
ATTTCAACCTCACGGAGATTCCGGAGGGCTCAGATCCATGAAGGCTTC  
CAGGAACTCCTCCGTACCCTCAACCAGCCAGACAGCCAGCTCCAGCT  
GACCACCGGCAATGGCCTGTTCTCAGCGAGGGCCTGAAGCTAGTGG  
ATAAGTTTTTGGAGGATGTTAAAAAGTTGTACCACTCAGAAGCCTTC  
ACTGTCAACTTCGGGGACACCGAAGAGGGCCAAGAAACAGATCAACG  
ATTACGTGGAGAAGGGTACTCAAGGGAAAATTGTGGATTTGGTCAAG  
GAGCTTGACAGAGACACAGTTTTTGTCTCTGGTGAATTACATCTTCTTT  
AAAGGCAAATGGGAGAGACCCTTTGAAGTCAAGGACACCGAGGAAG  
AGGACTTCCACGTGGACCAGGTGACCACCGTGAAGGTGCCTATGATG  
AAGCGTTTAGGCATGTTTAACATCCAGCACTGTAAGAAGCTGTCCAG  
CTGGGTGCTGCTGATGAAATACCTGGGCAATGCCACCGCCATCTTCT  
TCCTGCCTGATGAGGGGAAACTACAGCACCTGGAAAATGAACTCACC  
CACGATATCATCACCAAGTTCCTGGAAAATGAAGACAGAAGGTCTGC  
CAGCTTACATTTACCCAAACTGTCCATTACTGGAACCTATGATCTGAA  
GAGCGTCCTGGGTCAACTGGGCATCACTAAGGTCTTCAGCAATGGGG  
CTGACCTCTCCGGGGTCACAGAGGAGGCACCCCTGAAGCTCTCCAAG  
GCCGTGCATAAGGCTGTGCTGACCATCGACGAGAAAGGGACTGAAGC  
TGCTGGGGCCATGTTTTTAGAGGGCCATACCCATGTCTATCCCCCCCCGA  
GGTCAAGTTCAACAAACCCTTTGTCTTCTTAATGATTGAACAAAATAC  
CAAGTCTCCCCTCTTCATGGGAAAAGTGGTGAATCCCACCCAAAAAT  
AACTGCCTCTCGCTCCTCAACCCCTCCCCTCCATCCCTGGCCCCCTCC  
CTGGATGACATTAAAGAAGGGTTGAGCTGG

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FIG. 68B

Met Pro Ser Ser Val Ser Trp Gly Ile Leu Leu Leu Ala Gly Leu Cys Cys Leu Val  
Pro Val Ser Leu Ala Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser  
His His Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu Phe  
Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr Asn Ile Phe Phe  
Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu Ser Leu Gly Thr Lys Ala Asp  
Thr His Asp Glu Ile Leu Glu Gly Leu Asn Phe Asn Leu Thr Glu Ile Pro Glu Ala  
Gln Ile His Glu Gly Phe Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln  
Leu Gln Leu Thr Thr Gly Asn Gly Leu Phe Leu Ser Glu Gly Leu Lys Leu Val  
Asp Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr Val  
Asn Phe Gly Asp Thr Glu Glu Ala Lys Lys Gln Ile Asn Asp Tyr Val Glu Lys  
Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu Asp Arg Asp Thr Val  
Phe Ala LeuVal Asn Tyr Ile Phe Phe Lys Gly Lys Trp Glu Arg Pro Phe Glu Val  
Lys Asp Thr Glu Glu Glu Asp Phe His Val Asp Gln Val Thr Thr Val Lys Val  
Pro Met Met Lys Arg Leu Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser  
Ser Trp Val Leu Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro  
Asp Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile Thr Lys  
Phe Leu Glu Asn Glu AspArg Arg Ser Ala Ser Leu His Leu Pro Lys Leu Ser Ile  
Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly Gln Leu Gly Ile Thr Lys Val Phe  
Ser Asn Gly Ala Asp Leu Ser Gly Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys  
Ala Val His Lys Ala Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala  
Met Phe Leu Glu Ala Ile Pro Met Ser Ile Pro Pro Glu Val Lys Phe Asn Lys Pro  
Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe Met Gly Lys Val  
Val Asn Pro Thr Gln Lys

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FIG. 69A-1

GCTAACCTAGTGCCTATAGCTAAGGCAGGTACCTGCATCCTTGTTTTT  
GTTTAGTGGATCCTCTATCCTTCAGAGACTCTGGAACCCCTGTGGTCT  
TCTCTTCATCTAATGACCCTGAGGGGATGGAGTTTTCAAGTCCTTCCA  
GAGAGGAATGTCCCAAGCCTTTGAGTAGGGTAAGCATCATGGCTGGC  
AGCCTCACAGGTTTGCTTCTACTTCAGGCAGTGTCTGTTGGGCATCAGGT  
GCCCCGCCCTGCATCCCTAAAAGCTTCGGCTACAGCTCGGTGGTGTGT  
GTCTGCAATGCCACATACTGTGACTCCTTTGACCCCCCGACCTTTCCT  
GCCCTTGGTACCTTCAGCCGCTATGAGAGTACACGCAGTGGGCGACG  
GATGGAGCTGAGTATGGGGCCCATCCAGGCTAATCACACGGGCACAG  
GCCTGCTACTGACCCTGCAGCCAGAACAGAAGTTCCAGAAAGTGAAG  
GGATTTGGAGGGGGCCATGACAGATGCTGCTGCTCTCAACATCCTTGCC  
CTGTCACCCCCTGCCCAAATTTGCTACTTAAATCGTACTTCTCTGAA  
GAAGGAATCGGATATAACATCATCCGGGTACCCATGGCCAGCTGTGA  
CTTCTCCATCCGCACCTACACCTATGCAGACACCCCTGATGATTTCCA  
GTTGCACAACCTTCAGCCTCCCAGAGGAAGATAACCAAGCTCAAGATAC  
CCCTGATTCACCGAGCCCTGCAGTTGGCCCAGCGTCCCGTTTCACTCC  
TTGCCAGCCCCCTGGACATCACCCACTTGGCTCAAGACCAATGGAGCG  
GTGAATGGGAAGGGGTCACTCAAGGGACAGCCCGGAGACATCTACC  
ACCAGACCTGGGGCCAGATACTTTGTGAAGTTCCTGGATGCCTATGCTG  
AGCACAAGTTACAGTTCTGGGCAGTGACAGCTGAAAATGAGCCTTCT  
GCTGGGCTGTTGAGTGGATACCCCTTCCAGTGCCTGGGCTTCACCCCT  
GAACATCAGCGAGACTTCATTGCCCGTGACCTAGGTCCCTACCCTCGCC  
AACAGTACTCACCACAATGTCCGCCTACTCATGCTGGATGACCAACGC  
TTGCTGCTGCCCCACTGGGCAAAGGTGGTACTGACAGACCCAGAAGC  
AGCTAAATATGTTTCATGGCATTGCTGTACATTGGTACCTGGACTTTCT  
GGCTCCAGCCAAAGCCACCCTAGGGGAGACACACCGCCTGTTCCCCA  
ACACCATGCTCTTTGCCTCAGAGGCCTGTGTGGGCTCCAAGTTCTGGG  
AGCAGAGTGTGCGGCTAGGCTCCTGGGATCGAGGGATGCAGTACAGC  
CACAGCATCATCACGAACCTCCTGTACCATGTGGTTCGGCTGGACCGAC  
TGGAACCTTGCCCTGAACCCCGAAGGAGGACCCAATTGGGTGCGTAA  
CTTTGTGACAGTCCCATCATTGTAGACATCACCAAGGACACGTTTTA  
CAAACAGCCCATGTTCTACCACCTTGGCCACTTCAGCAAGTTTCATTCC  
TGAGGGCTCCCAGAGAGTGGGGCTGGTTGCCAGTCAGAAGAACGACC  
TGGAACGAGTGGCACTGATGCATCCCGATGGCTCTGCTGTTGTGGTCG  
TGCTAAACCGCTCCTCTAAGGATGTGCCTCTTACCATCAAGGATCCTG  
CTGTGGGCTTCTGAGACAATCTCACCTGGCTACTCCATTACACCT  
ACCTGTGGCATCGCCAGTGATGGAGCAGATACTCAAGGAGGCACTGG  
GCTCAGCCTGGGCATTAAAGGGACAGAGTCAGCTCACACGCTGTCTG  
TGACTAAAGAGGGCACAGCAGGGCCAGTGTGAGCTTACAGCGACGT

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FIG. 69A-2

AAGCCCAGGGGCAATGGTTTGGGTGACTCACTTTCCCCTCTAGGTGGT  
GCCCAGGGGCTGGAGGCCCTAGAAAAAGATCAGTAAGCCCCAGTGTC  
CCCCAGCCCCCATGCTTATGTGAACATGCGCTGTGTGCTGCTTGCTT  
TGGAAACT

FIG. 69B

Met Glu Phe Ser Ser Pro Ser Arg Glu Glu Cys Pro Lys Pro Leu Ser Arg Val Ser  
Ile Met Ala Gly Ser Leu Thr Gly Leu Leu Leu Leu Gln Ala Val Ser Trp Ala Ser  
Gly Ala Arg Pro Cys Ile Pro Lys Ser Phe Gly Tyr Ser Ser Val Val Cys Val Cys  
Asn Ala Thr Tyr Cys Asp Ser Phe Asp Pro Pro Thr Phe Pro Ala Leu Gly Thr  
Phe Ser Arg Tyr Glu Ser Thr Arg Ser Gly Arg Arg Met Glu Leu Ser Met Gly  
Pro Ile Gln Ala Asn His Thr Gly Thr Gly Leu Leu Leu Thr Leu Gln Pro Glu Gln  
Lys Phe Gln Lys Val Lys Gly Phe Gly Gly Ala Met Thr Asp Ala Ala Ala Leu  
Asn Ile Leu Ala Leu Ser Pro Pro Ala Gln Asn Leu Leu Leu Lys Ser Tyr Phe Ser  
Glu Glu Gly Ile Gly Tyr Asn Ile Ile Arg Val Pro Met Ala Ser Cys Asp Phe Ser  
Ile Arg Thr Tyr Thr Tyr Ala Asp Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser  
Leu Pro Glu Glu Asp Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu  
Ala Gln Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu Lys  
Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro Gly Asp Ile  
Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu Asp Ala Tyr Ala Glu  
His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu Asn Glu Pro Ser Ala Gly Leu  
Leu Ser Gly Tyr Pro Phe Gln Cys Leu Gly Phe Thr Pro Glu His Gln Arg Asp  
Phe Ile Ala Arg Asp Leu Gly Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg  
Leu Leu Met Leu Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val  
Leu Thr Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr Leu  
Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg Leu Phe Pro  
Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser Lys Phe Trp Glu Gln Ser  
Val Arg Leu Gly Ser Trp Asp Arg Gly Met Gln Tyr Ser His Ser Ile Ile Thr Asn  
Leu Leu Tyr His Val Val Gly Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu  
Gly Gly Pro Asn Trp Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Ile Thr  
Lys Asp Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys  
Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys Asn Asp Leu  
Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val Val Val Val Leu Asn  
Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys Asp Pro Ala Val Gly Phe Leu Glu  
Thr Ile Ser Pro Gly Tyr Ser Ile His Thr Tyr Leu Trp His Arg Gln

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FIG. 70A

ATGGATGCAATGAAGAGAGGGCTCTGCTGTGTGCTGCTGCTGTGTGG  
AGCAGTCTTCGTTTCGCCCAGCCAGGAAATCCATGCCCCGATTCAGAA  
GAGGAGCCAGATCTTACCAAGTGATCTGCAGAGATGAAAAACGCA  
GATGATATAACCAGCAACATCAGTCATGGCTGCGCCCTGTGCTCAGAA  
GCAACCGGGTGGAATATTGCTGGTGCAACAGTGGCAGGGGCACAGTGC  
CACTCAGTGCCTGTCAAAGTTGCAGCGAGCCAAGGTGTTTCAACGG  
GGGCACCTGCCAGCAGGCCCTGTACTTCTCAGATTTTCGTGTGCCAGTG  
CCCCGAAGGATTTGCTGGGAAGTGCTGTGAAATAGATAACCAGGGCCA  
CGTGCTACGAGGACCAGGGGCATCAGCTACAGGGGGCACGTGGAGCAC  
AGCGGAGAGTGCGCGCCGAGTGCACCAACTGGAACAGCAGCGCGTTG  
GCCCAGAAGCCCTACAGCGGGCGGAGGCCAGACGCCATCAGGCTGG  
GCCTGGGGAACCACTACTGCAGAAACCCAGATCGAGACTCAA  
GCCCTGGTGCTACGTCTTTAAGGCGGGGAAGTACAGCTCAGAGTTCT  
GCAGCACCCCTGCCTGCTCTGAGGGAAACAGTGACTGCTACTTTGGG  
AATGGGTCAGCCTACCGTGGCACGCACAGCCTCACCGAGTCGGGTGC  
CTCCTGCCTCCCGTGGAATTCCATGATCCTGATAGGCAAGGTTTACAC  
AGCACAGAACCCAGTGCCCAGGCACTGGGCCTGGGCAAACATAATT  
ACTGCCGGAATCCTGATGGGGATGCCAAGCCCTGGTGCCACGTGCTG  
AAGAACCGCAGGCTGACGTGGGAGTACTGTGATGTGCCCTCCTGCTC  
CACCTGCGGCCTGAGACAGTACAGCCAGCCTCAGTTTCGCATCAAAG  
GAGGGCTCTTCGCCGACATCGCCTCCCACCCCTGGCAGGCTGCCATCT  
TTGCCAAGCACAGGAGGTGCGCCGGGAGAGCGGTTCTGTGCGGGGGC  
ATACTCATCAGCTCCTGCTGGATTCTCTCTGCCGCCCCTGCTTCCAG  
GAGAGGTTTCCGCCCCACCACCTGACGGTGATCTTGGGCAGAACATA  
CCGGGTGGTCCCTGGCGAGGAGGAGCAGAAATTTGAAGTCGAAAAA  
TACATTGTCCATAAGGAATTCGATGATGACACTTACGACAATGACAT  
TGCGCTGCTGCAGCTGAAATCGGATTCGTCCCGCTGTGCCAGGAGA  
GCAGCGTGGTCCGCACTGTGTGCCTTCCCCCGGCGGACCTGCAGCTG  
CCGGA CTGGACGGAGTGTGAGCTCTCCGGCTACGGCAAGCATGAGGC  
CTTGCTCTCCTTTCTATTCGGAGCGGCTGAAGGAGGCTCATGTCAGACT  
GTACCCATCCAGCCGCTGCACATCACAACATTTACTTAACAGAACAG  
TCACCGACAACATGCTGTGTGCTGGAGACACTCGGAGCGGCGGGCCC  
CAGGCAAACCTTGCACGACGCCTGCCAGGGCGATTTCGGGAGGCCCCCT  
GGTGTGTCTGAACGATGGCCGCATGACTTTGGTGGGCATCATCAGCT  
GGGGCCTGGGCTGTGGACAGAAGGATGTCCCGGGTGTGTACACCAAG  
GTTACCAACTACCTAGACTGGATTTCGTGACAACATGCGACCGTGACC  
AGGAACACCCGACTCCTCAAAGCAAATGAGATCC

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FIG. 70B

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly Ala Val  
Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg Gly Ala Arg Ser Tyr  
Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln Gln His Gln Ser Trp  
Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly  
Arg Ala Gln Cys His Ser Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn  
Gly Gly Thr Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro  
Glu Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu  
Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu Cys  
Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly Arg Arg Pro Asp  
Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys Arg Asn Pro Asp Arg Asp  
Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser  
Thr Pro Ala Cys Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr  
Arg Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met  
Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu Gly Leu  
Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys Pro Trp Cys His  
Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys Asp Val Pro Ser Cys Ser  
Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe  
Ala Asp Ile Ala Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser  
Pro Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser  
Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile Leu Gly  
Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe Glu Val Glu Lys  
Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr Asp Asn Asp Ile Ala Leu  
Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg  
Thr Val Cys Leu Pro Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu  
Leu Ser Gly Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys  
Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn  
Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly Gly Pro  
Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys  
Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly  
Gln Lys Asp Val Pro Gly Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg  
Asp Asn Met Arg Pro

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FIG. 71A

ATCACTCTCTTTAATCACTACTCACATTAACCTCAACTCCTGCCACAA  
TGTACAGGATGCAACTCCTGTCTTGCAATTGCACTAATTCTTGCACTTG  
TCACAAACAGTGCACTACTTCAAGTTCGACAAAGAAAACAAAGAAA  
ACACAGCTACAACCTGGAGCATTACTGCTGGATTTACAGATGATTTTG  
AATGGAATTAATAATTACAAGAATCCCAAACCTCACCAGGATGCTCAC  
ATTTAAGTTTTACATGCCCAAGAAGGCCACAGAACTGAAACAGCTTC  
AGTGTCTAGAAGAAGAAGCTCAAACCTCTGGAGGAAGTGCTGAATTTA  
GCTCAAAGCAAAAACCTTTCACCTTAAGACCCAGGGACTTAATCAGCAA  
TATCAACGTAATAGTTCTGGAACCTAAAGGGATCTGAAACAACATTCA  
TGTGTGAATATGCAGATGAGACAGCAACCATTGTAGAATTTCTGAAC  
AGATGGATTACCTTTTGTCAAAGCATCATCTCAACACTAACTTGATAA  
TTAAGTGCTTCCCACCTTAAAACATATCAGGCCTTCTATTTATTTATTTA  
AATATTTAAATTTTATATTTATTGTTGAATGTATGGTTGCTACCTATTG  
TAACTATTATTCTTAATCTTAAACTATAAATATGGATCTTTTATGAT  
TCTTTTTGTAAGCCCTAGGGGCTCTAAAATGGTTTACCTTATTTATCC  
CAAAAATATTTATTATTATGTTGAATGTTAAATATAGTATCTATGTAG  
ATTGGTTAGTAAACTATTTAATAAATTTGATAAATATAAAAAAAA  
AAACAAAAA

FIG. 71B

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ile Leu Ala Leu Val Thr Asn  
Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Lys Lys Thr Gln Leu Gln Leu Glu  
His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile Asn Asn Tyr Lys Asn  
Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe Tyr Met Pro Lys Lys Ala Thr  
Glu Leu Lys Gln Leu Gln Cys Leu Glu Glu Glu Leu Lys Pro Leu Glu Glu Val  
Leu Asn Leu Ala Gln Ser Lys Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser  
Asn Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu  
Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe Cys  
Gln Ser Ile Ile Ser Thr Leu Thr

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FIG. 72A-1

ATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTTTTTCGATTCT  
GCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGTCA  
TGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAG  
ATTCCTCCTAGAGTGCCAAAATCTTTTCCATTCAACACCTCAGTCGT  
GTACAAAAAGACTCTGTTTGTAGAATTCACGGATCACCTTTTCAACAT  
CGCTAAGCCAAGGCCACCCTGGATGGGTCTGCTAGGTCCTACCATCC  
AGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCT  
TCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCT  
TCTGAGGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAG  
AAGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTGGCAG  
GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTAC  
CTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATTCAGG  
CCTCATTGGAGCCCTACTAGTATGTAGAGAAGGGAGTCTGGCCAAGG  
AAAAGACACAGACCTTGCACAAATTTATACTACTTTTTTGCTGTATTTG  
ATGAAGGGAAAAGTTGGCACTCAGAAACAAAGAACTCCTTGATGCA  
GGATAGGGATGCTGCATCTGCTCGGGCCTGGCCTAAAATGCACACAG  
TCAATGGTTATGTAAACAGGTCTCTGCCAGGTCTGATTGGATGCCACA  
GGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA  
GTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCAT  
CGCCAGGCGTCCTTGGAATCTCGCCAATAACTTTCCTTACTGCTCAA  
ACACTCTTGATGGACCTTGGACAGTTTCTACTGTTTTTGTATATCTCTT  
CCCACCAACATGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT  
CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCGGAAG  
ACTATGATGATGATCTTACTGATTCTGAAATGGATGTGGTCAGGTTTG  
ATGATGACAACTCTCCTTCTTTATCCAAATTCGCTCAGTTGCCAAGA  
AGCATCCTAAAACCTTGGGTACATTACATTGCTGCTGAAGAGGAGGAC  
TGGGACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGAAGTTATAAA  
AGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAA  
AAAAGTCCGATTTATGGCATAACAGATGAAACCTTTAAGACTCGTG  
AAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTACTTTATGGGG  
AAGTTGGAGACACACTGTTGATTATATTTAAGAATCAAGCAAGCAGA  
CCATATAACATCTACCCTCACGGAATCACTGATGTCCGTCCTTTGTAT  
TCAAGGAGATTACCAAAGGTGTAAACATTTGAAGGATTTTCCAAT  
TCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGAAGTGTAGAAG  
ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTA  
GTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC  
TCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACAGATA  
ATGTCAGACAAGAGGAATGTCATCCTGTTTTCTGTATTTGATGAGAAC  
CGAAGCTGGTACCTCACAGAGAATATACAACGCTTTCTCCCAATCCA  
GCTGGAGTGCAGCTTGAGGATCCAGAGTTCCAAGCCTCCAACATCAT  
GCACAGCATCAATGGCTATGTTTTTGATAGTTTGCAGTTGTGAGTTG  
TTTGCATGAGGTGGCATACTGGTACATTCTAAGCATTGGAGCACAGA  
CTGACTTCCTTTCTGTCTTCTCTCTGGATATACCTTCAAACACAAAAT



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FIG. 72A-2

GGTCTATGAAGACACACTCACCCCTATTCCCATTCTCAGGAGAAACTGT  
CTTCATGTGCGATGGAAAACCCAGGTCTATGGATTCTGGGGGTGCCACA  
ACTCAGACTTTCGGAACAGAGGCATGACCGCCTTACTGAAGGTTTCT  
AGTTGTGACAAGAACACTGGTGATTATTACGAGGACAGTTATGAAGA  
TATTTTCAGCATACTTGCTGAGTAAAAACAATGCCATTGAACCAAGAA  
GCTTCTCCCAGAATTCAAGACACCGTAGCACTAGGCAAAAAGCAATTT  
AATGCCACCACAATTCCAGAAAATGACATAGAGAAGACTGACCCTTG  
GTTTGCACACAGAACACCTATGCCTAAAATACAAAATGTCTCCTCTA  
GTGATTTGTTGATGCTCTTGCGACAGAGTCCTACTCCACATGGGCTAT  
CCTTATCTGATCTCCAAGAAGCCAAATATGAGACTTTTTTCTGATGATC  
CATCACCTGGAGCAATAGACAGTAATAACAGCCTGTCTGAAATGACA  
CACTTCAGGCCACAGCTCCATCACAGTGGGGACATGGTATTTACCCC  
TGAGTCAGGCCTCCAATTAAGATTAAATGAGAACTGGGGACAACCTG  
CAGCAACAGAGTTGAAGAACTTGATTTCAAAGTTTCTAGTACATCA  
AATAATCTGATTTCAACAATTCCATCAGACAATTTGGCAGCAGGTACT  
GATAATACAAGTTCCTTAGGACCCCCAAGTATGCCAGTTCATTATGAT  
AGTCAATTAGATACCACTCTATTTGGCAAAAAGTCATCTCCCCTTACT  
GAGTCTGGTGGACCTCTGAGCTTGAGTGAAGAAAATAATGATTCAAA  
GTTGTTAGAATCAGGTTTAATGAATAGCCAAGAAAGTTCATGGGGAA  
AAAATGTATCGTCAACAGAGAGTGGTAGGTTATTTAAAGGGAAAAGA  
GCTCATGGACCTGCTTTGTTGACTAAAGATAATGCCTTATTCAAAGTT  
AGCATCTCTTTGTTAAAGACAAACAAAACCTTCCAATAATTCAGCAACT  
AATAGAAAGACTCACATTGATGGCCCATCATTATTAATTGAGAATAG  
TCCATCAGTCTGGCAAAATATATTAGAAAGTGACACTGAGTTTAAAA  
AAGTGACACCTTTGATTCATGACAGAATGCTTATGGACAAAAATGCT  
ACAGCTTTGAGGCTAAATCATATGTCAAATAAAACTACTTCATCAAA  
AAACATGGAAATGGTCCAACAGAAAAAAGAGGGCCCCATTCCACCA  
GATGCACAAAATCCAGATATGTGCTTCTTTAAGATGCTATTCTTGCCA  
GAATCAGCAAGGTGGATACAAAGGACTCATGGAAAGAACTCTCTGAA  
CTCTGGGCAAGGCCCCAGTCCAAAGCAATTAGTATCCTTAGGACCAG  
AAAAATCTGTGGAAGGTCAGAATTTCTTGTCTGAGAAAAACAAAGTG  
GTAGTAGGAAAGGGTGAATTTACAAAGGACGTAGGACTCAAAGAGA  
TGGTTTTTCCAAGCAGCAGAAACCTATTTCTTACTAACTTGGATAATT  
TACATGAAAATAATACACACAATCAAGAAAAAAAATTCAGGAAGA  
AATAGAAAAGAAGGAAACATTAATCCAAGAGAATGTAGTTTTGCCTC  
AGATACATACAGTGACTGGCACTAAGAATTTTCATGAAGAACCTTTTC  
TACTGAGCACTAGGCAAAATGTAGAAGGTTTCATATGACGGGGCATA  
TGCTCCAGTACTTCAAGATTTTAGGTCATTAAATGATTCAACAAATAG  
AACAAAGAAACACACAGCTCATTCTCAAAAAAAGGGGAGGAAGAA  
AACTTGGAAAGGCTTGGGAAATCAAACCAGCAAATTGTAGAGAAATAT  
GCATGCACCACAAGGAATATCTCCTAATAACAAGCCAGCAGAATTTTG  
TCACGCAACGTAGTAAGAGAGCTTTGAAACAATTCAGACTCCCCTA

FIG. 72A-3

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GAAGAAACAGAACTTGAAAAAAGGATAATTGTGGATGACACCTCAAC  
CCAGTGGTCCAAAAACATGAAACATTTGACCCCGAGCACCTCACAC  
AGATAGACTACAATGAGAAGGAGAAAGGGGCCATTACTCAGTCTCCC  
TTATCAGATTGCCTTACGAGGAGTCATAGCATCCCTCAAGCAAATAGA  
TCTCCATTACCCATTGCAAAGGTATCATCATTTCCATCTATTAGACCTA  
TATATCTGACCAGGGTCCTATTCCAAGACAACTCTTCTCATCTTCCAG  
CAGCATCTTATAGAAAGAAAGATTCTGGGGTCCAAGAAAGCAGTCAT  
TTCTTACAAGGAGCCAAAAAAAATAACCTTTCTTTAGCCATTCTAACC  
TTGGAGATGACTGGTGATCAAAGAGAGGTTGGCTCCCTGGGGACAAG  
TGCCACAAATTCAGTCACATACAAGAAAGTTGAGAACACTGTTCTCCC  
GAAACCAGACTTGCCCAAAACATCTGGCAAAGTTGAATTGCTTCCAA  
AAGTTCACATTTATCAGAAGGACCTATTCCCTACGGAAACTAGCAATG  
GGTCTCCTGGCCATCTGGATCTCGTGGAAGGGAGCCTTCTTCAGGGAA  
CAGAGGGAGCGATTAAAGTGGAATGAAGCAAACAGACCTGGAAAAGT  
TCCCTTTCTGAGAGTAGCAACAGAAAGCTCTGCAAAGACTCCCTCCAA  
GCTATTGGATCCTCTTGCTTGGGATAACCACTATGGTACTCAGATACC  
AAAAGAAGAGTGGAATCCCAAGAGAAGTCACCAGAAAAAACAGCT  
TTTAAGAAAAAGGATACCATTTTGTCCCTGAACGCTTGTGAAAGCAAT  
CATGCAATAGCAGCAATAAATGAGGGACAAAATAAGCCCGAAATAG  
AAGTCACCTGGGCAAAGCAAGGTAGGACTGAAAGGCTGTGCTCTCAA  
AACCCACCAGTCTTGAAACGCCATCAACGGGAAATAACTCGTACTAC  
TCTTCAGTCAGATCAAGAGGAAATTGACTATGATGATACCATATCAGT  
TGAAATGAAGAAGGAAGATTTTGACATTTATGATGAGGATGAAAATC  
AGAGCCCCCGCAGCTTTCAAAGAAAACACGACACTATTTTATTGCTG  
CAGTGGAGAGGCTCTGGGATTATGGGATGAGTAGCTCCCCACATGTT  
CTAAGAAACAGGGCTCAGAGTGGCAGTGTCCCTCAGTTCAAGAAAGT  
TGTTTTCCAGGAATTTACTGATGGCTCCTTTACTCAGCCCTTATACCGT  
GGAGAATAAATGAACATTTGGGACTCCTGGGGCCATATATAAGAGC  
AGAAGTTGAAGATAATATCATGGTAACTTTCAGAAATCAGGCCTCTC  
GTCCCTATTCTTCTATTCTAGCCTTATTTCTTATGAGGAAGATCAGAG  
GCAAGGAGCAGAACCTAGAAAAAACTTTGTCAAGCCTAATGAAACCA  
AACTTACTTTTGGAAGGTGCAACATCATATGGCACCCACTAAAGAT  
GAGTTTGACTGCAAAGCCTGGGCTTATTTCTCTGATGTTGACCTGGAA  
AAAGATGTGCACTCAGGCCTGATTGGACCCCTTCTGGTCTGCCACACT  
AACACACTGAACCCTGCTCATGGGAGACAAGTGACAGTACAGGAATT  
TGCTCTGTTTTTTCACCATCTTTGATGAGACCAAAAGCTGGTACTTCACT  
GAAAATATGGAAAGAACTGCAGGGCTCCCTGCAATATCCAGATGGA  
AGATCCCCTTTTAAAGAGAATTATCGCTTCCATGCAATCAATGGCTA  
CATAATGGATACACTACCTGGCTTAGTAATGGCTCAGGATCAAAGGA  
TTCGATGGTATCTGCTCAGCATGGGCAGCAATGAAAACATCCATTCT  
ATTCATTTTCAGTGGACATGTGTTCACTGTACGAAAAAAGAGGAGTA  
TAAATGGCACTGTACAATCTCTATCCAGGTGTTTTTGAGACAGTGGA

FIG. 72A-4

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AATGTTACCATCCAAAGCTGGAATTTGGCGGGTGGGAATGCCTTATTGG  
CGAGCATCTACATGCTGGGATGAGCACACTTTTTCTGGTGTACAGCAA  
TAAGTGTGAGACTCCCCTGGGAATGGCTTCTGGACACATTAGAGATTT  
TCAGATTACAGCTTCAGGACAATATGGACAGTGGGCCCCAAAGCTGG  
CCAGACTTCATTATTCCGGATCAATCAATGCCTGGAGCACCAAGGAG  
CCCTTTTCTTGGATCAAGGTGGATCTGTTGGCACCAATGATTATTCAC  
GGCATCAAGACCCAGGGTGCCCGTCAGAAGTTCTCCAGCCTCTACAT  
CTCTCAGTTTATCATCATGTATAGTCTTGATGGGAAGAAGTGGCAGA  
CTTATCGAGGAAATTCCACTGGAACCTTAATGGTCTTCTTTGGCAATG  
TGGATTCATCTGGGATAAAACACAATATTTTAAACCCTCCAATTATTG  
CTCGATACATCCGTTTGCACCCAACCTCATTATAGCATTTCGCAGCACTC  
TTCGCATGGAGTTGATGGGCTGTGATTTAAATAGTTGCAGCATGCCAT  
TGGGAATGGAGAGTAAAGCAATATCAGATGCACAGATTACTGCTTCA  
TCCTACTTTACCAATATGTTTGGCCACCTGGTCTCCTTCAAAGCTCGA  
CTTCACCTCCAAGGGAGGAGTAATGCCTGGAGACCTCAGGTGAATAA  
TCCAAAAGAGTGGCTGCAAGTGGACTTCCAGAAGACAATGAAAGTCA  
CAGGAGTAACTACTCAGGGAGTAAATCTCTGCTTACCAGCATGTAT  
GTGAAGGAGTTCCTCATCTCCAGCAGTCAAGATGGCCATCAGTGGAC  
TCTCTTTTTTCAGAATGGCAAAGTAAAGGTTTTTCAGGGAAATCAAGA  
CTCCTTCACACCTGTGGTGAACCTCTCTAGACCCACCGTTACTGACTCG  
CTACCTTCGAATTCACCCCCAGAGTTGGGTGCACCAGATTGCCCTGAG  
GATGGAGGTCTGGGCTGCGAGGCACAGGACCTCTACTGAGGGTGGC  
CACTGCAGCACCTGCCACTGCCGTACCTCTCCCTCCTCAGCTCCAGG  
GCAGTGTCCCTCCCTGGCTTGCCTTCTACCTTTGTGCTAAATCCTAGC  
AGACACTGCCTTGAAGCCTCCTGAATTAACCTATCATCAGTCCTGCATT  
TCTTTGGTGGGGGGCCAGGAGGGTGCATCCAATTTAACTTAACTCTTA  
CCTATTTTCTGCAGCTGCTCCCAGATTACTCCTTCCTTCCAATATAACT  
AGGCAAAAAGAAGTGAGGAGAAACCTGCATGAAAGCATTCTTCCCTG  
AAAAGTTAGGCCTCTCAGAGTCACCACTTCTCTGTTGTAGAAAACT  
ATGTGATGAACTTTGAAAAAGATATTTATGATGTTAACATTTACAGGT  
TAAGCCTCATA CGTTTAAAATAAACTCTCAGTTGTTTATTATCCTGA  
TCAAGCATGGAACAAAGCATGTTTCAGGATCAGATCAATACAATCTT  
GGAGTCAAAGGCAAATCATTGGAACAATCTGCAAAATGGAGAGAA  
TACAATACTACTACAGTAAAGTCTGTTTCTGCTTCCTTACACATAGA  
TATAATTATGTTATTTAGTCATTATGAGGGGCACATTCTTATCTCCAA  
AACTAGCATTCTTAAACTGAGAATTATAGATGGGGTTCAAGAATCCC  
TAAGTCCCCTGAAATTATATAAGGCATTCTGTATAAATGCAAATGTGC  
ATTTTTCTGACGAGTGTCCATAGATATAAAGCCATTTGGTCTTAATTCT  
GACCAATAAAAAAATAAGTCAGGAGGATGCAATTGTTGAAAGCTTTG  
AAATAAAATAACAATGTCTTCTTGAAATTTGTGATGGCCAAGAAAGA  
AAATGATGA

FIG. 72B-1

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Met Gln Ile Glu Leu Ser Thr Cys Phe Phe Leu Cys Leu Leu Arg Phe Cys Phe Ser  
Ala Thr Arg Arg Tyr Tyr Leu Gly Ala Val Glu Leu Ser Trp Asp Tyr Met Gln Ser  
Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro Arg Val Pro Lys Ser Phe  
Pro Phe Asn Thr Ser Val Val Tyr Lys Lys Thr Leu Phe Val Glu Phe Thr Asp His  
Leu Phe Asn Ile Ala Lys Pro Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile  
Gln Ala Glu Val Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro  
Val Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala Glu Tyr  
Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val Phe Pro Gly Gly  
Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn Gly Pro Met Ala Ser Asp Pro  
Leu Cys Leu Thr Tyr Ser Tyr Leu Ser His Val Asp Leu Val Lys Asp Leu Asn  
Ser Gly Leu Ile Gly Ala Leu Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys  
Thr Gln Thr Leu His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser  
Trp His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser Ala Arg  
Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg Ser Leu Pro Gly Leu  
Ile Gly Cys His Arg Lys Ser Val Tyr Trp His Val Ile Gly Met Gly Thr Thr Pro  
Glu Val His Ser Ile Phe Leu Glu Gly His Thr Phe Leu Val Arg Asn His Arg Gln  
Ala Ser Leu Glu Ile Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp  
Leu Gly Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met Glu  
Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg Met Lys Asn  
Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp Ser Glu Met Asp Val  
Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe Ile Gln Ile Arg Ser Val Ala Lys  
Lys His Pro Lys Thr Trp Val His Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr  
Ala Pro Leu Val Leu Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn  
Asn Gly Pro Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr  
Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile Leu Gly Pro  
Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile Phe Lys Asn Gln Ala Ser  
Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile Thr Asp Val Arg Pro Leu Tyr Ser Arg  
Arg Leu Pro Lys Gly Val Lys His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile  
Phe Lys Tyr Lys Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg  
Cys Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala Ser  
Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp Gln Arg Gly Asn  
Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe Ser Val Phe Asp Glu Asn Arg  
Ser Trp Tyr Leu Thr Glu Asn Ile Gln Arg Phe Leu Pro Asn Pro Ala Gly Val Gln  
Leu Glu Asp Pro Glu Phe Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val  
Phe Asp Ser Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu  
Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr Thr Phe Lys  
His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro Phe Ser Gly Glu Thr Val  
Phe Met Ser Met Glu Asn Pro Gly Leu Trp Ile Leu Gly Cys His Asn Ser Asp Phe

FIG. 72B-2

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Arg Asn Arg Gly Met Thr Ala Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr  
Gly Asp Tyr Tyr Glu Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn  
Asn Ala Ile Glu Pro Arg Ser Phe Ser Gln Asn Ser Arg His Arg Ser Thr Arg Gln  
Lys Gln Phe Asn Ala Thr Thr Ile Pro Glu Asn Asp Ile Glu Lys Thr Asp Pro Trp  
Phe Ala His Arg Thr Pro Met Pro Lys Ile Gln Asn Val Ser Ser Ser Asp Leu Leu  
Met Leu Leu Arg Gln Ser Pro Thr Pro His Gly Leu Ser Leu Ser Asp Leu Gln Glu  
Ala Lys Tyr Glu Thr Phe Ser Asp Asp Pro Ser Pro Gly Ala Ile Asp Ser Asn Asn  
Ser Leu Ser Glu Met Thr His Phe Arg Pro Gln Leu His His Ser Gly Asp Met Val  
Phe Thr Pro Glu Ser Gly Leu Gln Leu Arg Leu Asn Glu Lys Leu Gly Thr Thr  
Ala Ala Thr Glu Leu Lys Lys Leu Asp Phe Lys Val Ser Ser Thr Ser Asn Asn Leu  
Ile Ser Thr Ile Pro Ser Asp Asn Leu Ala Ala Gly Thr Asp Asn Thr Ser Ser Leu  
Gly Pro Pro Ser Met Pro Val His Tyr Asp Ser Gln Leu Asp Thr Thr Leu Phe Gly  
Lys Lys Ser Ser Pro Leu Thr Glu Ser Gly Gly Pro Leu Ser Leu Ser Glu Glu Asn  
Asn Asp Ser Lys Leu Leu Glu Ser Gly Leu Met Asn Ser Gln Glu Ser Ser Trp Gly  
Lys Asn Val Ser Ser Thr Glu Ser Gly Arg Leu Phe Lys Gly Lys Arg Ala His Gly  
Pro Ala Leu Leu Thr Lys Asp Asn Ala Leu Phe Lys Val Ser Ile Ser Leu Leu  
Lys Thr Asn Lys Thr Ser Asn Asn Ser Ala Thr Asn Arg Lys Thr His Ile Asp  
Gly Pro Ser Leu Leu Ile Glu Asn Ser Pro Ser Val Trp Gln Asn Ile Leu Glu Ser  
Asp Thr Glu Phe Lys Lys Val Thr Pro Leu Ile His Asp Arg Met Leu Met Asp  
Lys Asn Ala Thr Ala Leu Arg Leu Asn His Met Ser Asn Lys Thr Thr Ser Ser  
Lys Asn Met Glu Met Val Gln Gln Lys Lys Glu Gly Pro Ile Pro Pro Asp Ala  
Gln Asn Pro Asp Met Ser Phe Phe Lys Met Leu Phe Leu Pro Glu Ser Ala Arg  
Trp Ile Gln Arg Thr His Gly Lys Asn Ser Leu Asn Ser Gly Gln Gly Pro Ser Pro  
Lys Gln Leu Val Ser Leu Gly Pro Glu Lys Ser Val Glu Gly Gln Asn Phe Leu  
Ser Glu Lys Asn Lys Val Val Val Gly Lys Gly Glu Phe Thr Lys Asp Val Gly  
Leu Lys Glu Met Val Phe Pro Ser Ser Arg Asn Leu Phe Leu Thr Asn Leu Asp  
Asn Leu His Glu Asn Asn Thr His Asn Gln Glu Lys Lys Ile Gln Glu Glu Ile  
Glu Lys Lys Glu Thr Leu Ile Gln Glu Asn Val Val Leu Pro Gln Ile His Thr  
Val Thr Gly Thr Lys Asn Phe Met Lys Asn Leu Phe Leu Leu Ser Thr Arg Gln  
Asn Val Glu Gly Ser Tyr Asp Gly Ala Tyr Ala Pro Val Leu Gln Asp Phe Arg  
Ser Leu Asn Asp Ser Thr Asn Arg Thr Lys Lys His Thr Ala His Phe Ser Lys  
Lys Gly Glu Glu Glu Asn Leu Glu Gly Leu Gly Asn Gln Thr Lys Gln Ile Val  
Glu Lys Tyr Ala Cys Thr Thr Arg Ile Ser Pro Asn Thr Ser Gln Gln Asn Phe  
Val Thr Gln Arg Ser Lys Arg Ala Leu Lys Gln Phe Arg Leu Pro Leu Glu Glu  
Thr Glu Leu Glu Lys Arg Ile Ile Val Asp Asp Thr Ser Thr Gln Trp Ser Lys Asn  
Met Lys His Leu Thr Pro Ser Thr Leu Thr Gln Ile Asp Tyr Asn Glu Lys Glu  
Lys Gly Ala Ile Thr Gln Ser Pro Leu Ser Asp Cys Leu Thr Arg Ser His Ser Ile  
Pro Gln Ala Asn Arg Ser Pro Leu Pro Ile Ala Lys Val Ser Ser Phe Pro Ser Ile  
Arg Pro Ile Tyr Leu Thr Arg Val Leu Phe Gln Asp Asn Ser Ser His Leu Pro

## FIG. 72B-3 304/498

Ala Ala Ser Tyr Arg Lys Lys Asp Ser Gly Val Gln Glu Ser Ser His Phe Leu  
Gln Gly Ala Lys Lys Asn Asn Leu Ser Leu Ala Ile Leu Thr Leu Glu Met Thr  
Gly Asp Gln Arg Glu Val Gly Ser Leu Gly Thr Ser Ala Thr Asn Ser Val Thr  
Tyr Lys Lys Val Glu Asn Thr Val Leu Pro Lys Pro Asp Leu Pro Lys Thr Ser  
Gly Lys Val Glu Leu Leu Pro Lys Val His Ile Tyr Gln Lys Asp Leu Phe Pro  
Thr Glu Thr Ser Asn Gly Ser Pro Gly His Leu Asp Leu Val Glu Gly Ser Leu  
Leu Gln Gly Thr Glu Gly Ala Ile Lys Trp Asn Glu Ala Asn Arg Pro Gly Lys  
Val Pro Phe Leu Arg Val Ala Thr Glu Ser Ser Ala Lys Thr Pro Ser Lys Leu  
Leu Asp Pro Leu Ala Trp Asp Asn His Tyr Gly Thr Gln Ile Pro Lys Glu Glu  
Trp Lys Ser Gln Glu Lys Ser Pro Glu Lys Thr Ala Phe Lys Lys Lys Asp Thr Ile  
Leu Ser Leu Asn Ala Cys Glu Ser Asn His Ala Ile Ala Ala Ile Asn Glu Gly  
Gln Asn Lys Pro Glu Ile Glu Val Thr Trp Ala Lys Gln Gly Arg Thr Glu Arg  
Leu Cys Ser Gln Asn Pro Pro Val Leu Lys Arg His Gln Arg Glu Ile Thr Arg  
Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile Asp Tyr Asp Asp Thr Ile Ser Val Glu  
Met Lys Lys Glu Asp Phe Asp Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg  
Ser Phe Gln Lys Lys Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp  
Tyr Gly Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser Val  
Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser Phe Thr Gln Pro  
Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu Leu Gly Pro Tyr Ile Arg  
Ala Glu Val Glu Asp Asn Ile Met Val Thr Phe Arg Asn Gln Ala Ser Arg Pro  
Tyr Ser Phe Tyr Ser Ser Leu Ile Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu  
Pro Arg Lys Asn Phe Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val  
Gln His His Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr  
Phe Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro Leu  
Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln Val Thr Val Gln  
Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr Lys Ser Trp Tyr Phe Thr Glu  
Asn Met Glu Arg Asn Cys Arg Ala Pro Cys Asn Ile Gln Met Glu Asp Pro Thr  
Phe Lys Glu Asn Tyr Arg Phe His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro  
Gly Leu Val Met Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly  
Ser Asn Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg Lys  
Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val Phe Glu Thr  
Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val Glu Cys Leu Ile Gly Glu  
His Leu His Ala Gly Met Ser Thr Leu Phe Leu Val Tyr Ser Asn Lys Cys Gln Thr  
Pro Leu Gly Met Ala Ser Gly His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln  
Tyr Gly Gln Trp Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala  
Trp Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro Met Ile  
Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser Ser Leu Tyr Ile Ser  
Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys Lys Trp Gln Thr Tyr Arg Gly  
Asn Ser Thr Gly Thr Leu Met Val Phe Phe Gly Asn Val Asp Ser Ser Gly Ile

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FIG. 72B-4

Lys His Asn Ile Phe Asn Pro Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr  
His Tyr Ser Ile Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn  
Ser Cys Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile Thr  
Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser Lys Ala Arg Leu  
His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln Val Asn Asn Pro Lys Glu  
Trp Leu Gln Val Asp Phe Gln Lys Thr Met Lys Val Thr Gly Val Thr Thr Gln  
Gly Val Lys Ser Leu Leu Thr Ser Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser  
Gln Asp Gly His Gln Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe  
Gln Gly Asn Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu  
Leu Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala Leu Arg  
Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr



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FIG. 73A

TCCACCTGTCCCCGCAGCGCCGGCTCGCGCCCTCCTGCCGCAGCCACC  
GAGCCGCCGTCTAGCGCCCCGACCTCGCCACCATGAGAGCCCTGCTG  
GCGCGCCTGCTTCTCTGCGTCCTGGTCGTGAGCGACTCCAAAGGCAGC  
AATGAAC TTCATCAAGTTCCATCGAACTGTGACTGTCTAAATGGAGGA  
ACATGTGTGTCCAACAAGTACTTCTCCAACATTCACTGGTGCAACTGC  
CCAAAGAAATTCGGAGGGGCAGCACTGTGAAATAGATAAGTCAAAAAC  
CTGCTATGAGGGGGAATGGTCACTTTTACCGAGGAAAGGCCAGCACTG  
ACACCATGGGCGCGCCCTGCCTGCCCTGGAAC TCTGCCACTGTCCTTC  
AGCAAACGTACCATGCCCACAGATCTGATGCTCTTCAGCTGGGGCCTGG  
GGAAACATAATTACTGCAGGAACCCAGACAACCGGAGGGCGACCCTGG  
TGCTATGTGCAGGTGGGCCTAAAGCCGCTTGTCCAAGAGTGCATGGT  
GCATGACTGCGCAGATGGAAAAAAGCCCTCCTCTCCTCCAGAAGAAT  
TAAAATTTCAGTGTGGCCAAAAGACTCTGAGGCCCCGCTTTAAGATTA  
TTGGGGGGAGAATTCACCACCATCGAGAACCAGCCCTGGTTTTCGGGCC  
ATCTACAGGAGGCACCGGGGGGGGCTCTGTACCTACGTGTGTGGAGG  
CAGCCTCATCAGCCCTTGCTGGGTGATCAGCGCCACACACTGCTTCAT  
TGATTACCCAAAGAAGGAGGACTACATCGTCTACCTGGGTCGCTCAA  
GGCTTA ACTCCAACACGCAAGGGGAGATGAAGTTTGAGGTGGAAAAC  
CTCATCCTACACAAGGACTACAGCGCTGACACGCTTGCTCACCACAAC  
GACATTGCCTTGCTGAAGATCCGTTCCAAGGAGGGCAGGTGTGCGCA  
GCCATCCCGGACTATACAGACCATCTGCCTGCCCTCGATGTATAACGA  
TCCCCAGTTTGGCACAAGCTGTGAGATCACTGGCTTTGGAAAAGAGA  
ATTCTACCGACTATCTCTATCCGGAGCAGCTGAAGATGACTGTTGTGA  
AGCTGATTTCCCACCGGGAGTGTGAGCAGCCCCACTACTACGGCTCTG  
AAGTCACCACCAAAATGCTGTGTGCTGCTGACCCACAGTGGAACA  
GATTCCTGCCAGGGAGACTCAGGGGGACCCCTCGTCTGTTCCCTCCAA  
GGCCGCATGACTTTGACTGGAATTGTGAGCTGGGGCCGTGGATGTGC  
CCTGAAGGACAAGCCAGGCGTCTACACGAGAGTCTCACACTTCTTAC  
CCTGGATCCGCAGTCACACCAAGGAAGAGAATGGCCTGGCCCTCTGA  
GGGTCCCCAGGGAGGAAACGGGGCACCACCCGCTTTCTTGCTGGTTGTC  
ATTTTTCAGTAGAGTCATCTCCATCAGCTGTAAGAAGAGACTGGGA  
AGAT



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FIG. 73B

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser Asp Ser  
Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp Cys Leu Asn Gly  
Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile His Trp Cys Asn Cys Pro Lys  
Lys Phe Gly Gly Gln His Cys Glu Ile Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn  
Gly His Phe Tyr Arg Gly Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro  
Trp Asn Ser Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu  
Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg Arg Arg  
Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln Glu Cys Met Val His  
Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys  
Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile  
Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr  
Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys  
Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu  
Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys  
Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg  
Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro  
Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys  
Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys  
Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr  
Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp  
Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val  
Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser  
His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Glu Asn Gly Leu Ala Leu

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FIG.74A

TCCTGCACAGGCAGTGCCTTGAAGTGCTTCTTCAGAGACCTTTCTTCA  
TAGACTACTTTTTTTTTCTTTAAGCAGCAAAAGGAGAAAATTGTCATCA  
AGGATATTCCAGATTCTTGACAGCATTCTCGTCATCTCTGAGGACATC  
ACCATCATCTCAGGATGAGGGGCATGAAGCTGCTGGGGGGCGCTGCTG  
GCACTGGCGGCCCTACTGCAGGGGGGCCGTGTCCCTGAAGATCGCAGC  
CTTCAACATCCAGACATTTGGGGAGACCAAGATGTCCAATGCCACCCT  
CGTCAGCTACATTGTGTCAGATCCTGAGCCGCTATGACATCGCCCTGGT  
CCAGGAGGTCAGAGACAGCCACCTGACTGCCGTGGGGAAGCTGCTGG  
ACAACCTCAATCAGGATGCACCAGACACCTATCACTACGTGGTCAGT  
GAGCCACTGGGACGGAACAGCTATAAGGAGCGCTACCTGTTCGTGTA  
CAGGCCTGACCAGGTGTCTGCGGTGGACAGCTACTACTACGATGATG  
GCTGCGAGCCCTGCGGGAACGACACCTTCAACCGAGAGCCAGCCATT  
GTCAGGTTCTTCTCCCGGTTACAGAGGTCAGGGAGTTTGCCATTGTT  
CCCCTGCATGCGGCCCCGGGGGACGCAGTAGCCGAGATCGACGCTCT  
CTATGACGTCTACCTGGATGTCCAAGAGAAATGGGGCTTGGAGGACG  
TCATGTTGATGGGCGACTTCAATGCGGGCTGCAGCTATGTGAGACCCT  
CCCAGTGGTCATCCATCCGCCTGTGGACAAGCCCCACCTTCCAGTGGC  
TGATCCCCGACAGCGCTGACACCACAGCTACACCCACGCACTGTGCCT  
ATGACAGGATCGTGGTTGCAGGGATGCTGCTCCGAGGCGCCGTTGTTC  
CCGACTCGGCTCTTCCCTTTAACTTCCAGGCTGCCTATGGCCTGAGTG  
ACCAACTGGCCCAAGCCATCAGTGACCACTATCCAGTGGAGGTGATG  
CTGAAGTGAGCAGCCCCTCCCCACACCAGTTGAACTGCAG

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## FIG. 74B

Met Arg Gly Met Lys Leu Leu Gly Ala Leu Leu Ala Leu Ala Ala Leu Leu Gln  
Gly Ala Val Ser Leu Lys Ile Ala Ala Phe Asn Ile Gln Thr Phe Gly Glu Thr Lys  
Met Ser Asn Ala Thr Leu Val Ser Tyr Ile Val Gln Ile Leu Ser Arg Tyr Asp Ile  
Ala Leu Val Gln Glu Val Arg Asp Ser His Leu Thr Ala Val Gly Lys Leu Leu  
Asp Asn Leu Asn Gln Asp Ala Pro Asp Thr Tyr His Tyr Val Val Ser Glu Pro  
Leu Gly Arg Asn Ser Tyr Lys Glu Arg Tyr Leu Phe Val Tyr Arg Pro Asp Gln  
Val Ser Ala Val Asp Ser Tyr Tyr Tyr Asp Asp Gly Cys Glu Pro Cys Gly Asn  
Asp Thr Phe Asn Arg Glu Pro Ala Ile Val Arg Phe Phe Ser Arg Phe Thr Glu Val  
Arg Glu Phe Ala Ile Val Pro Leu His Ala Ala Pro Gly Asp Ala Val Ala Glu Ile  
Asp Ala Leu Tyr Asp Val Tyr Leu Asp Val Gln Glu Lys Trp Gly Leu Glu Asp  
Val Met Leu Met Gly Asp Phe Asn Ala Gly Cys Ser Tyr Val Arg Pro Ser Gln  
Trp Ser Ser Ile Arg Leu Trp Thr Ser Pro Thr Phe Gln Trp Leu Ile Pro Asp Ser  
Ala Asp Thr Thr Ala Thr Pro Thr His Cys Ala Tyr Asp Arg Ile Val Val Ala Gly  
Met Leu Leu Arg Gly Ala Val Val Pro Asp Ser Ala Leu Pro Phe Asn Phe Gln  
Ala Ala Tyr Gly Leu Ser Asp Gln Leu Ala Gln Ala Ile Ser Asp His Tyr Pro Val  
Glu Val Met Leu Lys

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FIG. 75A

GCTGCATCAGAAGAGGCCATCAAGCACATCACTGTCCTTCTGCCATGG  
CCCTGTGGATGCGCCTCCTGCCCCCTGCTGGCGCTGCTGGCCCTCTGGG  
GACCTGACCCAGCCGCAGCCTTTGTGAACCAACACCTGTGCGGCTCAC  
ACCTGGTGGAAGCTCTCTACCTAGTGTGCGGGGAACGAGGCTTCTTCT  
ACACACCCAAGACCCGCCGGGAGGCAGAGGACCTGCAGGTGGGGCA  
GGTGGAGCTGGGCGGGGGGCCCTGGTGCAGGCAGCCTGCAGCCCTTGG  
CCCTGGAGGGGTCCCTGCAGAAGCGTGGCATTGTGGAACAATGCTGT  
ACCAGCATCTGCTCCCTCTACCAGCTGGAGAACTACTGCAACTAGACG  
CAGCCCGCAGGCAGCCCCCACC CGCCGCTCCTGCACCGAGAGAGA  
TGGAATAAAGCCCTTGAACCAGC

FIG. 75B

Met Ala Leu Trp Met Arg Leu Leu Pro Leu Leu Ala Leu Leu Ala Leu Trp Gly  
Pro Asp Pro Ala Ala Ala Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val  
Glu Ala Leu Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr  
Arg Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly Pro  
Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln Lys Arg Gly Ile  
Val Glu Gln Cys Cys Thr Ser Ile Cys Ser Leu Tyr Gln Leu Glu Asn Tyr Cys Asn

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FIG. 76A

ATGGGAGGTTGGTCTTCCAAACCTCGACAAGGCATGGGGACGAATCT  
TTCTGTTCCCAATCCTCTGGGATTCTTTCCCGATCACCAGTTGGACCCT  
GCGTTCGGAGCCAACTCAAACAATCCAGATTGGGACTTCAACCCCAA  
CAAGGATCACTGGCCAGAGGCAATCAAGGTAGGAGCGGGAGACTTC  
GGGCCAGGGTTACCCCCACACACGGCGGTCTTTTGGGGTGGAGCCC  
TCAGGCTCAGGGCATATTGACAACAGTGCCAGCAGCGCCTCCTCCTG  
TTTCCACCAATCGGCAGTCAGGAAGACAGCCTACTCCCATCTCTCCAC  
CTCTAAGAGACAGTCATCCTCAGGCCATGCAGTGGAATCCACAACA  
TTCCACCAAGCTCTGCTAGATCCCAGAGTGAGGGGCCTATATTTTCCT  
GCTGGTGGCTCCAGTTCCGGAACAGTAAACCCTGTTCCGACTACTGTC  
TCACCCATATCGTCAATCTTCTCGAGGACTGGGGACCCTGCACCGAAC  
ATGGAGAGCACAACATCAGGATTCCTAGGACCCCTGCTCGTGTTACA  
GGCGGGGTTTTTCTTGTTGACAAGAATCCTCACAATACCACAGAGTCT  
AGACTCGTGGTGGACTTCTCTCAATTTTCTAGGGGGAGCACCCACGTG  
TCCTGGCCAAAATTCGCAGTCCCCAACCTCCAATCACTCACCAACCTC  
TTGTCCTCCAATTTGTCCTGGTTATCGCTGGATGTGTCTGCGGCGTTTT  
ATCATATTCTCTTCATCCTGCTGCTATGCCTCATCTTCTTGTTGGTTC  
TTCTGGACTACCAAGGTATGTTGCCCGTTTGTCTCTACTTCCAGGAA  
CATCAACTACCAGCACGGGACCATGCAAGACCTGCACGATTCTGCT  
CAAGGAACCTCTATGTTTCCCTCTTGTTGCTGTACAAAACCTTCGGAC  
GGAAACTGCACTTGTAATCCCATCCCATCATCCTGGGCTTTCGCAAGA  
TTCCTATGGGAGTGGGCCTCAGTCCGTTTCTCCTGGCTCAGTTTACTA  
GTGCCATTTGTTCAGTGGTTCGCAGGGCTTTCCCCCACTGTTTGGCTTT  
CAGTTATATGGATGATGTGGTATTGGGGGCCAAGTCTGTACAACATCT  
TGAGTCCCTTTTTACCTCTATTACCAATTTTCTTTTGTCTTTGGGTATAC  
ATTTGA

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FIG. 76B

Met Gly Gly Trp Ser Ser Lys Pro Arg Gln Gly Met Gly Thr Asn Leu Ser Val Pro  
Asn Pro Leu Gly Phe Phe Pro Asp His Gln Leu Asp Pro Ala Phe Gly Ala Asn  
Ser Asn Asn Pro Asp Trp Asp Phe Asn Pro Asn Lys Asp His Trp Pro Glu Ala Ile  
Lys Val Gly Ala Gly Asp Phe Gly Pro Gly Phe Thr Pro Pro His Gly Gly Leu Leu  
Gly Trp Ser Pro Gln Ala Gln Gly Ile Leu Thr Thr Val Pro Ala Ala Pro Pro Pro  
Val Ser Thr Asn Arg Gln Ser Gly Arg Gln Pro Thr Pro Ile Ser Pro Pro Leu Arg  
Asp Ser His Pro Gln Ala Met Gln Trp Asn Ser Thr Thr Phe His Gln Ala Leu Leu  
Asp Pro Arg Val Arg Gly Leu Tyr Phe Pro Ala Gly Gly Ser Ser Ser Gly Thr Val  
Asn Pro Val Pro Thr Thr Val Ser Pro Ile Ser Ser Ile Phe Ser Arg Thr Gly Asp  
Pro Ala Pro Asn Met Glu Ser Thr Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu  
Gln Ala Gly Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser  
Trp Trp Thr Ser Leu Asn Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser  
Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr  
Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu  
Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu  
Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro Cys Lys Thr Cys Thr Ile Pro Ala  
Gln Gly Thr Ser Met Phe Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn  
Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp  
Ala Ser Val Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Ala  
Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro  
Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu  
Trp Val Tyr Ile

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FIG. 77A

CGAACCACTCAGGGTCCTGTGGACAGCTCACCTAGCTGCAATGGCTA  
CAGGCTCCCGGACGTCCCTGCTCCTGGCTTTTGGCCTGCTCTGCCTGC  
CCTGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGC  
CTTTTGACAACGCTATGCTCCGCGCCCATCGTCTGCACCAGCTGGCCT  
TTGACACCTACCAGGAGTTTGAAGAAGCCTATATCCCAAAGGAACAG  
AAGTATTCATTCCTGCAGAACCCCCAGACCTCCCTCTGTTTCTCAGAG  
TCTATTCCGACACCCTCCAACAGGGAGGAAACACAACAGAAATCCAA  
CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGGA  
GCCCCGTGCAGTTCCTCAGGAGTGTCTTCGCCAACAGCCTGGTGTACGG  
CGCCTCTGACAGCAACGTCTATGACCTCCTAAAGGACCTAGAGGAAG  
GCATCCAAACGCTGATGGGGAGGCTGGAAGATGGCAGCCCCCGGACT  
GGGCAGATCTTCAAGCAGACCTACAGCAAGTTTCGACACAAACTCACA  
CAACGATGACGCACTACTCAAGAACTACGGGGCTGCTCTACTGCTTCAG  
GAAGGACATGGCAAGGTCGAGACATTCTGCGCATCGTGCAGTGCCG  
CTCTGTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGGGTGGCATCCCTG  
TGACCCCTCCCCAGTGCCTCTCCTGGCCCTGGAAGTTGCCACTCCAGT  
GCCACCAAGCCTTGTCCTAATAAAATTAAGTTGCATC

FIG. 77B

Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu  
Pro Trp Leu Gln Glu Gly Ser Ala Phe Pro Thr Ile Pro Leu Ser Arg Pro Phe Asp  
Asn Ala Met Leu Arg Ala His Arg Leu His Gln Leu Ala Phe Asp Thr Tyr Gln  
Glu Phe Glu Glu Ala Tyr Ile Pro Lys Glu Gln Lys Tyr Ser Phe Leu Gln Asn Pro  
Gln Thr Ser Leu Cys Phe Ser Glu Ser Ile Pro Thr Pro Ser Asn Arg Glu Glu Thr  
Gln Gln Lys Ser Asn Leu Glu Leu Leu Arg Ile Ser Leu Leu Leu Ile Gln Ser Trp  
Leu Glu Pro Val Gln Phe Leu Arg Ser Val Phe Ala Asn Ser Leu Val Tyr Gly Ala  
Ser Asp Ser Asn Val Tyr Asp Leu Leu Lys Asp Leu Glu Glu Gly Ile Gln Thr Leu  
Met Gly Arg Leu Glu Asp Gly Ser Pro Arg Thr Gly Gln Ile Phe Lys Gln Thr Tyr  
Ser Lys Phe Asp Thr Asn Ser His Asn Asp Asp Ala Leu Leu Lys Asn Tyr Gly  
Leu Leu Tyr Cys Phe Arg Lys Asp Met Asp Lys Val Glu Thr Phe Leu Arg Ile  
Val Gln Cys Arg Ser Val Glu Gly Ser Cys Gly Phe

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FIG. 78A

ATGTATTCCAATGTGATAGGAACTGTAACCTCTGGAAAAAGGAAGGT  
TTATCTTTTGTCTTGCTGCTCATTGGCTTCTGGGACTGCGTGACCTGT  
CACGGGAGCCCTGTGGACATCTGCACAGCCAAGCCGCGGGACATTCC  
CATGAATCCCATGTGCATTTACCGCTCCCCGGAGAAGAAGGCAACTG  
AGGATGAGGGCTCAGAACAGAAGATCCCGGAGGCCACCAACCGGCG  
TGTCTGGGAACTGTCCAAGGCCAATTCCCGCTTTGCTACCACTTTCTA  
TCAGCACCTGGCAGATTCCAAGAATGACAATGATAACATTTTCCTGTC  
ACCCCTGAGTATCTCCACGGCTTTTGCTATGACCAAGCTGGGTGCCTG  
TAATGACACCCTCCAGCAACTGATGGAGGTATTTAAGTTTGACACCAT  
ATCTGAGAAAACATCTGATCAGATCCACTTCTTCTTTGCCAACTGAA  
CTGCCGACTCTATCGAAAAGCCAACAAATCCTCCAAGTTAGTATCAGC  
CAATCGCCTTTTTGGAGACAAATCCCTTACCTTCAATGAGACCTACCA  
GGACATCAGTGAGTTGGTATATGGAGCCAAGCTCCAGCCCCCTGGACT  
TCAAGGAAAATGCAGAGCAATCCAGAGCGGCCATCAACAAATGGGTG  
TCCAATAAGACCGAAGGCCGAATCACCGATGTCATTCCCTCGGAAGC  
CATCAATGAGCTCACTGTTCTGGTGCTGGTTAACACCATTTACTTCAA  
GGGCCTGTGGAAGTCAAAGTTCAGCCCTGAGAACACAAGGAAGGAAC  
TGTTCTACAAGGCTGATGGAGAGTCGTGTTTCAGCATCTATGATGTACC  
AGGAAGGCAAGTTCCGTTATCGGCGCGTGGCTGAAGGCACCCAGGTG  
CTTGAGTTGCCCTTCAAAGGTGATGACATCACCATGGTCCCTCATCTTG  
CCCAAGCCTGAGAAGAGCCTGGCCAAGGTGGAGAAGGAACTCACCCC  
AGAGGTGCTGCAGGAGTGGCTGGATGAATTGGAGGAGATGATGCTGG  
TGGTCCACATGCCCCGCTTCCGCATTGAGGACGGCTTCAGTTTGAAGG  
AGCAGCTGCAAGACATGGGCCTTGTCGATCTGTTTCAGCCCTGAAAAG  
TCCAAACTCCCAGGTATTGTTGCAGAAGGCCGAGATGACCTCTATGTC  
TCAGATGCATTCCATAAGGCATTTCTTGAGGTAAATGAAGAAGGCAG  
TGAAGCAGCTGCAAGTACCGCTGTTGTGATTGCTGGCCGTTTCGCTAAA  
CCCAACAGGGTGACTTTCAAGGCCAACAGGCCTTTCCTGGTTTTTAT  
AAGAGAAGTTCCTCTGAACACTATTATCTTCATGGGCAGAGTAGCCA  
ACCCTTGTGTAAAGTAA



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FIG. 78B

Met Tyr Ser Asn Val Ile Gly Thr Val Thr Ser Gly Lys Arg Lys Val Tyr Leu Leu  
Ser Leu Leu Leu Ile Gly Phe Trp Asp Cys Val Thr Cys His Gly Ser Pro Val Asp  
Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn Pro Met Cys Ile Tyr Arg Ser  
Pro Glu Lys Lys Ala Thr Glu Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr  
Asn Arg Arg Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr  
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser  
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr Leu Gln Gln  
Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Ile His  
Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser  
Lys Leu Val Ser Ala Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu  
Thr Tyr Gln Asp Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe  
Lys Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr  
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu Thr Val Leu  
Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Ser Pro Glu  
Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser  
Met Met Tyr Gln Glu Gly Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln  
Val Leu Glu Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys  
Pro Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu  
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg Phe Arg  
Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met Gly Leu Val Asp  
Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile Val Ala Glu Gly Arg Asp Asp  
Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser  
Glu Ala Ala Ala Ser Thr Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg  
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn  
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys

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FIG. 79A

ATGGATTACTACAGAAAATATGCAGCTATCTTTCTGGTCACATTGTCG  
GTGTTTCTGCATGTTCTCCATTCCGCTCCTGATGTGCAGGATTGCCAG  
AATGCACGCTACAGGAAAACCCATTCTTCTCCCAGCCGGGTGCCCA  
ATACTTCAGTGCATGGGCTGCTGCTTCTCTAGAGCATATCCCCTCCA  
CTAAGGTCCAAGAAGACGATGTTGGTCCAAAAGAACGTCACCTCAGA  
GTCCACTTGCTGTGTAGCTAAATCATATAACAGGGTCACAGTAATGGG  
GGGTTTCAAAGTGGAGAACCACACGGCGTGCCACTGCAGTACTTGTT  
ATTATCACAAATCTTAA

FIG. 79B

Met Asp Tyr Tyr Arg Lys Tyr Ala Ala Ile Phe Leu Val Thr Leu Ser Val Phe Leu  
His Val Leu His Ser Ala Pro Asp Val Gln Asp Cys Pro Glu Cys Thr Leu Gln Glu  
Asn Pro Phe Phe Ser Gln Pro Gly Ala Pro Ile Leu Gln Cys Met Gly Cys Cys Phe  
Ser Arg Ala Tyr Pro Thr Pro Leu Arg Ser Lys Lys Thr Met Leu Val Gln Lys Asn  
Val Thr Ser Glu Ser Thr Cys Cys Val Ala Lys Ser Tyr Asn Arg Val Thr Val Met  
Gly Gly Phe Lys Val Glu Asn His Thr Ala Cys His Cys Ser Thr Cys Tyr Tyr His  
Lys Ser

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FIG. 79C

ATGGAGATGTTCCAGGGGCTGCTGCTGTTGCTGCTGCTGAGCATGGGC  
GGGACATGGGCATCCAAGGAGCCGCTTCGGCCACGGTGCCGCCCCAT  
CAATGCCACCCTGGCTGTGGAGAAGGAGGGCTGCCCCGTGTGCATCA  
CCGTCAACACCACCATCTGTGCCGGCTACTGCCCCACCATGACCCGCG  
TGCTGCAGGGGGTCCCTGCCGGCCCTGCCTCAGGTGGTGTGCAACTACC  
GCGATGTGCGCTTCGAGTCCATCCGGCTCCCTGGCTGCCCGCGCGGCG  
TGAACCCCGTGGTCTCCTACGCCGTGGCTCTCAGCTGTCAATGTGCAC  
TCTGCCGCCGCAGCACCACTGACTGCGGGGGTCCCAAGGACCACCCC  
TTGACCTGTGATGACCCCCGCTTCCAGGACTCCTCTTCTCAAAGGCC  
CCTCCCCCAGCCTTCCAAAGCCCATCCCGACTCCCGGGGCCCTCGGAC  
ACCCCGATCCTCC CACAATAA

FIG. 79D

Met Glu Met Phe Gln Gly Leu Leu Leu Leu Leu Leu Ser Met Gly Gly Thr  
Trp Ala Ser Lys Glu Pro Leu Arg Pro Arg Cys Arg Pro Ile Asn Ala Thr Leu Ala  
Val Glu Lys Glu Gly Cys Pro Val Cys Ile Thr Val Asn Thr Thr Ile Cys Ala Gly  
Tyr Cys Pro Thr Met Thr Arg Val Leu Gln Gly Val Leu Pro Ala Leu Pro Gln Val  
Val Cys Asn Tyr Arg Asp Val Arg Phe Glu Ser Ile Arg Leu Pro Gly Cys Pro Arg  
Gly Val Asn Pro Val Val Ser Tyr Ala Val Ala Leu Ser Cys Gln Cys Ala Leu Cys  
Arg Arg Ser Thr Thr Asp Cys Gly Gly Pro Lys Asp His Pro Leu Thr Cys Asp  
Asp Pro Arg Phe Gln Asp Ser Ser Ser Ser Lys Ala Pro Pro Pro Ser Leu Pro Ser  
Pro Ser Arg Leu Pro Gly Pro Ser Asp Thr Pro Ile Leu Pro Gln

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FIG. 80A

ATGCGTCCCCTGCGCCCCCGCGCCGCGCTGCTGGCGCTCCTGGCCTCG  
CTCCTGGCCGCGCCCCCGGTGGCCCCGGCCGAGGCCCGCACCTGGT  
GCAGGTGGACGCGGCCCGCGCGCTGTGGCCCCCTGCGGCGCTTCTGGA  
GGAGCACAGGCTTCTGCCCCCGCTGCCACACAGCCAGGCTGACCA  
TACGTCTCAGCTGGGACCAGCAGCTCAACCTCGCCTATGTGGGCGCC  
GTCCCTCACCGCGGCATCAAGCAGGTCCGGACCCACTGGCTGCTGGA  
GCTTGTCACCACCAGGGGGTCCACTGGACGGGGCCTGAGCTACAACT  
TCACCCACCTGGACGGGTACTTGGACCTTCTCAGGGAGAACCAGCTCC  
TCCCAGGGTTTGAGCTGATGGGCAGCGCCTCGGGCCACTTCACTGACT  
TTGAGGACAAGCAGCAGGTGTTTGAGTGGAAGGACTTGGTCTCCAGC  
CTGGCCAGGAGATACATCGGTAGGTACGGACTGGCGCATGTTTCCAA  
GTGGAACCTTCGAGACGTGGAATGAGCCAGACCACCACGACTTTGACA  
ACGTCTCCATGACCATGCAAGGCTTCCTGAACTACTACGATGCCTGCT  
CGGAGGGTCTGCGCGCCGCCAGCCCCGCCCTGCGGCTGGGAGGCCCC  
GGCGACTCCTTCCACACCCCCACCGCGATCCCCGCTGAGCTGGGGCCTC  
CTGCGCCACTGCCACGACGGTACCAACTTCTTCACTGGGGAGGCGGG  
CGTGCGGCTGGACTACATCTCCCTCCACAGGAAGGGTGCGCGCAGCT  
CCATCTCCATCCTGGAGCAGGAGAAGGTCGTGCGCGCAGCAGATCCGG  
CAGCTCTTCCCAAGTTCGCGGACACCCCCATTTACAACGACGAGGCG  
GACCCGCTGGTGGGCTGGTCCCTGCCACAGCCGTGGAGGGCGGACGT  
GACCTACGCGGCCATGGTGGTGAAGGTCATCGCGCAGCATCAGAACC  
TGCTACTGGCCAACACCACCTCCGCCTTCCCCTACGCGCTCCTGAGCA  
ACGACAATGCCTTCTGAGCTACCACCCGCAACCCCTTCGCGCAGCGCA  
CGCTCACCGCGCGCTTCCAGGTCAACAACACCCGCCCGCCGCACGTG  
CAGCTGTTGCGCAAGCCGGTGCTCACGGCCATGGGGCTGCTGGCGCT  
GCTGGATGAGGAGCAGCTCTGGGCGGAAGTGTCGCAGGCCGGGACCG  
TCCTGGACAGCAACCACACGGTGGGCGTCTTGGCCAGCGCCACCGC  
CCCCAGGGCCCCGGCCGACGCCTGGCGCGCCGCGGTGCTGATCTACGC  
GAGCGACGACACCCGCGCCCAACCCGACGCTCGCGGTGACCC  
TGCGGCTGCGCGGGGTGCCCCCGGCCCGGGCCTGGTCTACGTCACG  
CGCTACCTGGACAACGGGCTCTGCAGCCCCGACGGCGAGTGGCGGCG  
CCTGGGGCCGGCCCGTCTTCCCCACGGCAGAGCAGTTCCGGCGCATGC  
GCGCGGCTGAGGACCCGGTGGCCGCGGCGCCCCGCCCTTACCCGCC  
GGCGGCCGCTGACCCTGCGCCCCGCGCTGCGGCTGCCGTCGCTTTTG  
CTGGTGACGTGTGTGCGCGCCCCGAGAAGCCGCCCGGGCAGGTCAC  
GCGGCTCCGCGCCCTGCCCCCTGACCCAAGGGCAGCTGGTTCTGGTCTG  
GTCGGATGAACACGTGGGCTCCAAGTGCCTGTGGACATACGAGATCC  
AGTTCTCTCAGGACGGTAAGGCGTACACCCCGGTCAGCAGGAAGCCA  
TCGACCTTCAACCTCTTTGTGTTTACGCCAGACACAGGTGCTGTCTCT  
GGCTCCTACCGAGTTCGAGCCCTGGACTACTGGGCCCCGACCAGGCC  
CTTCTCGGACCCTGTGCCGTACCTGGAGGTCCCTGTGCCAAGAGGGCC  
CCCATCCCCGGGCAATCCAT GA

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FIG. 80B

Met Arg Pro Leu Arg Pro Arg Ala Ala Leu Leu Ala Leu Leu Ala Ser Leu Leu  
Ala Ala Pro Pro Val Ala Pro Ala Glu Ala Pro His Leu Val Gln Val Asp Ala Ala  
Arg Ala Leu Trp Pro Leu Arg Arg Phe Trp Arg Ser Thr Gly Phe Cys Pro Pro Leu  
Pro His Ser Gln Ala Asp Gln Tyr Val Leu Ser Trp Asp Gln Gln Leu Asn Leu Ala  
Tyr Val Gly Ala Val Pro His Arg Gly Ile Lys Gln Val Arg Thr His Trp Leu Leu  
Glu Leu Val Thr Thr Arg Gly Ser Thr Gly Arg Gly Leu Ser Tyr Asn Phe Thr His  
Leu Asp Gly Tyr Leu Asp Leu Leu Arg Glu Asn Gln Leu Leu Pro Gly Phe Glu  
Leu Met Gly Ser Ala Ser Gly His Phe Thr Asp Phe Glu Asp Lys Gln Gln Val  
Phe Glu Trp Lys Asp Leu Val Ser Ser Leu Ala Arg Arg Tyr Ile Gly Arg Tyr Gly  
Leu Ala His Val Ser Lys Trp Asn Phe Glu Thr Trp Asn Glu Pro Asp His His Asp  
Phe Asp Asn Val Ser Met Thr Met Gln Gly Phe Leu Asn Tyr Tyr Asp Ala Cys  
Ser Glu Gly Leu Arg Ala Ala Ser Pro Ala Leu Arg Leu Gly Gly Pro Gly Asp Ser  
Phe His Thr Pro Pro Arg Ser Pro Leu Ser Trp Gly Leu Leu Arg His Cys His Asp  
Gly Thr Asn Phe Phe Thr Gly Glu Ala Gly Val Arg Leu Asp Tyr Ile Ser Leu His  
Arg Lys Gly Ala Arg Ser Ser Ile Ser Ile Leu Glu Gln Glu Lys Val Val Ala Gln  
Gln Ile Arg Gln Leu Phe Pro Lys Phe Ala Asp Thr Pro Ile Tyr Asn Asp Glu Ala  
Asp Pro Leu Val Gly Trp Ser Leu Pro Gln Pro Trp Arg Ala Asp Val Thr Tyr Ala  
Ala Met Val Val Lys Val Ile Ala Gln His Gln Asn Leu Leu Leu Ala Asn Thr Thr  
Ser Ala Phe Pro Tyr Ala Leu Leu Ser Asn Asp Asn Ala Phe Leu Ser Tyr His Pro  
His Pro Phe Ala Gln Arg Thr Leu Thr Ala Arg Phe Gln Val Asn Asn Thr Arg  
Pro Pro His Val Gln Leu Leu Arg Lys Pro Val Leu Thr Ala Met Gly Leu Leu Ala  
Leu Leu Asp Glu Glu Gln Leu Trp Ala Glu Val Ser Gln Ala Gly Thr Val Leu  
Asp Ser Asn His Thr Val Gly Val Leu Ala Ser Ala His Arg Pro Gln Gly Pro Ala  
Asp Ala Trp Arg Ala Ala Val Leu Ile Tyr Ala Ser Asp Asp Thr Arg Ala His Pro  
Asn Arg Ser Val Ala Val Thr Leu Arg Leu Arg Gly Val Pro Pro Gly Pro Gly Leu  
Val Tyr Val Thr Arg Tyr Leu Asp Asn Gly Leu Cys Ser Pro Asp Gly Glu Trp  
Arg Arg Leu Gly Arg Pro Val Phe Pro Thr Ala Glu Gln Phe Arg Arg Met Arg  
Ala Ala Glu Asp Pro Val Ala Ala Ala Pro Arg Pro Leu Pro Ala Gly Gly Arg Leu  
Thr Leu Arg Pro Ala Leu Arg Leu Pro Ser Leu Leu Leu Val His Val Cys Ala  
Arg Pro Glu Lys Pro Pro Gly Gln Val Thr Arg Leu Arg Ala Leu Pro Leu Thr Gln  
Gly Gln Leu Val Leu Val Trp Ser Asp Glu His Val Gly Ser Lys Cys Leu Trp Thr  
Tyr Glu Ile Gln Phe Ser Gln Asp Gly Lys Ala Tyr Thr Pro Val Ser Arg Lys Pro  
Ser Thr Phe Asn Leu Phe Val Phe Ser Pro Asp Thr Gly Ala Val Ser Gly Ser Tyr  
Arg Val Arg Ala Leu Asp Tyr Trp Ala Arg Pro Gly Pro Phe Ser Asp Pro Val Pro  
Tyr Leu Glu Val Pro Val Pro Arg Gly Pro Pro Ser Pro Gly Asn Pro

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FIG. 81A

ATGCAGCTGAGGAACCCAGAACTACATCTGGGCTGCGCGCTTGCGCT  
TCGCTTCCTGGCCCTCGTTTCCTGGGACATCCCTGGGGCTAGAGCACT  
GGACAATGGATTGGCAAGGACGCCTACCATGGGCTGGCTGCACTGGG  
AGCGCTTCATGTGCAACCTTGACTGCCAGGAAGAGCCAGATTCCTGC  
ATCAGTGAGAAGCTCTTCATGGAGATGGCAGAGCTCATGGTCTCAGA  
AGGCTGGAAGGATGCAGGTTATGAGTACCTCTGCATTGATGACTGTTG  
GATGGCTCCCCAAAGAGATTCAGAAGGCAGACTTCAGGCAGACCCTC  
AGCGCTTTCCTCATGGGATTCGCCAGCTAGCTAATTATGTTACAGCA  
AAGGACTGAAGCTAGGGATTTATGCAGATGTTGGAAATAAAACCTGC  
GCAGGCTTCCCTGGGAGTTTTGGATACTACGACATTGATGCCCAGACC  
TTTGCTGACTGGGGAGTAGATCTGCTAAAATTTGATGGTTGTTACTGT  
GACAGTTTGGAATAATTTGGCAGATGGTTATAAGCACATGTCCTTGGCC  
CTGAATAGGACTGGCAGAAGCATTGTGTACTCCTGTGAGTGGCCTCTT  
TATATGTGGCCCTTTCAAAGCCCAATTATACAGAAATCCGACAGTAC  
TGCAATCACTGGCGAAATTTTGCTGACATTGATGATTCCTGGAAAAGT  
ATAAAGAGTATCTTGGACTGGACATCTTTTAACCAGGAGAGAATTGTT  
GATGTTGCTGGACCAGGGGGTTGGAATGACCCAGATATGTTAGTGAT  
TGGCAACTTTGGCCTCAGCTGGAATCAGCAAGTAACTCAGATGGCCCT  
CTGGGCTATCATGGCTGCTCCTTTATTCATGTCTAATGACCTCCGACA  
CATCAGCCCTCAAGCCAAAGCTCTCCTTCAGGATAAGGACGTAATTGC  
CATCAATCAGGACCCCTTGGGCAAGCAAGGGTACCAGCTTAGACAGG  
GAGACAACTTTGAAGTGTGGGAACGACCTCTCTCAGGCTTAGCCTGG  
GCTGTAGCTATGATAAACCGGCAGGAGATTGGTGGACCTCGCTCTTAT  
ACCATCGCAGTTGCTTCCCTGGGTAAAGGAGTGGCCTGTAATCCTGCC  
TGCTTCATCACACAGCTCCTCCCTGTGAAAAGGAAGCTAGGGTTCTAT  
GAATGGACTTCAAGGTTAAGAAGTCACATAAATCCCACAGGCACTGT  
TTTGCTTCAGCTAGAAAATACAATGCAGATGTCATTAAAAGACTTACT  
TTAA

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FIG. 81B

Met Gln Leu Arg Asn Pro Glu Leu His Leu Gly Cys Ala Leu Ala Leu Arg Phe  
Leu Ala Leu Val Ser Trp Asp Ile Pro Gly Ala Arg Ala Leu Asp Asn Gly Leu Ala  
Arg Thr Pro Thr Met Gly Trp Leu His Trp Glu Arg Phe Met Cys Asn Leu Asp  
Cys Gln Glu Glu Pro Asp Ser Cys Ile Ser Glu Lys Leu Phe Met Glu Met Ala Glu  
Leu Met Val Ser Glu Gly Trp Lys Asp Ala Gly Tyr Glu Tyr Leu Cys Ile Asp Asp  
Cys Trp Met Ala Pro Gln Arg Asp Ser Glu Gly Arg Leu Gln Ala Asp Pro Gln  
Arg Phe Pro His Gly Ile Arg Gln Leu Ala Asn Tyr Val His Ser Lys Gly Leu Lys  
Leu Gly Ile Tyr Ala Asp Val Gly Asn Lys Thr Cys Ala Gly Phe Pro Gly Ser Phe  
Gly Tyr Tyr Asp Ile Asp Ala Gln Thr Phe Ala Asp Trp Gly Val Asp Leu Leu Lys  
Phe Asp Gly Cys Tyr Cys Asp Ser Leu Glu Asn Leu Ala Asp Gly Tyr Lys His  
Met Ser Leu Ala Leu Asn Arg Thr Gly Arg Ser Ile Val Tyr Ser Cys Glu Trp Pro  
Leu Tyr Met Trp Pro Phe Gln Lys Pro Asn Tyr Thr Glu Ile Arg Gln Tyr Cys Asn  
His Trp Arg Asn Phe Ala Asp Ile Asp Asp Ser Trp Lys Ser Ile Lys Ser Ile Leu  
Asp Trp Thr Ser Phe Asn Gln Glu Arg Ile Val Asp Val Ala Gly Pro Gly Gly Trp  
Asn Asp Pro Asp Met Leu Val Ile Gly Asn Phe Gly Leu Ser Trp Asn Gln Gln  
Val Thr Gln Met Ala Leu Trp Ala Ile Met Ala Ala Pro Leu Phe Met Ser Asn Asp  
Leu Arg His Ile Ser Pro Gln Ala Lys Ala Leu Leu Gln Asp Lys Asp Val Ile Ala  
Ile Asn Gln Asp Pro Leu Gly Lys Gln Gly Tyr Gln Leu Arg Gln Gly Asp Asn  
Phe Glu Val Trp Glu Arg Pro Leu Ser Gly Leu Ala Trp Ala Val Ala Met Ile Asn  
Arg Gln Glu Ile Gly Gly Pro Arg Ser Tyr Thr Ile Ala Val Ala Ser Leu Gly Lys  
Gly Val Ala Cys Asn Pro Ala Cys Phe Ile Thr Gln Leu Leu Pro Val Lys Arg Lys  
Leu Gly Phe Tyr Glu Trp Thr Ser Arg Leu Arg Ser His Ile Asn Pro Thr Gly Thr  
Val Leu Leu Gln Leu Glu Asn Thr Met Gln Met Ser Leu Lys Asp Leu Leu

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FIG. 82A

ATGGCGCCCGTCGCCGTCTGGGCGCGCTGGCCGTCGGACTGGAGCT  
CTGGGCTGCGGCGCACGCCTTGCCCCGCCAGGTGGCATTACACCCTA  
CGCCCCGGAGCCCGGGAGCACATGCCGGCTCAGAGAATACTATGACC  
AGACAGCTCAGATGTGCTGCAGCAAATGCTCGCCGGGCCAACATGCA  
AAAGTCTTCTGTACCAAGACCTCGGACACCGTGTGTGACTCCTGTGAG  
GACAGCACATAACCCAGCTCTGGAAGTGGGTTCCCGAGTGCTTGAG  
CTGTGGCTCCCGCTGTAGCTCTGACCAGGTGGAACTCAAGCCTGCAC  
TCGGGAACAGAACCGCATCTGCACCTGCAGGCCCGGCTGGTACTGCG  
CGCTGAGCAAGCAGGAGGGGTGCCGGCTGTGCGCGCCGCTGCGCAAG  
TGCCGCCCCGGGCTTCGGCGTGGCCAGACCAGGAACTGAAACATCAGA  
CGTGGTGTGCAAGCCCTGTGCCCCGGGGACGTTCTCCAACACGACTTC  
ATCCACGGATATTTGCAGGCCCCACCAGATCTGTAACGTGGTGGCCAT  
CCCTGGGAATGCAAGCATGGATGCAGTCTGCACGTCCACGTCCCCCA  
CCCGGAGTATGGCCCCAGGGGCGAGTACACTTACCCAGCCAGTGTCC  
ACACGATCCCAACACACGCAGCCAACTCCAGAACCCAGCACTGCTCC  
AAGCACCTCCTTCCTGCTCCCAATGGGCCCCAGCCCCCAGCTGAAGG  
GAGCACTGGCGACTTCGCTCTTCCAGTTGGACTGATTGTGGGTGTGAC  
AGCCTTGGGTCTACTAATAATAGGAGTGGTGAAGTGTGTCATCATGAC  
CCAGGTGAAAAAGAAGCCCTTGTGCCTGCAGAGAGAAGCCAAGGTGC  
CTCACTTGCCCTGCCGATAAGGCCCGGGGTACACAGGGCCCCCGAGCAG  
CAGCACCTGCTGATCACAGCGCCGAGCTCCAGCAGCAGCTCCCTGGA  
GAGCTCGGCCAGTGCGTTGGACAGAAGGGCGCCCACTCGGAACCAAGC  
CACAGGCACCAGGCGTGGAGGCCAGTGGGGCCGGGGAGGCCCGGGC  
CAGCACCGGGAGCTCAGATTCTTCCCCTGGTGGCCATGGGACCCAGG  
TCAATGTACCTGCATCGTGAACGTCTGTAGCAGCTCTGACCACAGCT  
CACAGTGCTCCTCCCAAGCCAGCTCCACAATGGGAGACACAGATTCC  
AGCCCCTCGGAGTCCCCGAAGGACGAGCAGGTCCCCTTCTCCAAGGA  
GGAATGTGCCTTTCGGTCACAGCTGGAGACGCCAGAGACCCTGCTGG  
GGAGCACCGAAGAGAAGCCCCTGCCCTTGGAGTGCCTGATGCTGGG  
ATGAAGCCCAGTTAACCAGGCCGGTGTGGGCTGTGTGCTAGCCAAGG  
TGGGCTGAGCCCTGGCAGGATGACCCTGCGAAGGGGCCCTGGTCCTT  
CCAGGC



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FIG. 82B

Met Ala Pro Val Ala Val Trp Ala Ala Leu Ala Val Gly Leu Glu Leu Trp Ala Ala  
Ala His Ala Leu Pro Ala Gln Val Ala Phe Thr Pro Tyr Ala Pro Glu Pro Gly Ser  
Thr Cys Arg Leu Arg Glu Tyr Tyr Asp Gln Thr Ala Gln Met Cys Cys Ser Lys  
Cys Ser Pro Gly Gln His Ala Lys Val Phe Cys Thr Lys Thr Ser Asp Thr Val Cys  
Asp Ser Cys Glu Asp Ser Thr Tyr Thr Gln Leu Trp Asn Trp Val Pro Glu Cys  
Leu Ser Cys Gly Ser Arg Cys Ser Ser Asp Gln Val Glu Thr Gln Ala Cys Thr Arg  
Glu Gln Asn Arg Ile Cys Thr Cys Arg Pro Gly Trp Tyr Cys Ala Leu Ser Lys Gln  
Glu Gly Cys Arg Leu Cys Ala Pro Leu Arg Lys Cys Arg Pro Gly Phe Gly Val  
Ala Arg Pro Gly Thr Glu Thr Ser Asp Val Val Cys Lys Pro Cys Ala Pro Gly Thr  
Phe Ser Asn Thr Thr Ser Ser Thr Asp Ile Cys Arg Pro His Gln Ile Cys Asn Val  
Val Ala Ile Pro Gly Asn Ala Ser Met Asp Ala Val Cys Thr Ser Thr Ser Pro Thr  
Arg Ser Met Ala Pro Gly Ala Val His Leu Pro Gln Pro Val Ser Thr Arg Ser Gln  
His Thr Gln Pro Thr Pro Glu Pro Ser Thr Ala Pro Ser Thr Ser Phe Leu Leu Pro  
Met Gly Pro Ser Pro Pro Ala Glu Gly Ser Thr Gly Asp Phe Ala Leu Pro Val Gly  
Leu Ile Val Gly Val Thr Ala Leu Gly Leu Leu Ile Ile Gly Val Val Asn Cys Val  
Ile Met Thr Gln Val Lys Lys Lys Pro Leu Cys Leu Gln Arg Glu Ala Lys Val Pro  
His Leu Pro Ala Asp Lys Ala Arg Gly Thr Gln Gly Pro Glu Gln Gln His Leu Leu  
Ile Thr Ala Pro Ser Ser Ser Ser Ser Ser Leu Glu Ser Ser Ala Ser Ala Leu Asp Arg  
Arg Ala Pro Thr Arg Asn Gln Pro Gln Ala Pro Gly Val Glu Ala Ser Gly Ala Gly  
Glu Ala Arg Ala Ser Thr Gly Ser Ser Asp Ser Ser Pro Gly Gly His Gly Thr Gln  
Val Asn Val Thr Cys Ile Val Asn Val Cys Ser Ser Ser Asp His Ser Ser Gln Cys  
Ser Ser Gln Ala Ser Ser Thr Met Gly Asp Thr Asp Ser Ser Pro Ser Glu Ser Pro  
Lys Asp Glu Gln Val Pro Phe Ser Lys Glu Glu Cys Ala Phe Arg Ser Gln Leu Glu  
Thr Pro Glu Thr Leu Leu Gly Ser Thr Glu Glu Lys Pro Leu Pro Leu Gly Val Pro  
Asp Ala Gly Met Lys Pro Ser

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## FIG. 83A

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Arg Ala Ser Gln Asp Val Asn Thr Ala Val Ala Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Ser Ala Ser Phe Leu Tyr Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Arg Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln His Tyr Thr Thr Pro  
Pro Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys

## FIG. 83B

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg  
Leu Ser Cys Ala Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg  
Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala Arg Ile Tyr Pro Thr Asn Gly Tyr  
Thr Arg Tyr Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Ala Asp Thr Ser Lys  
Asn Thr Ala Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr  
Tyr Cys Ser Arg Trp Gly Gly Asp Gly Phe Tyr Ala Met Asp Tyr Trp Gly Gln  
Gly Thr Leu Val Thr Val Ser Ser

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FIG. 84A

Gln Val Thr Leu Arg Glu Ser Gly Pro Ala Leu Val Lys Pro Thr Gln Thr Leu Thr  
Leu Thr Cys Thr Phe Ser Gly Phe Ser Leu Ser Thr Ser Gly Met Ser Val Gly Trp  
Ile Arg Gln Pro Ser Gly Lys Ala Leu Glu Trp Leu Ala Asp Ile Trp Trp Asp Asp  
Lys Lys Asp Tyr Asn Pro Ser Leu Lys Ser Arg Leu Thr Ile Ser Lys Asp Thr Ser  
Lys Asn Gln Val Val Leu Lys Val Thr Asn Met Asp Pro Ala Asp Thr Ala Thr  
Tyr Tyr Cys Ala Arg Ser Met Ile Thr Asn Trp Tyr Phe Asp Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ser

FIG. 84B

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Thr Cys Lys Cys Gln Leu Ser Val Gly Tyr Met His Trp Tyr Gln Gln Lys  
Pro Gly Lys Ala Pro Lys Leu Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val  
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser  
Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Phe Gln Gly Ser Gly Tyr Pro Phe  
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 85A

GACATCTTGCTGACTCAGTCTCCAGCCATCCTGTCTGTGAGTCCAGGA  
GAAAGAGTCAGTTTCTCCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGC  
ATCCACTGGTATCAGCAAAGAACAAATGGTTCTCCAAGGCTTCTCATA  
AAGTATGCTTCTGAGTCTATGTCTGGGATCCCTTCCAGGTTTAGTGGC  
AGTGGATCAGGGACAGATTTTACTCTTAGCATCAACACTGTGGAGTCT  
GAAGATATTGCAGATTATTACTGTCAACAAAGTCATAGCTGGCCATTC  
ACGTTTCGGCTCGGGGACAAATTTGGAAGTAAAAGAAGTGAAGCTTGA  
GGAGTCTGGAGGAGGCTTGGTGCAACCTGGAGGATCCATGAAACTCT  
CCTGTGTTGCCTCTGGATTCATTTTTCAGTAACCACTGGATGAACTGGG  
TCCGCCAGTCTCCAGAGAAGGGGCTTGAGTGGGTTGCTGAAATTAGA  
TCAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGG  
AGGTTACCATCTCAAGAGATGATTCCAAAAGTGCTGTCTACCTGCAA  
ATGACCGACTTAAGAAGTGAAGACACTGGCGTTTATTACTGTTCCAGG  
AATTACTACGGTAGTACCTACGACTACTGGGGCCAAGGCACCACTCTC  
ACAGTCTCC

FIG. 85B

Asp Ile Leu Leu Thr Gln Ser Pro Ala Ile Leu Ser Val Ser Pro Gly Glu Arg Val  
Ser Phe Ser Cys Arg Ala Ser Gln Phe Val Gly Ser Ser Ile His Trp Tyr Gln Gln  
Arg Thr Asn Gly Ser Pro Arg Leu Leu Ile Lys Tyr Ala Ser Glu Ser Met Ser Gly  
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Ser Ile Asn  
Thr Val Glu Ser Glu Asp Ile Ala Asp Tyr Tyr Cys Gln Gln Ser His Ser Trp Pro  
Phe Thr Phe Gly Ser Gly Thr Asn Leu Glu Val Lys Glu Val Lys Leu Glu Glu Ser  
Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu Ser Cys Val Ala Ser Gly  
Phe Ile Phe Ser Asn His Trp Met Asn Trp Val Arg Gln Ser Pro Glu Lys Gly Leu  
Glu Trp Val Ala Glu Ile Arg Ser Lys Ser Ile Asn Ser Ala Thr His Tyr Ala Glu  
Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Ala Val Tyr  
Leu Gln Met Thr Asp Leu Arg Thr Glu Asp Thr Gly Val Tyr Tyr Cys Ser Arg  
Asn Tyr Tyr Gly Ser Thr Tyr Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser

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FIG. 86A

ATGGAGACAGACACACTCCTGTTATGGGTGCTGCTGCTCTGGGTTCCA  
GGTTCCACTGGTGACGTCAGGCGAGGGCCCCGGAGCCTGCGGGGGCAG  
GGACGCGCCAGCCCCACGCCCTGCGTCCCGGCCGAGTGCTTCGACC  
TGCTGGTCCGCCACTGCGTGGCCTGCGGGCTCCTGCGCACGCCGCGGC  
CGAAACCGGCCGGGGCCAGCAGCCCTGCGCCCAGGACGGCGCTGCAG  
CCGCAGGAGTCGGTGGGCGCGGGGGCCGGCGAGGCGGCGGTTCGACA  
AACTCACACATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGA  
CCGTCAGTCTTCCTCTTCCCCCAAAACCAAGGACACCCTCATGATC  
TCCCGGACCCCTGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGA  
AGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGC  
ATAATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTA  
CCGTGTGGTCAGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGG  
CAAGGAGTACAAGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCA  
TCGAGAAAACCATCTCCAAAGCCAAAGGGCAGCCCCGAGAACCACAG  
GTGTACACCCTGCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGT  
CAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGT  
GGAGTGGGAGAGCAATGGGCAGCCGGAGAACAATAAGACCACG  
CCTCCCGTGTTGGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTC  
ACCGTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTC  
CGTGATGCATGAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCT  
CCCTGTCTCCCGGGAAATGA

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## FIG. 86B

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro Gly Ser  
Thr Gly Asp Val Arg Arg Gly Pro Arg Ser Leu Arg Gly Arg Asp Ala Pro Ala  
Pro Thr Pro Cys Val Pro Ala Glu Cys Phe Asp Leu Leu Val Arg His Cys Val Ala  
Cys Gly Leu Leu Arg Thr Pro Arg Pro Lys Pro Ala Gly Ala Ser Ser Pro Ala Pro  
Arg Thr Ala Leu Gln Pro Gln Glu Ser Val Gly Ala Gly Ala Gly Glu Ala Ala Val  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser  
Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu  
Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn  
Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys  
Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro  
Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly  
Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn  
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys  
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys

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FIG. 87

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Asp Gly Ile Val Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser  
Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro  
Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

FIG. 88

Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Gly Pro Gly Thr Ser Val Arg  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Lys  
Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Val Asp Lys Ser Ser  
Thr Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe  
Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Arg Gly Thr  
Leu Val Thr Val Ser Ala

FIG. 89

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys

FIG. 90

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser

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FIG. 91

Asp Ile Gln Met Thr Gln Thr Pro Ser Thr Leu Ser Ala Ser Val Gly Asp Arg Val  
Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Asn Asn Tyr Leu Asn Trp Tyr Gln Gln  
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Thr Ser Thr Leu His Ser Gly  
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser  
Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu  
Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu Val Lys Arg Thr Val Ala Ala Pro  
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val  
Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val  
Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys  
Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys  
His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr Lys  
Ser Phe Asn Arg Gly Glu Cys

FIG. 92

Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ser Ser Val Lys  
Val Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn Tyr Leu Ile Glu Trp Val Arg  
Gln Ala Pro Gly Gln Gly Leu Glu Trp Ile Gly Val Ile Tyr Pro Gly Ser Gly Gly  
Thr Asn Tyr Asn Glu Lys Phe Lys Gly Arg Val Thr Leu Thr Val Asp Glu Ser  
Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr  
Phe Cys Ala Arg Arg Asp Gly Asn Tyr Gly Trp Phe Ala Tyr Trp Gly Gln Gly  
Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala  
Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp  
Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val  
His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val  
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys  
Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His  
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe  
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val  
Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly  
Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu  
Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser  
Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp  
Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser  
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr  
Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp  
Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu  
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly



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FIG. 93A

ATGGATTTTCAGGTGCAGATTATCAGCTTCCTGCTAATCAGTGCTTCA  
GTCATAATGTCCAGAGGGCAAATTGTTCTCTCCCAGTCTCCAGCAATC  
CTGTCTGCATCTCCAGGGGAGAAGGTCACAATGACTTGCAGGGCCAG  
CTCAAGTGTAAGTTACATCCACTGGTTCCAGCAGAAGCCAGGATCCTC  
CCCCAAACCCTGGATTTATGCCACATCCAACCTGGCTTCTGGAGTCCC  
TGTTTCGCTTCAGTGGCAGTGGGTCTGGGACTTCTTACTCTCTCACAAT  
CAGCAGAGTGGAGGCTGAAGATGCTGCCACTTATTACTGCCAGCAGT  
GGACTAGTAACCCACCCACGTTCTGGAGGGGGGACCAAGCTGGAAATC  
AAA

FIG. 93B

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser Val Ile Met Ser  
Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly Glu  
Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Val Ser Tyr Ile His Trp Phe Gln  
Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser  
Gly Val Pro Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile  
Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp Thr Ser Asn  
Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys

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FIG. 94A

ATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTACGCGTG  
TCCTGTCCCAGGTACAACTGCAGCAGCCTGGGGCTGAGCTGGTGAAG  
CCTGGGGCCTCAGTGAAGATGTCCTGCAAGGCTTCTGGCTACACATTT  
ACCAGTTACAATATGCACTGGGTAAAACAGACACCTGGTCGGGGCCT  
GGAATGGATTGGAGCTATTTATCCCGGAAATGGTGATACTTCCTACAA  
TCAGAAGTTCAAAGGCAAGGCCACATTGACTGCAGACAAATCCTCCA  
GCACAGCCTACATGCAGCTCAGCAGCCTGACATCTGAGGACTCTGCG  
GTCTATTACTGTGCAAGATCGACTTACTACGGCGGTGACTGGTACTTC  
AATGTCTGGGGCGCAGGGACCACGGTCACCGTCTCTGCA

FIG. 94B

Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg Val Leu Ser  
Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala Ser Val Lys  
Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr Asn Met His Trp Val Lys  
Gln Thr Pro Gly Arg Gly Leu Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp  
Thr Ser Tyr Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser  
Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr  
Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn Val Trp Gly Ala Gly  
Thr Thr Val Thr Val Ser Ala

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FIG. 95A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGGCGGAAGTGGGCG  
GAGTTAGGGGCGGGATGGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATTCCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT  
TATGGGACTTTCCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGC  
GGTTTGACTCACGGGGATTTCCTCAAGTCTCCACCCCATTTGACGTCAATG  
GGAGTTTGTGGTGGCACCAGTCAACGGGACTTTCCAGTAAATGTCGTA  
ACAACCTCCGCCCCATTGACGCAATGGGCGGTAGGCGTGTACGGTGG  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTCACCATGAGGGTCCCCGCTCAGCTCCT  
GGGGCTCCTGCTGCTCTGGCTCCCAGGTGCACGATGTGATGGTACCAA  
GGTGGAAATCAAACGTACGGTGGCTGCACCATCTGTCTTCATCTTCCC  
GCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCT  
GCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAGGTGG  
ATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAG  
GACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG  
CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC  
ATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGGGAGAG  
TGTTGAATTCAGATCCGTTAACGGTTACCAACTACCTAGACTGGATT  
GTGACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTG  
CCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCT  
TGACCCTGGAAGGTGCCACTCCCCTGTCCTTTCTTAATAAAATGAGG  
AAATTGCATCGCATTGTCTGAGTAGGTGTCAATTCTATTCTGGGGGGTG  
GGGTGGGGCAGGACAGCAAGGGGGAGGATTGGGAAGACAATAGCAG  
GCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGAC  
AGCTATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGC  
CCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCCTACTT  
GGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGT  
TTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGGACTCACGGGGA  
TTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGGTGGCAC

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FIG. 95B

CAAAATCAACGGGACTTTCCAAAATGTCGTAACAACCTCCGCCCCATTG  
ACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAG  
AGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGAACACAGACCC  
GTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGTCGCTGTTGCTA  
CGCGTGTGCTAGCACCAAGGGGCCCATCGGTCTTCCCCCTGGCACCCCT  
CCTCCAAGAGCACCTCTGGGGGGCACAGCGGCCCTGGGCTGCCTGGTC  
AAGGACTACTTCCCCGAACCGGTGACGGTGTGCTGGAACCTCAGGCGC  
CCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAGG  
ACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGG  
CACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACCA  
AGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACACA  
TGCCCAACCGTGCCCAAGCACCTGAACTCCTGGGGGGGACCGTCAGTCTTC  
CTCTTCCCCCCTAAAACCCAAGGACACCCCTCATGATCTCCCGGACCCCT  
GAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGGT  
CAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAGA  
CAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAGC  
GTCCTCACCGTCCCTGCACCAGGACTGGCTGAATGGCAAGGACTACAA  
GTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACCA  
TCTCCAAGGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTG  
CCCCCATCCCGGGATGAGCTGACCAGGAACCAGGTCAGCCTGACCTG  
CCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAGA  
GCAATGGGCAGCCGGAGAACAACCTACAAGACCACGCCTCCCGTGCTG  
GACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAAG  
AGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATGA  
GGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGG  
TAAATGAGGATCCGTAAACGGTTACCAACTACCTAGACTGGATTCTGTG  
ACAACATGCGGCCGTGATATCTACGTATGATCAGCCTCGACTGTGCCT  
TCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCTTCCTTGA  
CCCTGGAAGGTGCCACTCCCAGTGTCTTTCCTAATAAAAATGAGGAAA  
TTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGGG  
TGGGGCAGGACAGCAAGGGGGGAGGATTGGGAAGACAATAGCAGGCA  
TGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGGCTCGACAGC  
GCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCATA  
ATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCAGTAGTTGAT  
TGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGG

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FIG. 95C

GCTGCGATTTTCGCGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTG  
GTAGGATTTTATCCCCGCTGCCATCATGGTTCGACCATTGAACTGCAT  
CGTCGCCGTGTCCCAAATATGGGGATTGGCAAGAACGGAGACCTAC  
CCTGGCCTCCGCTCAGGAACGAGTTCAAGTACTTCCAAAGAATGACC  
ACAACCTCTTCAGTGGAAGGTAAACAGAATCTGGTGATTATGGGTAG  
GAAAACCTGGTTCTCCATTCTGAGAACAAATCGACCTTTAAAGGACA  
GAATTAATATAGTTCTCAGTAGAGAACTCAAAGAACCACCACGAGGA  
GCTCATTTTCTTGCCAAAAGTTTGGATGATGCCTTAAGACTTATTGAA  
CAACCGGAATTGGCAAGTAAAGTAGACATGGTTTGGATAGTCGGAGG  
CAGTTCTGTTTACCAGGAAGCCATGAATCAACCAGGCCACCTTAGACT  
CTTTGTGACAAGGATCATGTCAGGAATTTGAAAGTGACACGTTTTTCCC  
AGAAATTGATTTGGGGAAATATAAACTTCTCCCAGAATACCCAGGCG  
TCCTCTCTGAGGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAA  
GTCTACGAGAAGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGC  
TCCCCCTCCTAAAGTCATGCATTTTTTATAAGACCATGGGACTTTTGCTG  
GCTTTAGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGT  
TTGCCCTCCCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAC  
TGTCCTTTCCTAATAAAAATGAGGAAATTGCATCGCATTGTCTGAGTAG  
GTGTCATTCTATTCTGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGG  
AGGATTGGGAAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCT  
ATGGAACCAGCTGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTT  
ATTTGCATAATGAGAAAAAAAGGAAAATTAATTTTAACACCAATTCA  
GTAGTTGATTGAGCAAATGCGTTGCCAAAAGGATGCTTTAGAGACA  
GTGTTCTCTGCACAGATAAGGACAAACATTATTCAGAGGGAGTACCC  
AGAGCTGAGACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGA  
AATATGCTTGTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGG  
TAAGGGCCAATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGG  
CAGAGCATATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTC  
TGACATAGTTGTGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAA  
GATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC  
GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGT  
GTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGA  
CCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCGGCTAT  
CGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTGCTCGACGTTG  
TCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGG  
CAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATC  
ATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGC  
CCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAATCG  
GATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATC  
AGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGCGCATG  
CCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCG

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FIG. 95D

AATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGC  
CGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCG  
TGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT  
GCTTTACGGTATCGCCGCTTCCCGATTTCGCAGCGCATCGCCTTCTATC  
GCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGAC  
CGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCG  
CCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCG  
GCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCC  
ACCCCAACTTGTTTATTGCGAGCTTATAATGGTTACAAATAAAGCAATA  
GCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTT  
GTGGTTTGTCCAAACTCATCAATCTATCTTATCATGTCTGGATCGCGG  
CCGCGATCCCGTCGAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCC  
TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG  
AGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC  
ATTAATTGCGTTGCGCTCACTGCCCGCTTTCAGTCGGGAAACCTGTC  
GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT  
TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC  
GGTCGTTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA  
TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA  
GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGC  
TGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATC  
GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC  
CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC  
CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG  
GCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC  
GTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC  
CGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCCGGTAAGA  
CACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG  
AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA  
ACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGA  
AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA  
CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATT  
ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC  
GGGGTCTGACGCTCAGTGGAACGAAACTCACGTAAAGGGATTTTGG  
TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA  
AATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG  
ACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTC  
TATTCGTTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTAC  
GATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGC  
GAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA  
GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTC  
CATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGC

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FIG. 95E

CAGTTAATAGTTTGGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGG  
TGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTCCCAAC  
GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT  
AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTG  
TTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGC  
CATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCAT  
TCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCCGGCGTCAA  
TACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATC  
ATTGGAAAACGTTCTTCGGGGCGAAAACCTCTCAAGGATCTTACCGCTG  
TTGAGATCCAGTTCGATGTAACCCACTCGTGACCCCAACTGATCTTCA  
GCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGG  
CAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAA  
TACTCATACTCTTCCTTTTTTCAATATTATTGAAGCATTATCAGGGTTA  
TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAACA  
AATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT

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FIG. 96A

GACGTCGCGGCCGCTCTAGGCCTCCAAAAAAGCCTCCTCACTACTTCT  
GGAATAGCTCAGAGGCCGAGGCGGCCTCGGCCTCTGCATAAATAAAA  
AAAATTAGTCAGCCATGCATGGGGCGGAGAATGGGCGGAAGTGGGCG  
GAGTTAGGGGCGGGATGGGCGGAGTTAGGGGCGGGACTATGGTTGCT  
GACTAATTGAGATGCATGCTTTGCATACTTCTGCCTGCTGGGGAGCCT  
GGGGACTTTCCACACCTGGTTGCTGACTAATTGAGATGCATGCTTTGC  
ATACTTCTGCCTGCTGGGGAGCCTGGGGACTTTCCACACCCTAACTGA  
CACACATTCCACAGAATTAATCCCCTAGTTATTAATAGTAATCAATT  
ACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAA  
CTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCC  
ATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGA  
CTTCCATTGACGTCAATGGGTGGACTATTTACGGTAAACTGCCCACT  
TGCGAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACG  
TCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCT  
TATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTA  
TTACCATGGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATACC  
GGTTTGACTCACGCGGATTTCCAAGTCTCCACCCCATTTGACGTCAATG  
GGAGTTTGTGGTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA  
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGG  
GAGGTCTATATAAGCAGAGCTGGGTACGTGAACCGTCAGATCGCCTG  
GAGACGCCATCACAGATCTCTCACTATGGATTTTTCAGGTGCAGATTAT  
CAGCTTCCTGCTAATCAGTGCTTCAGTCATAATGTCCAGAGGACAAAT  
TGTTCTCTCCCAGTCTCCAGCAATCCTGTCTGCATCTCCAGGGGAGAA  
GGTCACAATGACTTGCAGGGGCCAGCTCAAGTGTAAGTTACATCCACT  
GGTTCAGCAGAAGCCAGGATCCTCCCCCAAACCCTGGATTTATGCCA  
CATCCAACCTGGCTTCTGGAGTCCCTGTTTCGCTTCAGTGGCAGTGGGT  
CTGGGACTTCTTACTCTCTCACAATCAGCAGAGTGGAGGCTGAAGATG  
CTGCCACTTATTACTGCCAGCAGTGGACTAGTAACCCACCCACGTTCG  
GAGGGGGGACCAAGCTGGAAATCAAACGTACGGTGGCTGCACCATCT  
GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCC  
TCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTA  
CAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG  
TGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA  
CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCC  
TGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTT  
CAACAGGGGAGAGTGTTGAATTCAGATCCGTAAACGGTTACCAACTA  
CCTAGACTGGATTCGTGACAACATGCGGCCGTGATATCTACGTATGAT  
CAGCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTC  
CCCCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCACTGTCCTTTCC



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FIG. 96B

TAATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCT  
ATTCTGGGGGGGTGGGGGTGGGGGCAGGACAGCAAGGGGGGAGGATTGGG  
AAGACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCA  
GCTGGGGGCTCGACAGCTATGCCAAGTACGCCCCCTATTGACGTCAATG  
ACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGG  
ACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCAT  
GGTGATGCGGTTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTTG  
ACTCACGGGGATTTCCTCAAGTCTCCACCCCATTGACGTCAATGGGAGTT  
TGTTTTTGGCACCAAAATCAACGGGACTTTCCTCAAAATGTCGTAACAAC  
CCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTC  
TATATAAGCAGAGCTGGGTACGTCCTCACATTCAGTGATCAGCACTGA  
ACACAGACCCGTCGACATGGGTTGGAGCCTCATCTTGCTCTTCCTTGT  
CGCTGTTGCTACGCGTGTCTGTCCCAGGTACAACCTGCAGCAGCCTGG  
GGCTGAGCTGGTGAAGCCTGGGGCCTCAGTGAAGATGTCCTGCAAGG  
CTTCTGGCTACACATTTACCAGTTACAATATGCACTGGGTAAAACAGA  
CACCTGGTCGGGGGCCTGGAATGGATTGGAGCTATTTATCCCGGAAAT  
GGTGATACTTCCTACAATCAGAAGTTCAAAGGCAAGGCCACATTGAC  
TGCAGACAAATCCTCCAGCACAGCCTACATGCAGCTCAGCAGCCTGA  
CATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCGACTTACTACG  
GCGGTGACTGGTACTTCAATGTCTGGGGCGCAGGGACCACGGTCACC  
GTCTCTGCAGCTAGCACCAAGGGGCCATCGGTCTTCCCCCTGGCACCC  
TCCTCCAAGAGCACCTCTGGGGGCGACAGCGGCCCTGGGCTGCCTGGT  
CAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAACCTCAGGCG  
CCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCAG  
GACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGG  
GCACCCAGACCTACATCTGCAACGTGAATCACAAGCCCAGCAACACC  
AAGGTGGACAAGAAAGCAGAGCCCAAATCTTGTGACAAAACCTCACAC  
ATGCCACCGTGCCAGCACCTGAACTCCTGGGGGGACCGTCAGTCTT  
CCTCTTCCCCCCTAAAACCCAAGGACACCCTCATGATCTCCCGGACCCC  
TGAGGTCACATGCGTGGTGGTGGACGTGAGCCACGAAGACCCTGAGG  
TCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCATAATGCCAAG  
ACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTCAG  
CGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACA  
AGTGCAAGGTCTCCAACAAAGCCCTCCCAGCCCCCATCGAGAAAACC  
ATCTCCAAGCCAAAGGGCAGCCCCGAGAACCACAGGTGTACACCCT  
GCCCCCATCCCGGGATGAGCTGACCAAGAACCAGGTCAGCCTGACCT  
GCCTGGTCAAAGGCTTCTATCCCAGCGACATCGCCGTGGAGTGGGAG  
AGCAATGGGCAGCCGGAGAACAACTACAAGACCACGCCTCCCGTGGCT  
GGACTCCGACGGCTCCTTCTTCTCTACAGCAAGCTCACCGTGGACAA  
GAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCATG  
AGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGG  
GTAAATGAGGATCCGTAAACGGTTACCAACTACCTAGACTGGATTCTG

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FIG. 96C

GACAACATGCGGCCCGTGATATCTACGTATGATCAGCCTCGACTGTGCC  
TTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCCCCGTGCCCTTCCTTG  
ACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTAATAAAATGAGGAA  
ATTGCATCGCATTGTCTGAGTAGGTGTCATTCTATTCTGGGGGGGTGGG  
GTGGGGCAGGACAGCAAGGGGGGAGGATTGGGAAGACAATAGCAGGC  
ATGCTGGGGATGCGGTGGGCTCTATGGAACCAGCTGGGGCTCGACAG  
CGCTGGATCTCCCGATCCCCAGCTTTGCTTCTCAATTTCTTATTTGCAT  
AATGAGAAAAAAAGGAAAATTAATTTTAAACACCAATTCAGTAGTTGA  
TTGAGCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCT  
GCACAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAG  
ACTCCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTT  
GTCATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCC  
AATCTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCAT  
ATAAGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAG  
TTGTGTTGGGAGCTTGGATAGCTTGGACAGCTCAGGGCTGCGATTTTCG  
CGCCAAACTTGACGGCAATCCTAGCGTGAAGGCTGGTAGGATTTTATC  
CCCGCTGCCATCATGGTTCGACCATTGAACTGCATCGTCGCCGTGTCC  
CAAAATATGGGGATTGGCAAGAACGGAGACCTACCCTGGCCTCCGCT  
CAGGAACGAGTTCAAGTACTTCCAAAGAATGACCACAACCTCTTCAG  
TGGAAGGTAAACAGAATCTGGTGATTATGGGTAGGAAAACCTGGTTC  
TCCATTCTGAGAAGAATCGACCTTTAAAGGACAGAATTAATATAGTT  
CTCAGTAGAGAACTCAAAGAACCACGAGGAGCTCATTTTCTTGC  
CAAAAGTTTGGATGATGCCTTAAGACTTATTGAACAACCGGAATTGG  
CAAGTAAAGTAGACATGGTTTGGATAGTCGGAGGCAGTTCTGTTTACC  
AGGAAGCCATGAATCAACCAGGCCACCTTAGACTCTTTGTGACAAGG  
ATCATGCAGGAATTTGAAAGTGACACGTTTTTCCCAGAAATTGATTTG  
GGGAAATATAAACTTCTCCCAGAATACCCAGGCGTCCTCTCTGA  
GGTCCAGGAGGAAAAAGGCATCAAGTATAAGTTTGAAGTCTACGAGA  
AGAAAGACTAACAGGAAGATGCTTTCAAGTTCTCTGCTCCCCTCCTAA  
AGCTATGCATTTTTTATAAGACCATGGGACTTTTGCTGGCTTTAGATCA  
GCCTCGACTGTGCCTTCTAGTTGCCAGCCATCTGTTGTTTGCCCCCTCCC  
CCGTGCCTTCCTTGACCCTGGAAGGTGCCACTCCCAGTGTCTTTCTTA  
ATAAAATGAGGAAATTGCATCGCATTGTCTGAGTAGGTGTCATTCTAT  
TCTGGGGGGGTGGGGTGGGGCAGGACAGCAAGGGGGGAGGATTGGGAA  
GACAATAGCAGGCATGCTGGGGATGCGGTGGGCTCTATGGAACCAGC  
TGGGGCTCGAGCTACTAGCTTTGCTTCTCAATTTCTTATTTGCATAATG  
AGAAAAAAAGGAAAATTAATTTTAAACACCAATTCAGTAGTTGATTGA  
GCAAATGCGTTGCCAAAAAGGATGCTTTAGAGACAGTGTTCTCTGCA  
CAGATAAGGACAAACATTATTCAGAGGGAGTACCCAGAGCTGAGACT  
CCTAAGCCAGTGAGTGGCACAGCATTCTAGGGAGAAATATGCTTGTC  
ATCACCGAAGCCTGATTCCGTAGAGCCACACCTTGGTAAGGGCCAAT  
CTGCTCACACAGGATAGAGAGGGCAGGAGCCAGGGCAGAGCATATA  
AGGTGAGGTAGGATCAGTTGCTCCTCACATTTGCTTCTGACATAGTTG

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FIG. 96D

TGTTGGGAGCTTGGATCGATCCTCTATGGTTGAACAAGATGGATTGCA  
CGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTG  
GGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTC  
AGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGC  
CCTGAATGAACTGCAGGACGAGGCAGCGCGGCTATCGTGGCTGGCCA  
CGACGGGCGTTCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGG  
GAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGGCAGGATCTCCTG  
TCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCA  
ATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCGACCAC  
CAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGG  
TCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGGCTCGCGC  
CAGCCGAACCTGTTTCGCCAGGCTCAAGGCGCGCATGCCCCGACGGCGAG  
GATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG  
GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTG  
GCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGA  
AGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTAT  
CGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA  
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGAC  
GCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGA  
AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCT  
CCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCCACCCCAACTTGTT  
TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTT  
CACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAA  
ACTCATCAATCTATCTTATCATGTCTGGATCGCGGGCCGCGATCCCGTC  
GAGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGT  
TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG  
TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT  
GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA  
TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGC GTATTGGGC  
GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCTCGGCT  
GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA  
CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA  
GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC  
ATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT  
CAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCC  
CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC  
CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA  
ATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTGTTTCGCTCCAA  
GCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTT  
ATCCGGTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC

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FIG. 96E

GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG  
TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC  
ACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC  
TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGC  
TGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA  
AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC  
TCAGTGGAACGAAAACCTCACGTAAAGGGATTTTGGTTCATGAGATTATC  
AAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAAATGAAGTTTTAA  
ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATG  
CTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCC  
ATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGG  
CTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTC  
ACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCG  
AGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTA  
ATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGC  
GCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACGCTCGTCGT  
TTGGTATGGCTTCATTCAGCTCCGGTCCCAACGATCAAGGCGAGTTA  
CATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTC  
CGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTA  
TGGCAGCACTGCATAATTCTCTTACTGTTCATGCCATCCGTAAGATGCT  
TTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTA  
TGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACC  
GCGCCACATAGCAGAACTTTAAAGTGCTCATCATTGGAAAACGTTCT  
TCGGGGCGAAAACCTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCCG  
ATGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCA  
CCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAA  
AAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCT  
TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGG  
ATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGC  
GCACATTTCCCCGAAAAGTGCCACCT

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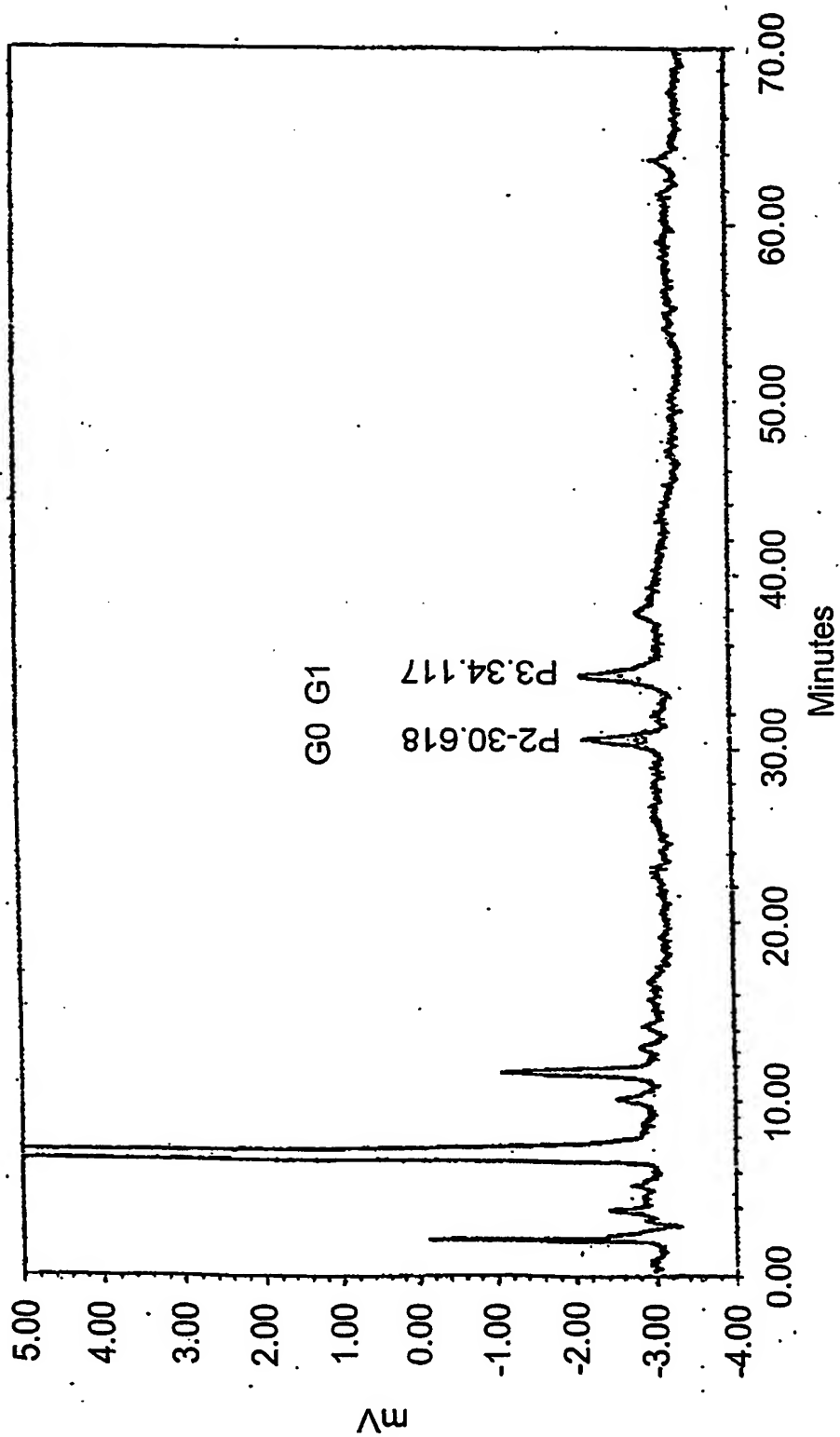


FIG. 97A

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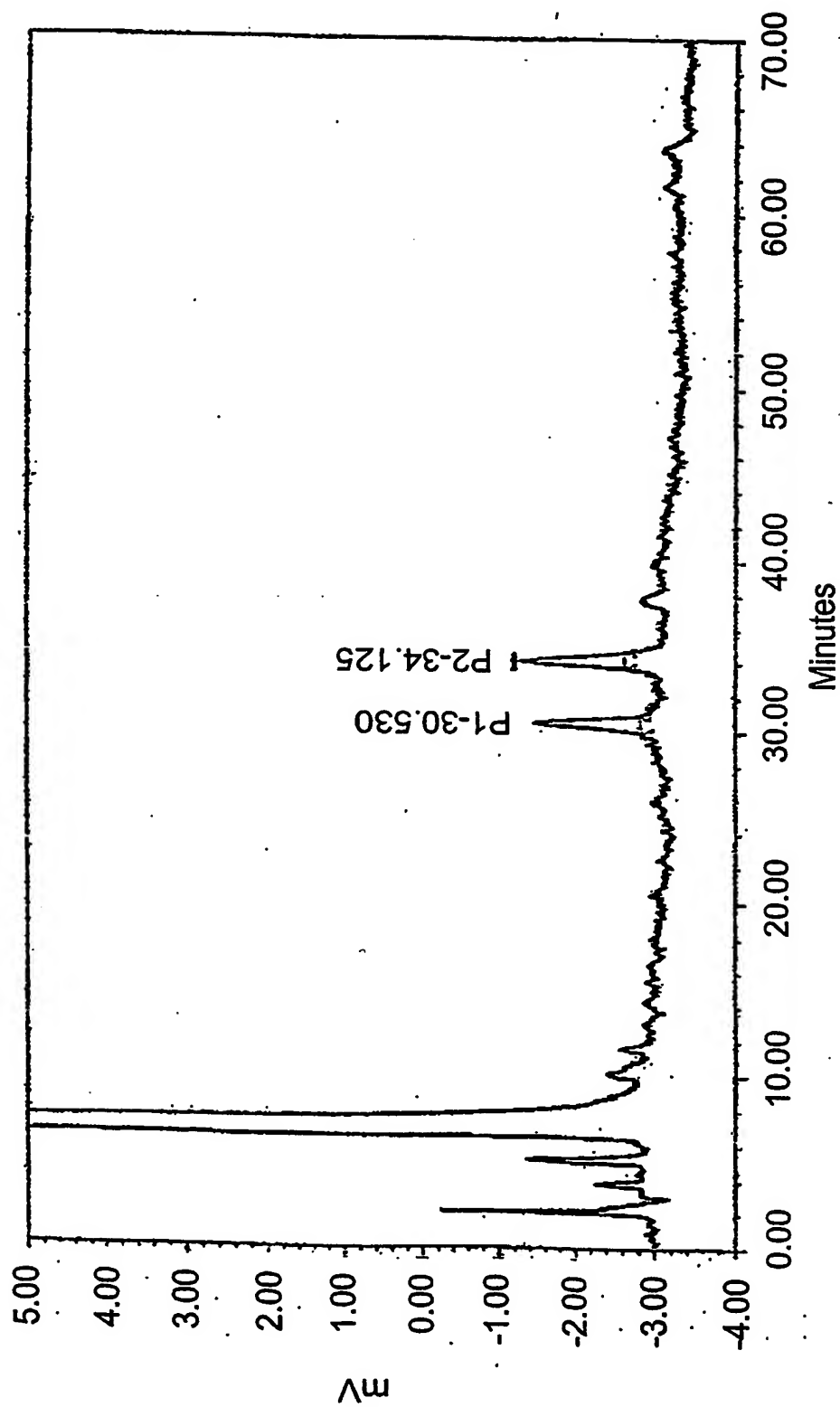


FIG. 97B

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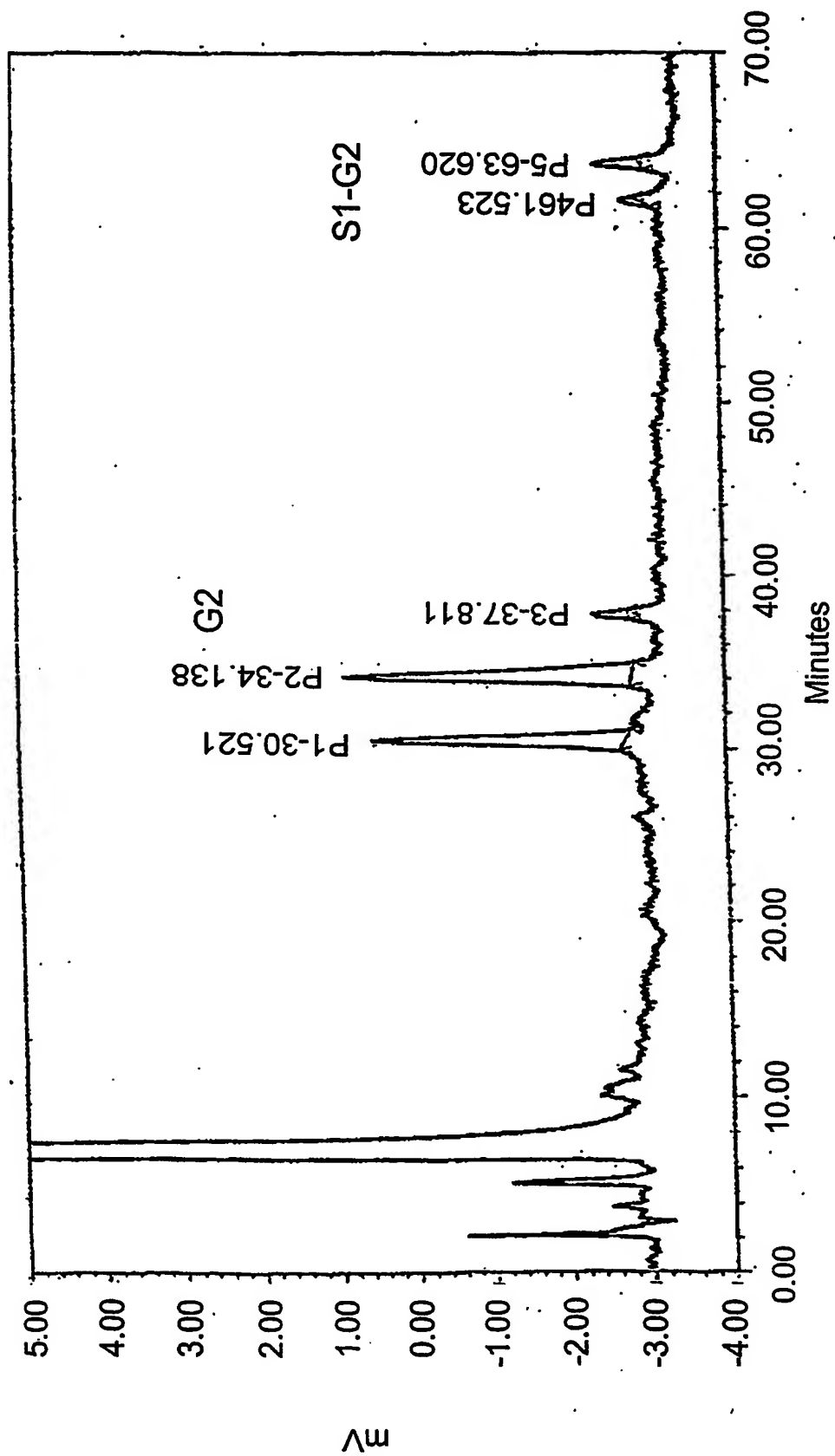


FIG. 97C

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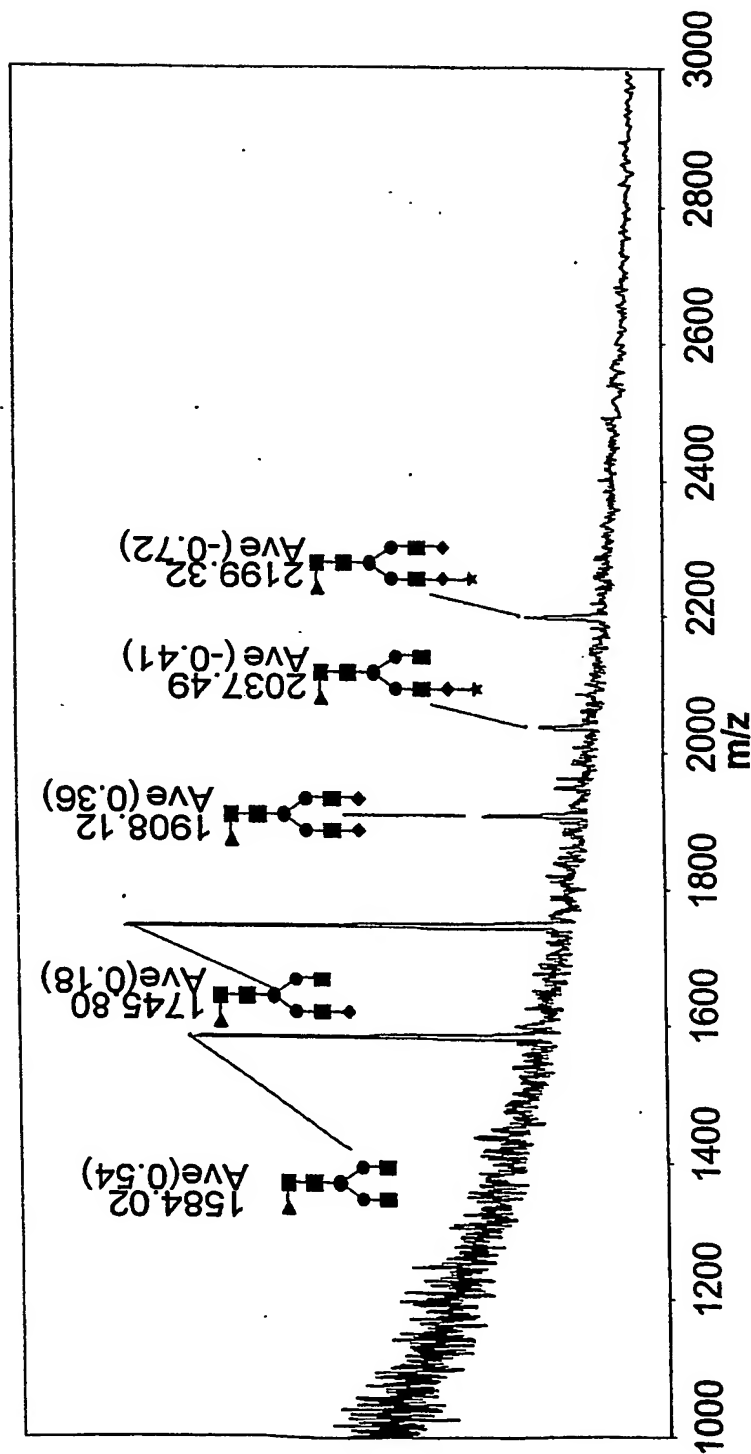


FIG. 98A



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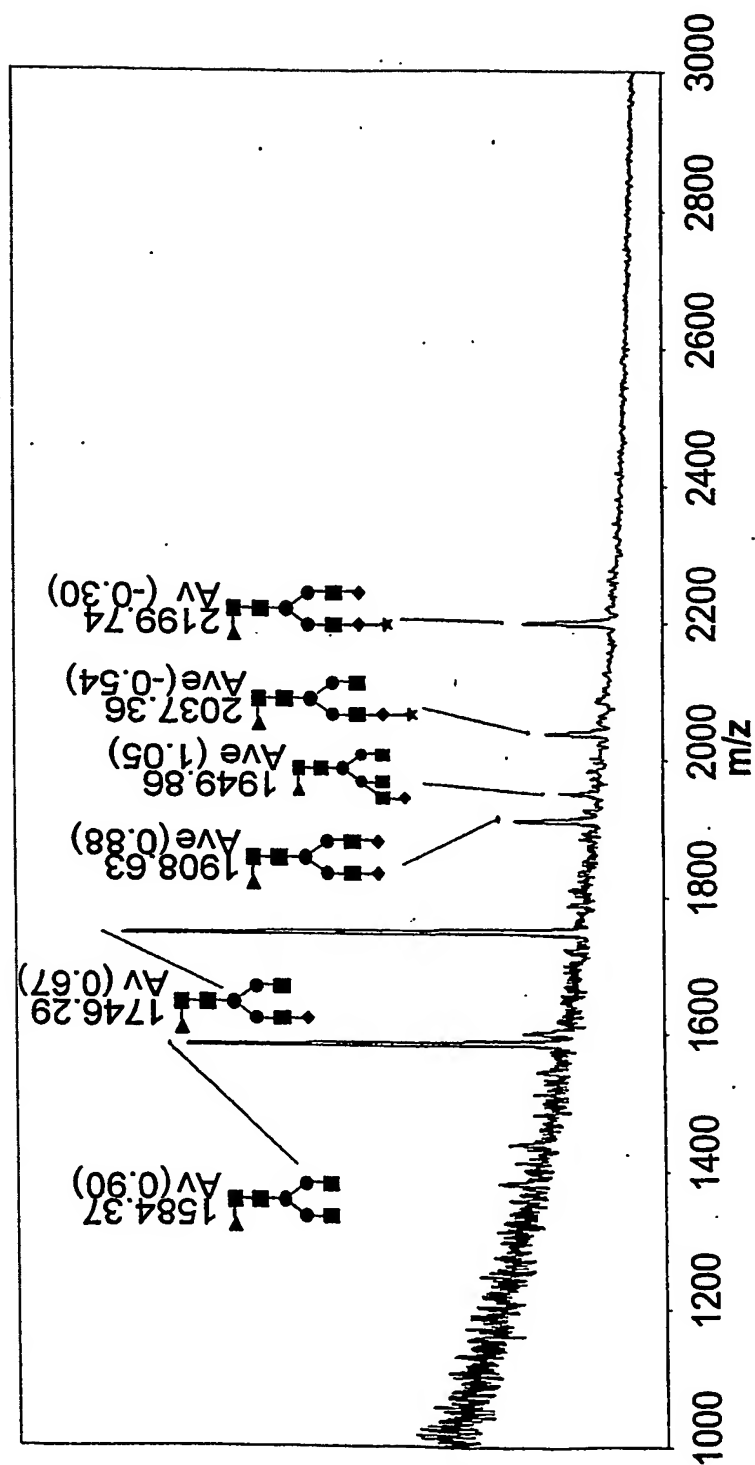


FIG. 98B

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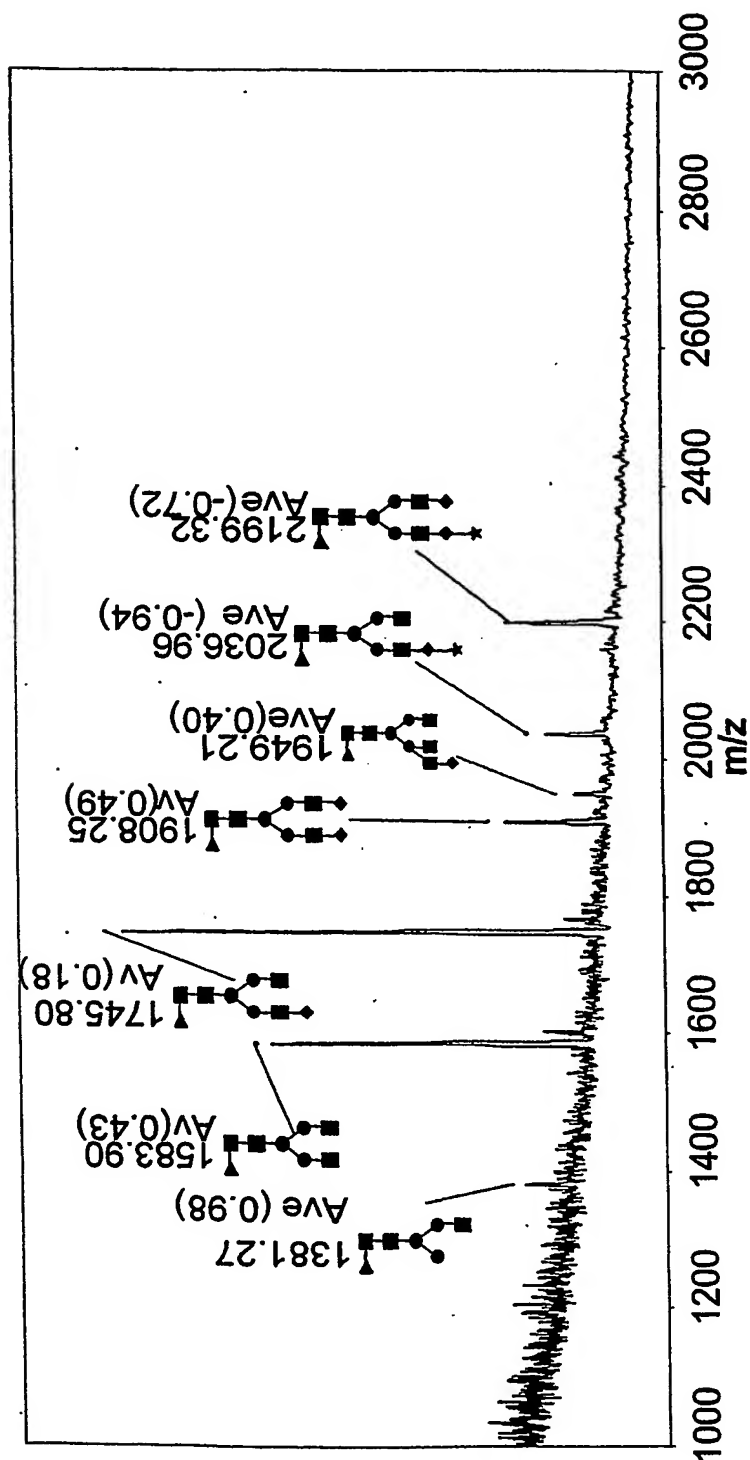


FIG. 98C

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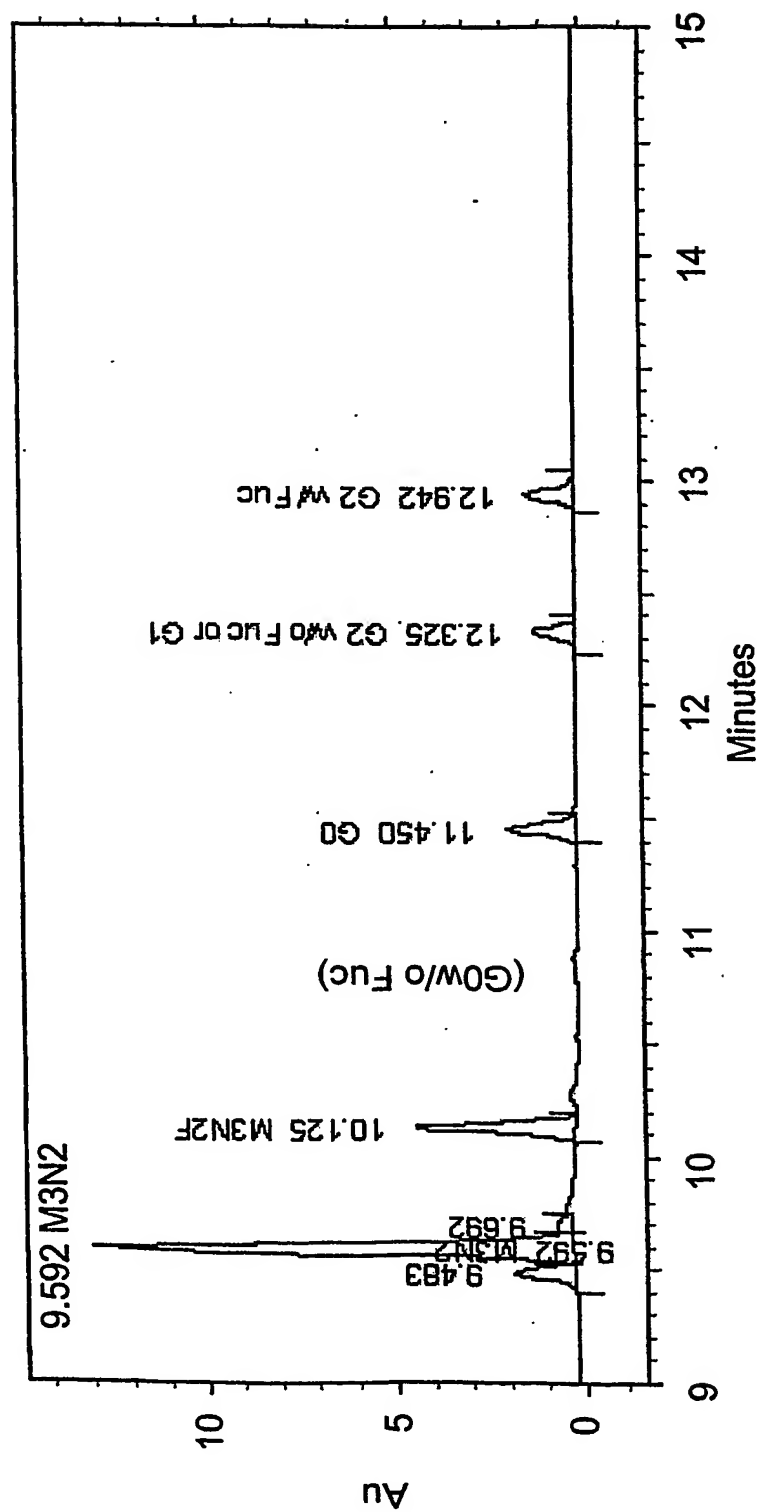


FIG. 99A

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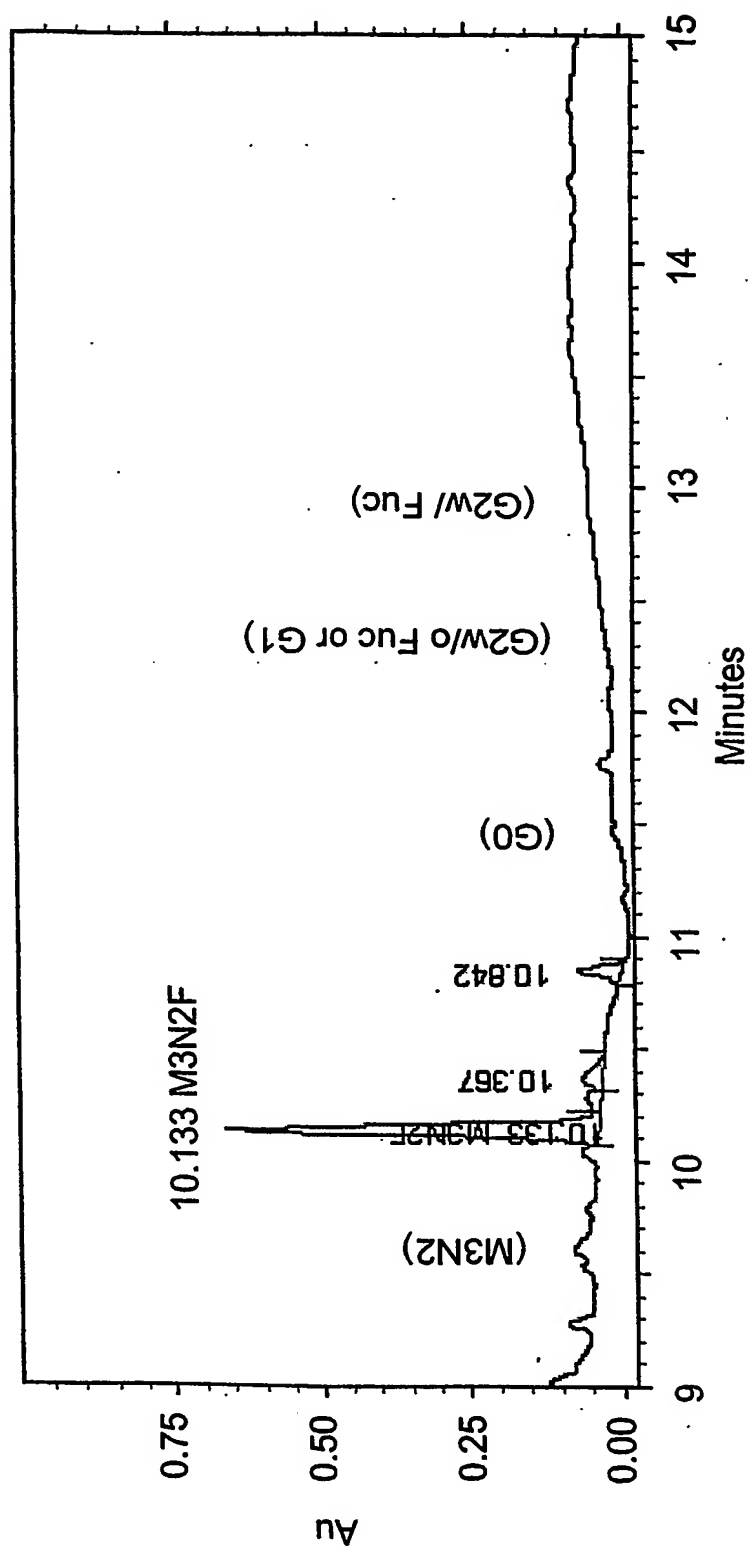


FIG. 99B

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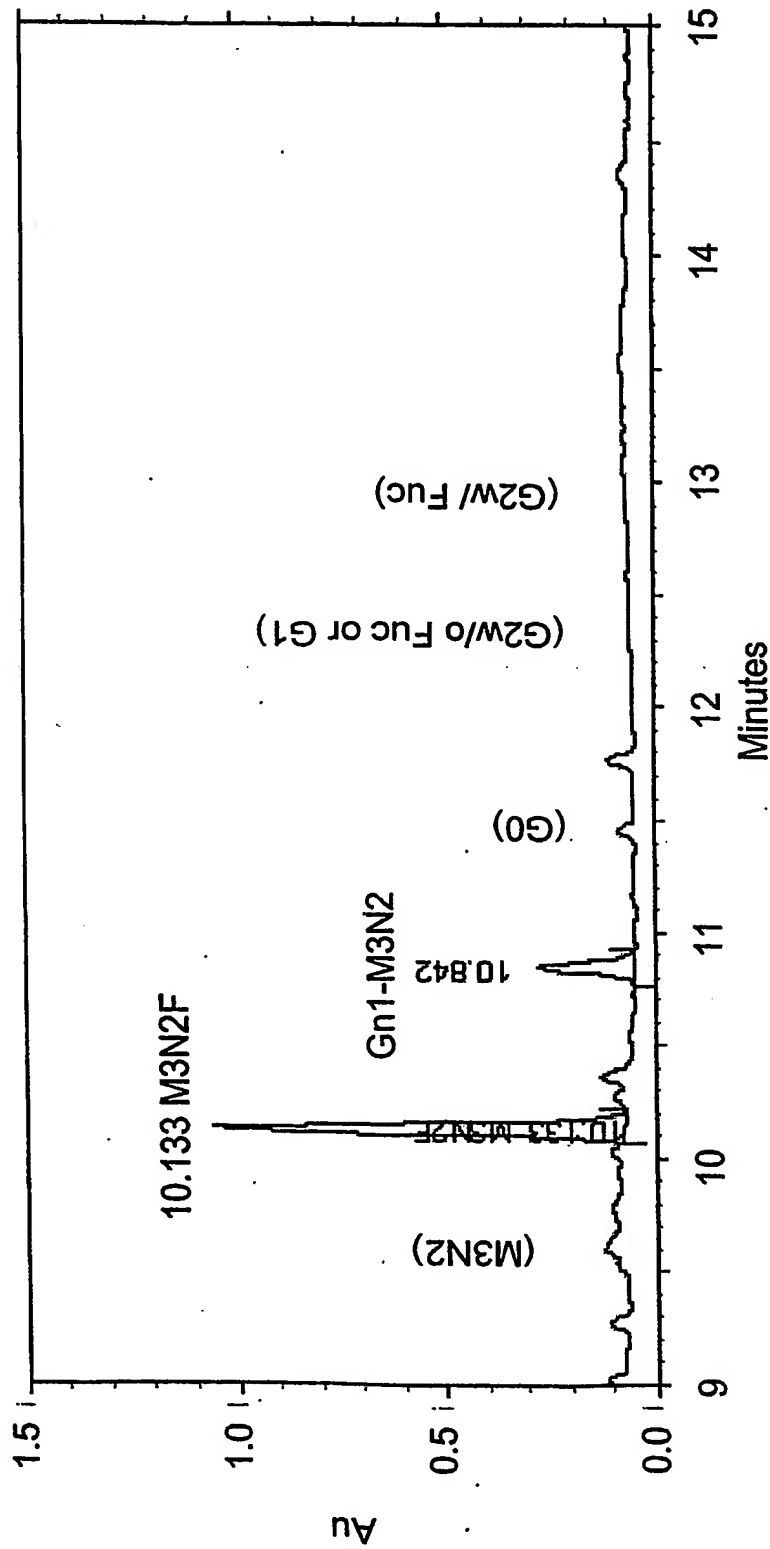


FIG. 99C

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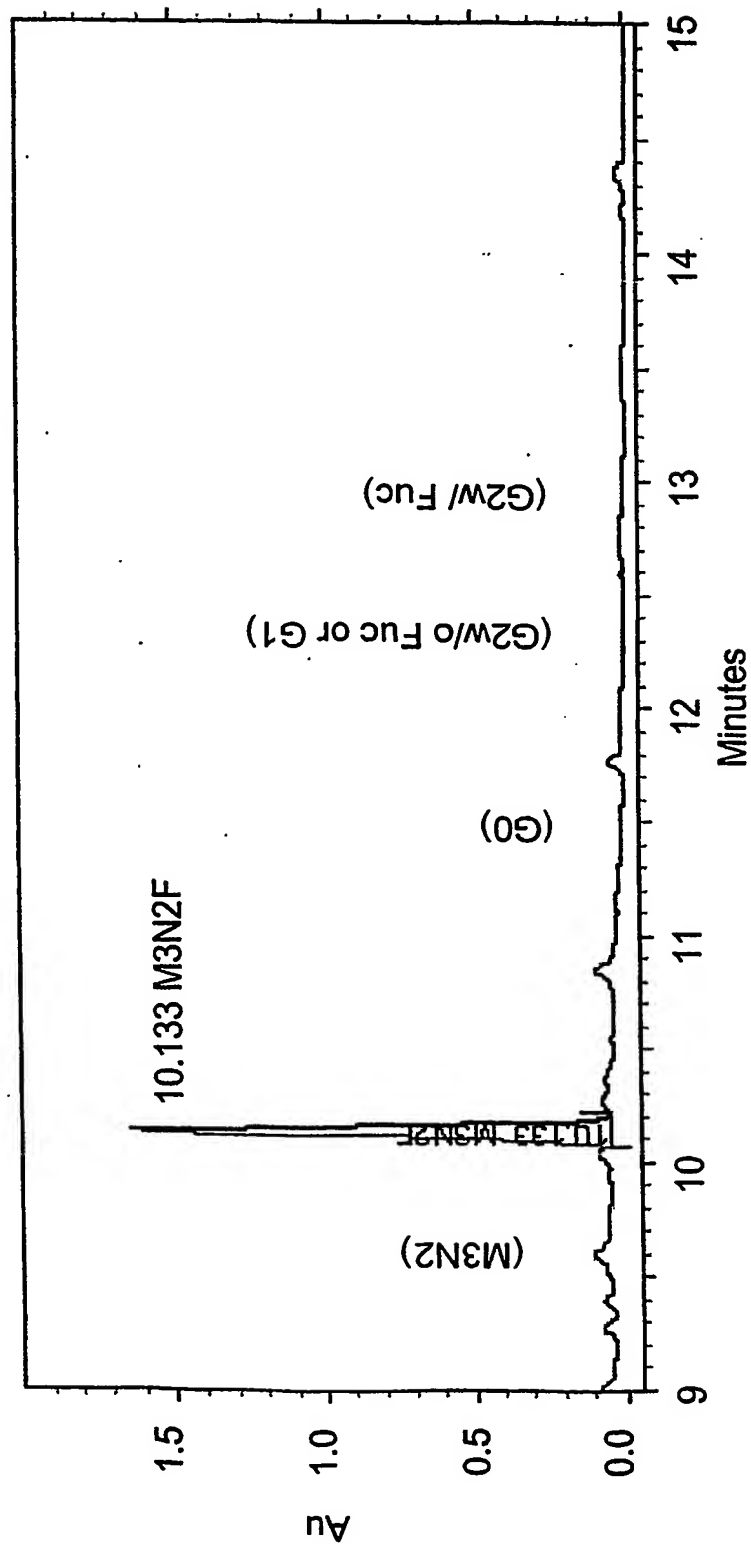


FIG. 99D

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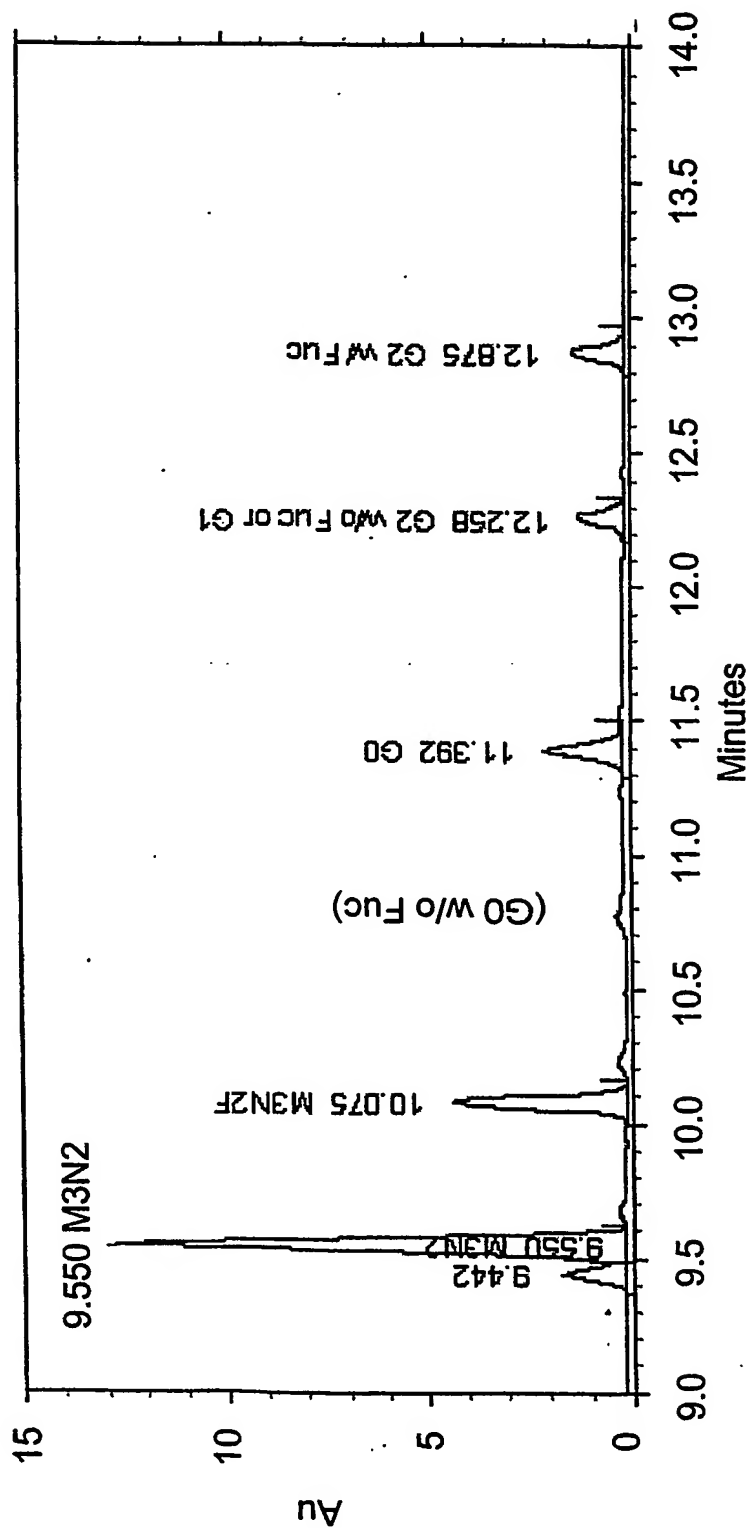


FIG. 100A

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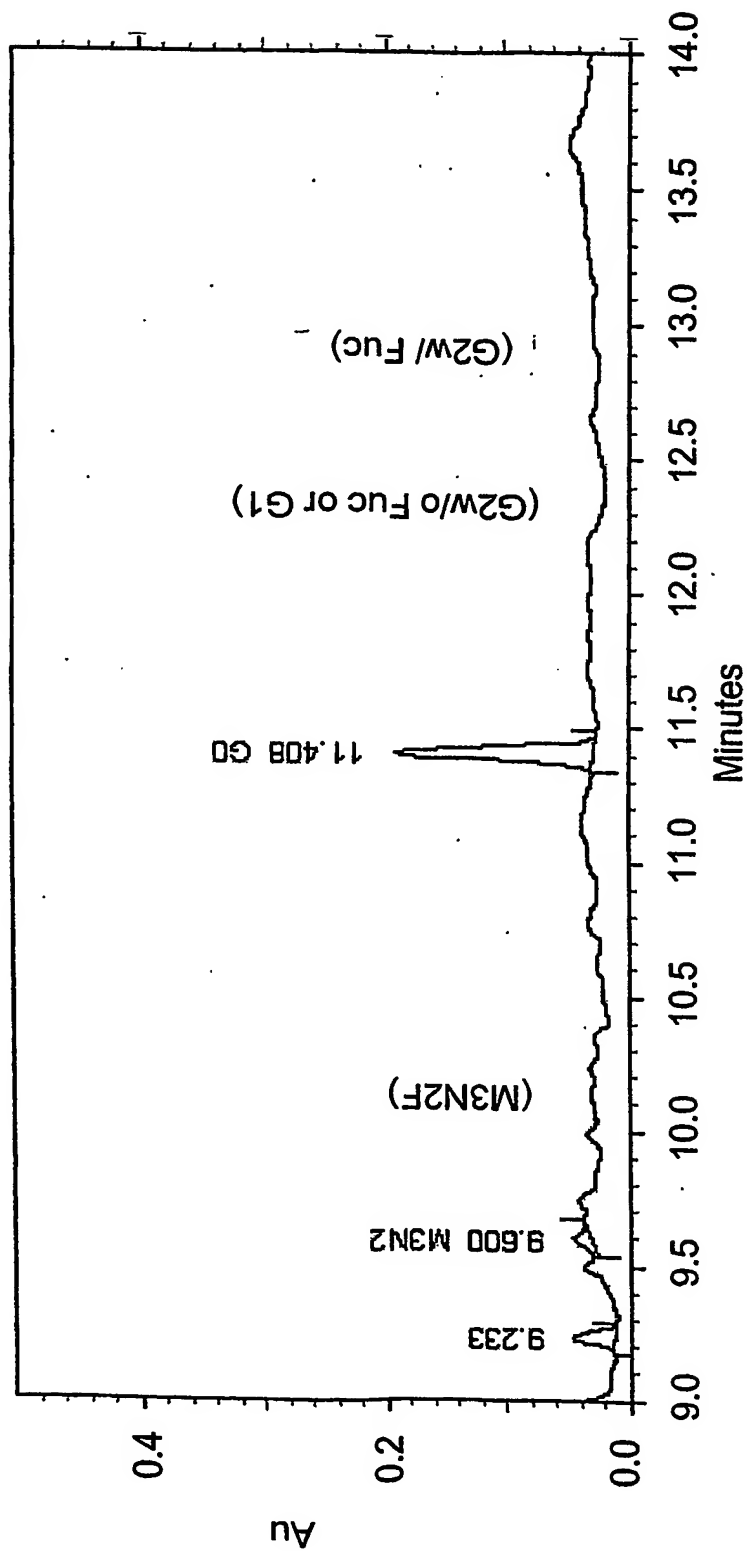


FIG. 100B



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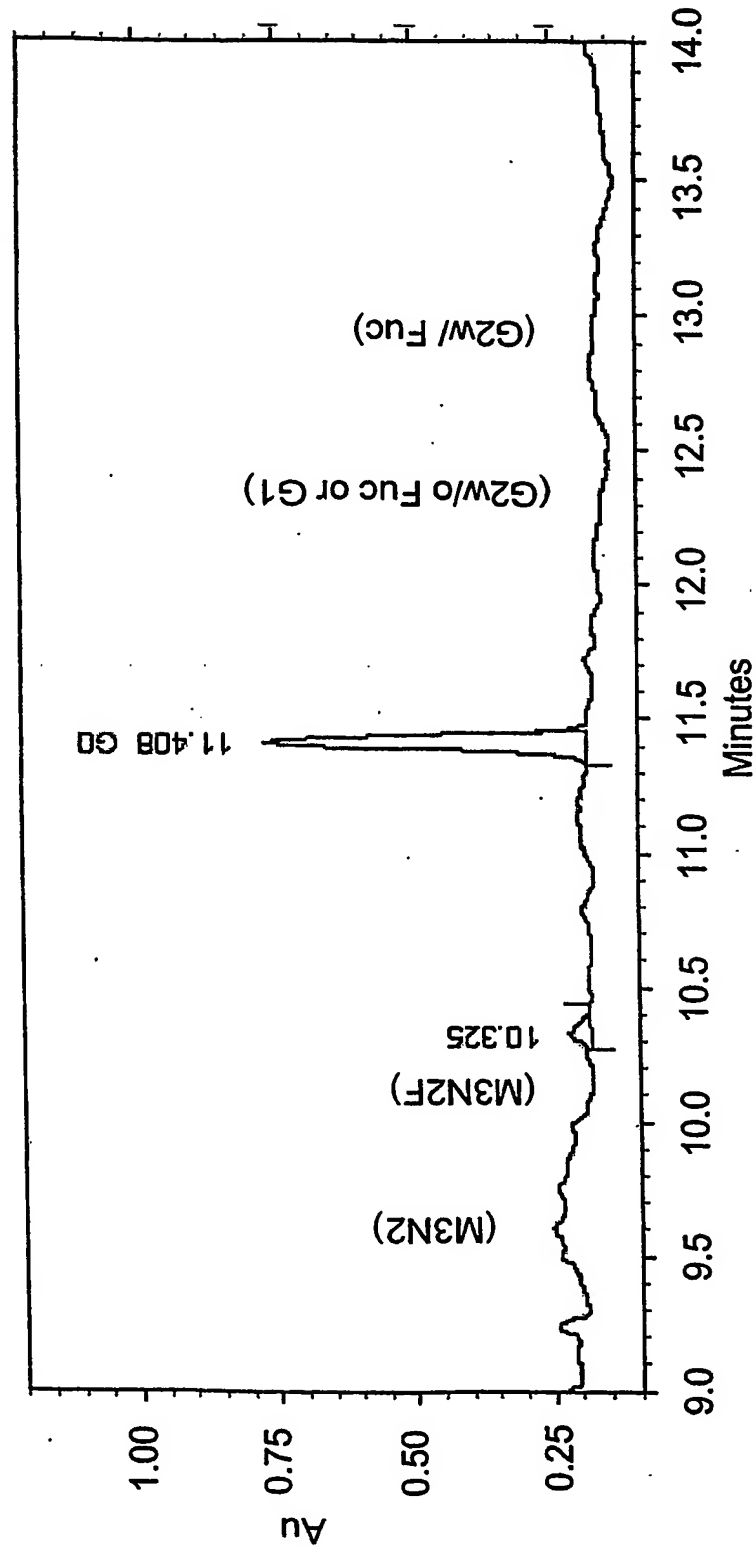


FIG. 100C

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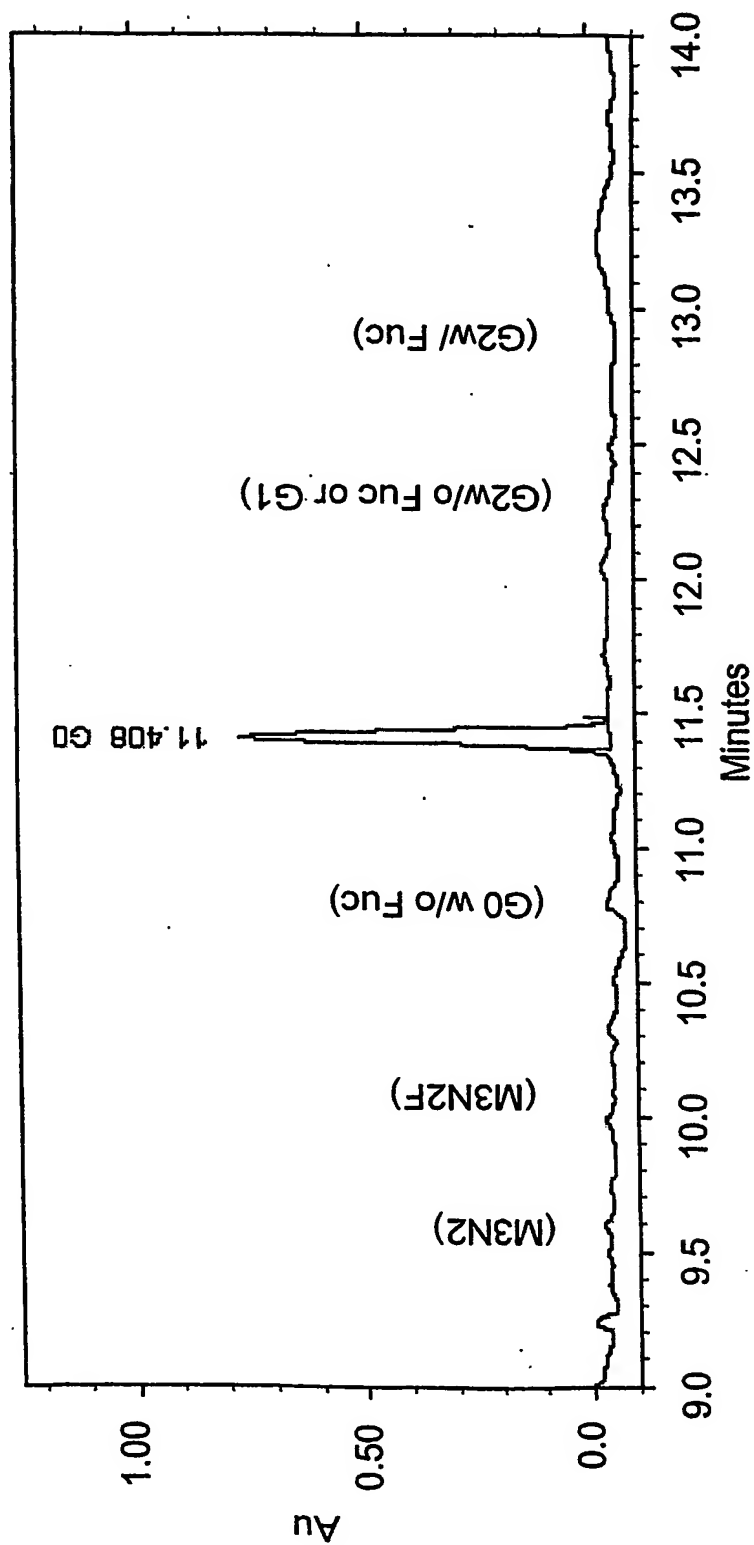


FIG. 100D

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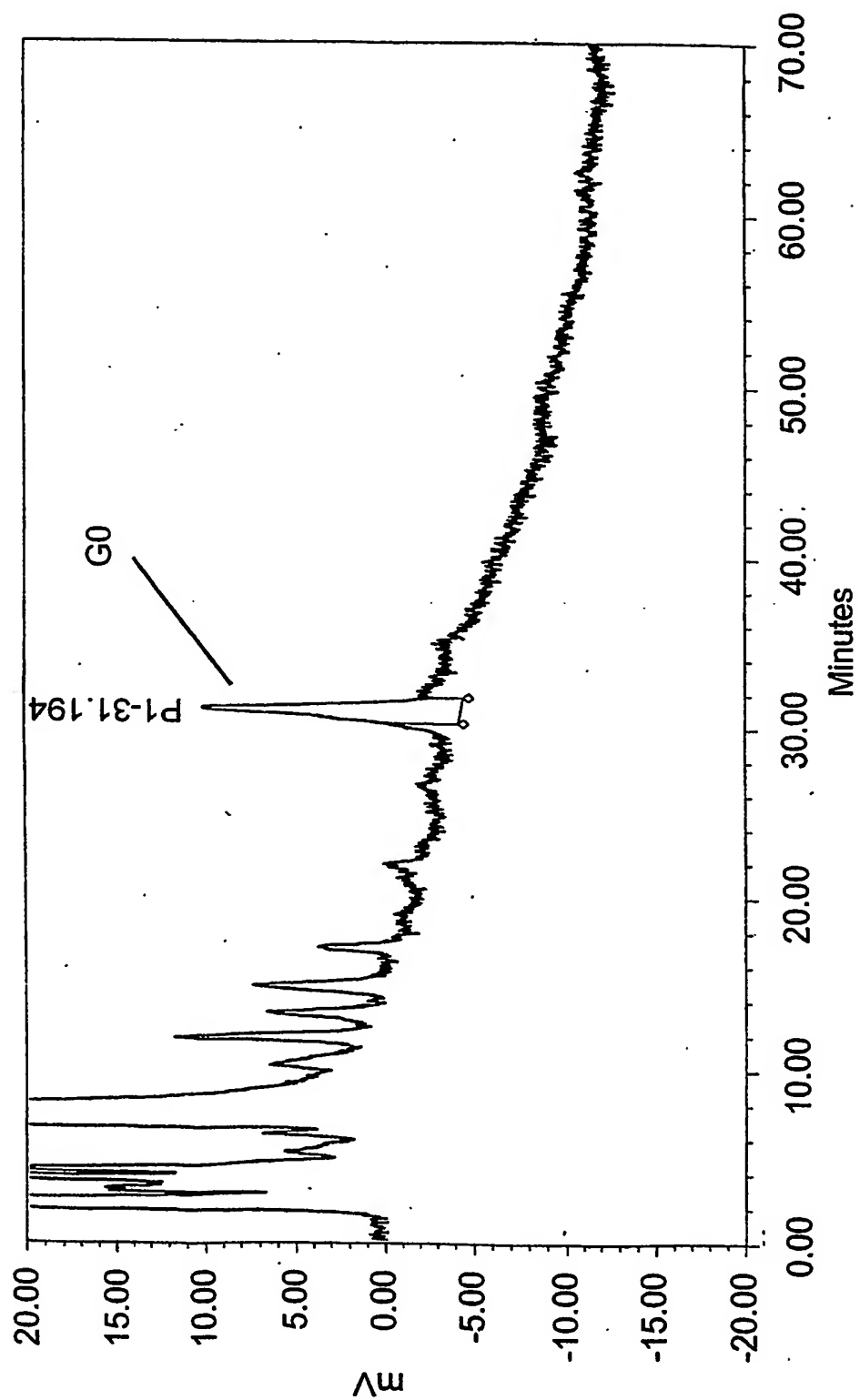


FIG. 101A

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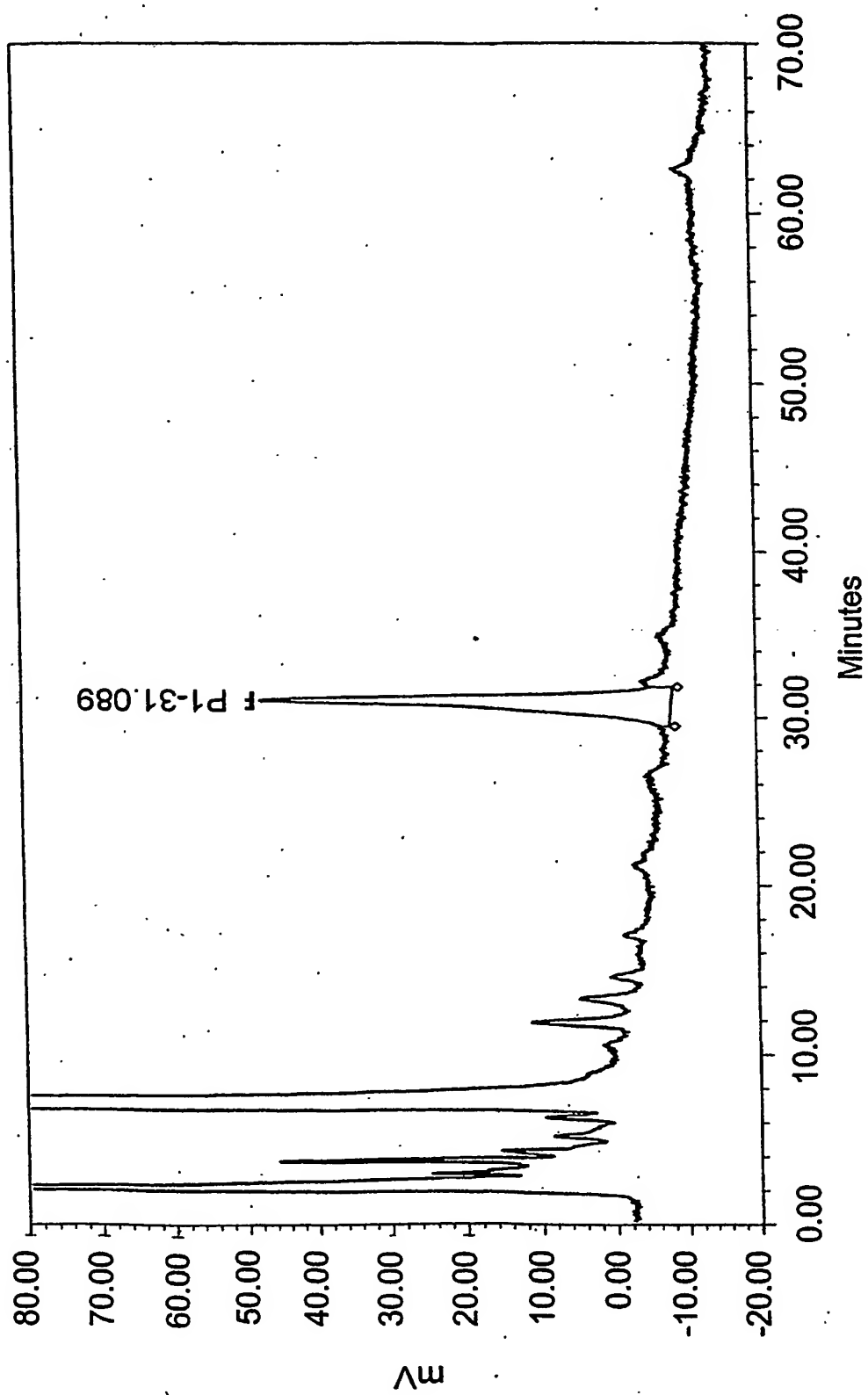


FIG. 101B

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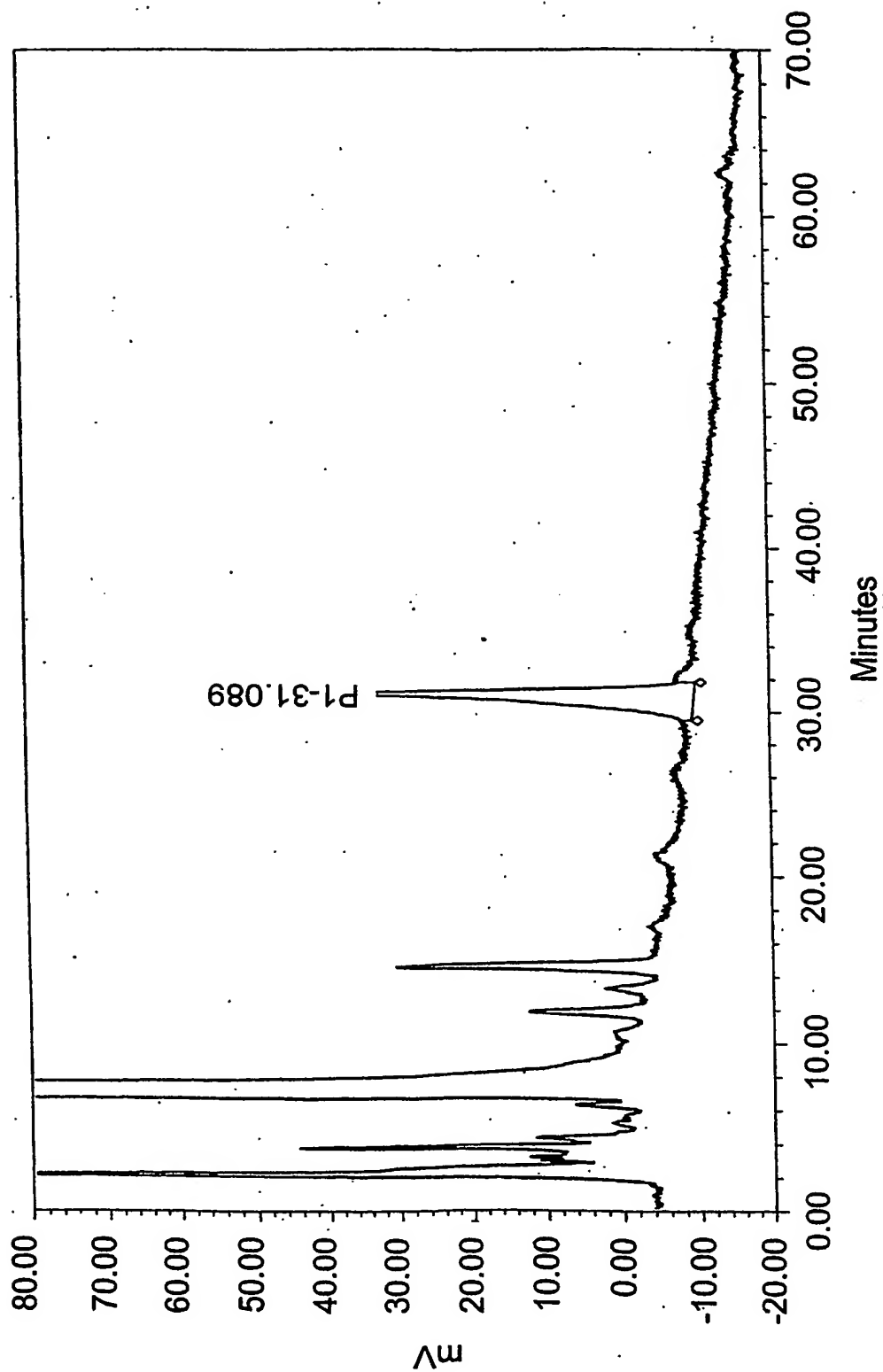


FIG. 101C

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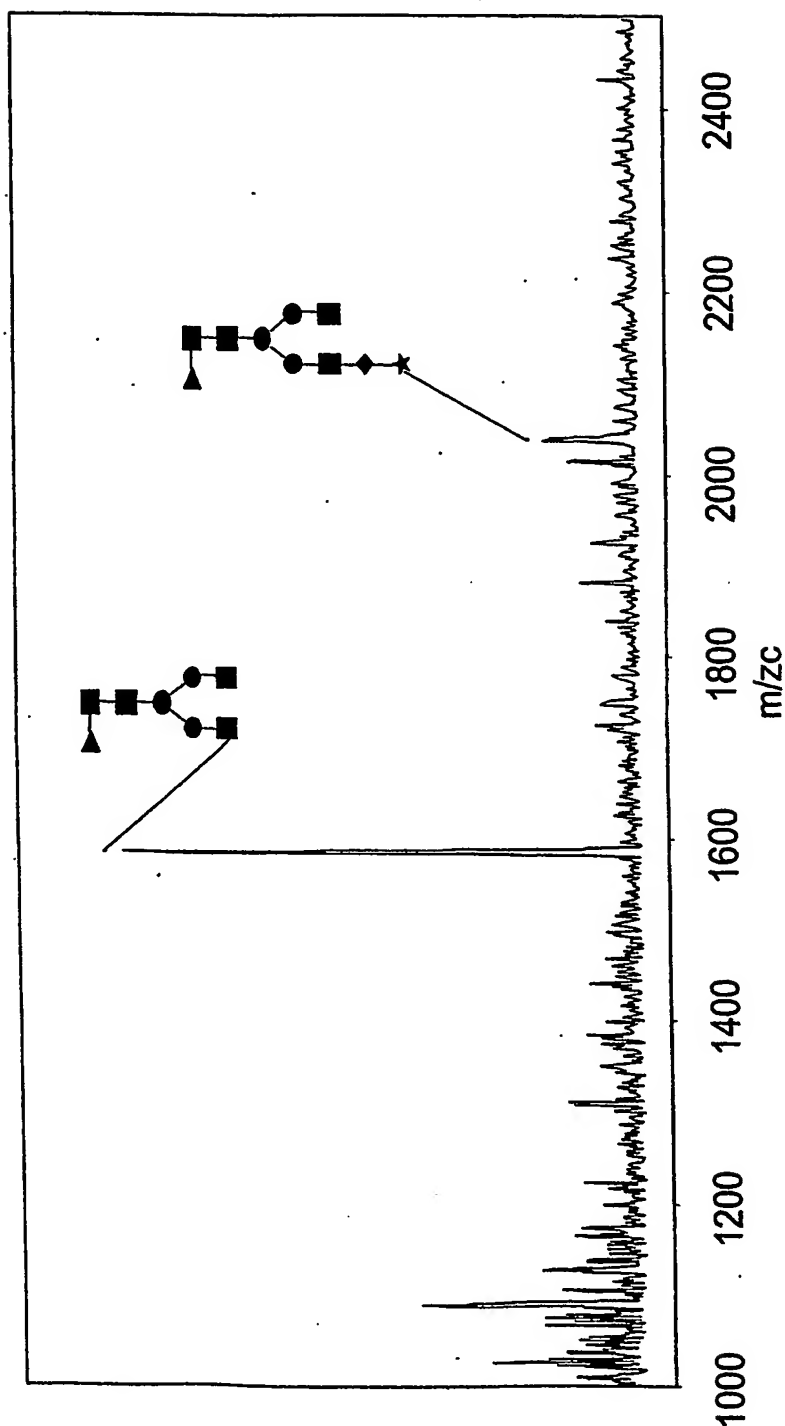


FIG. 102A

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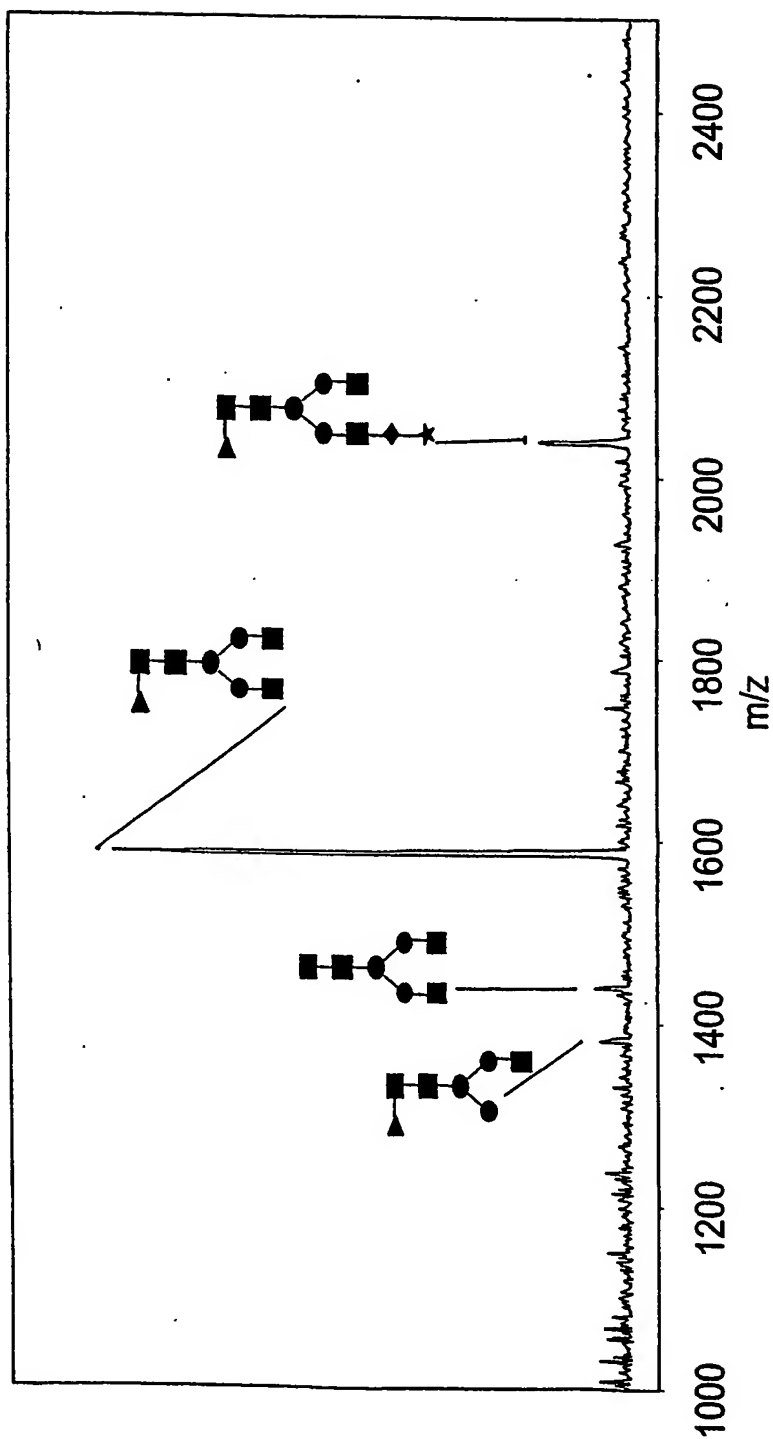


FIG. 102B

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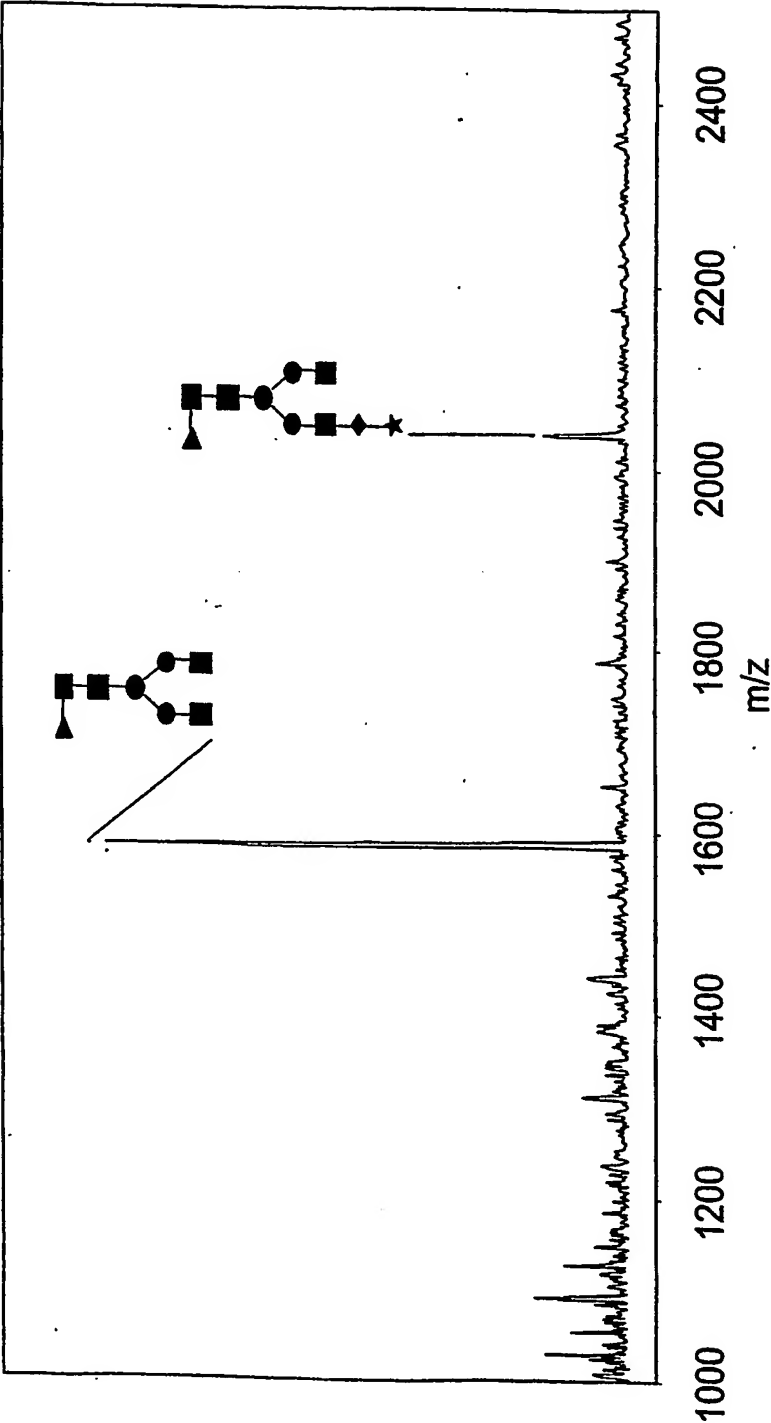


FIG. 102C



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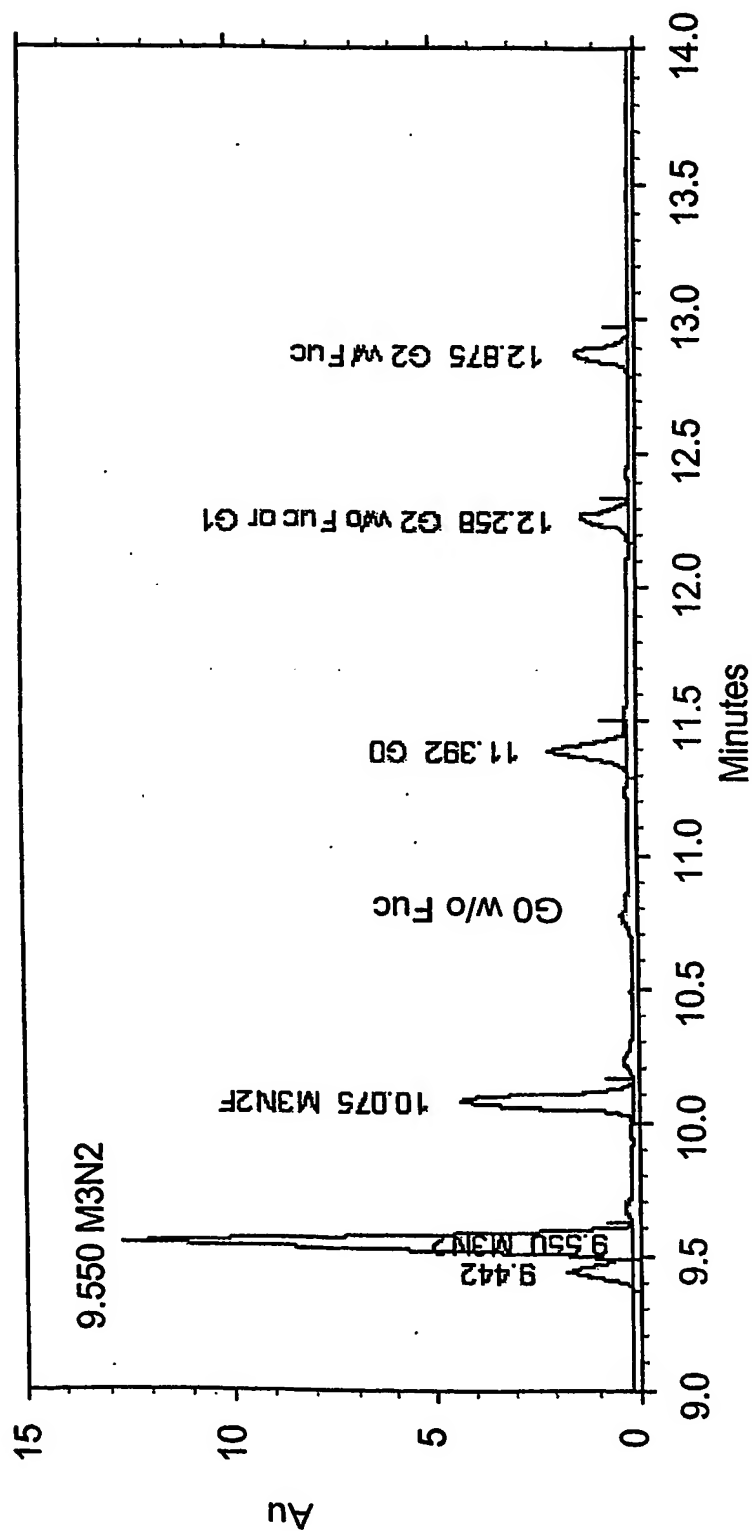


FIG. 103A

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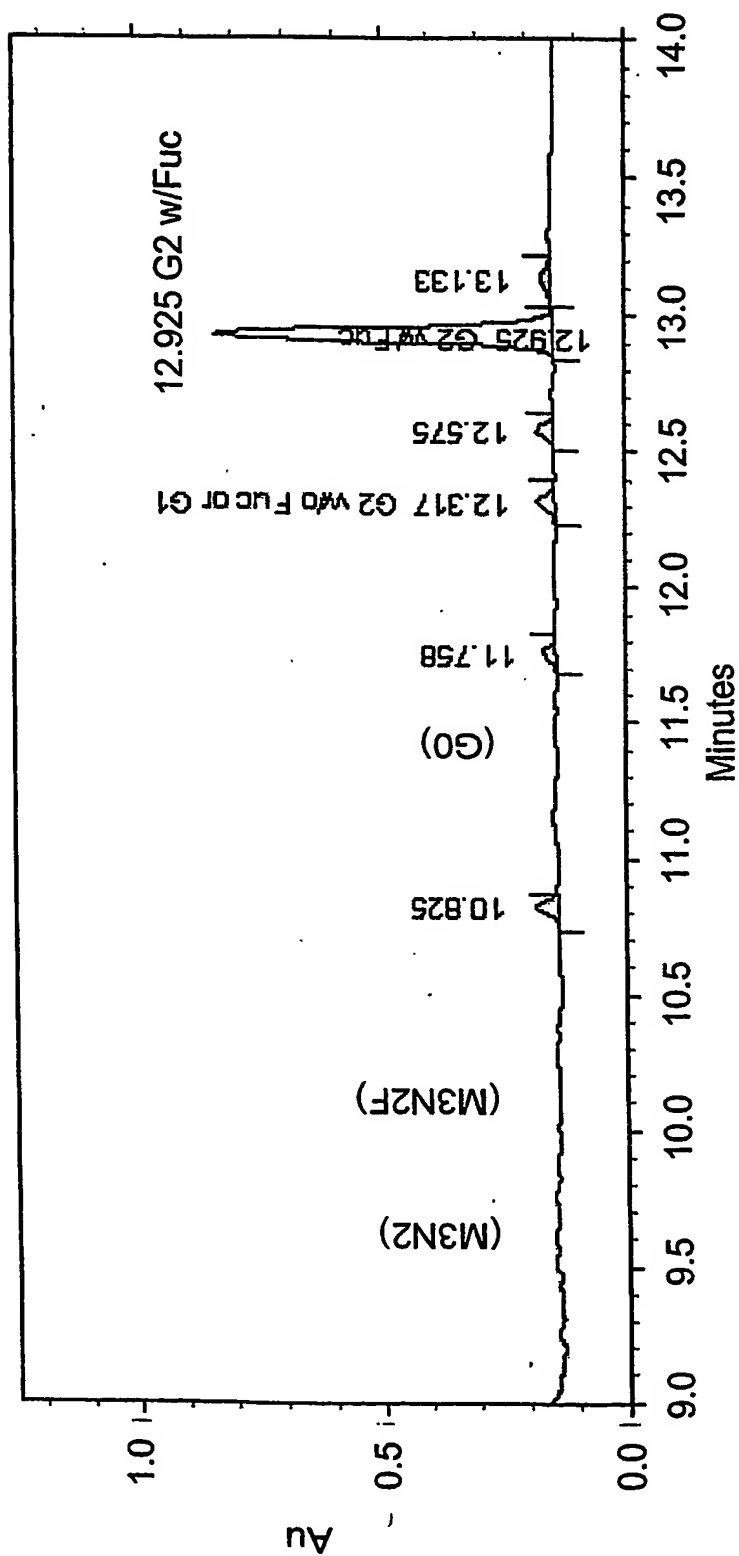


FIG. 103B

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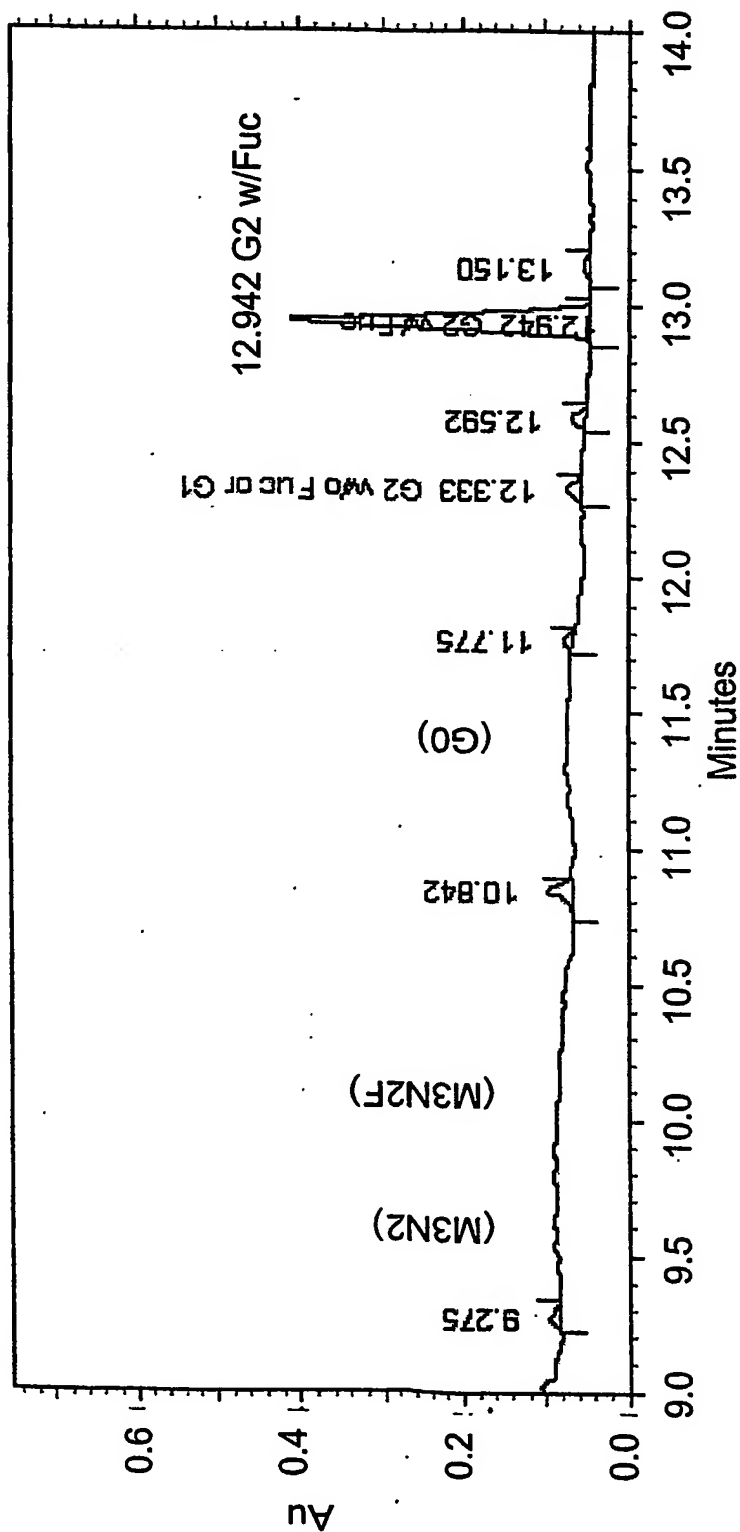


FIG. 103C

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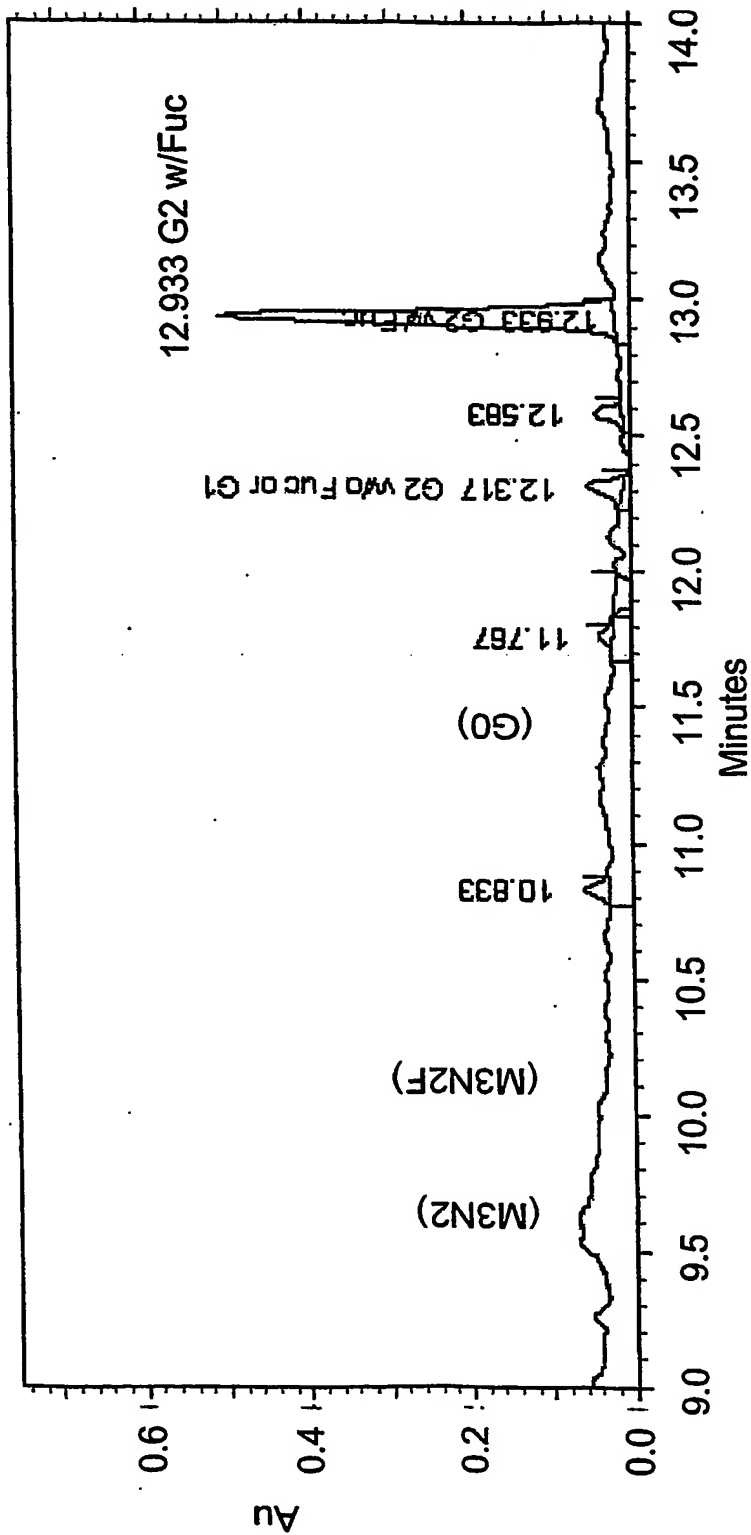


FIG. 103D

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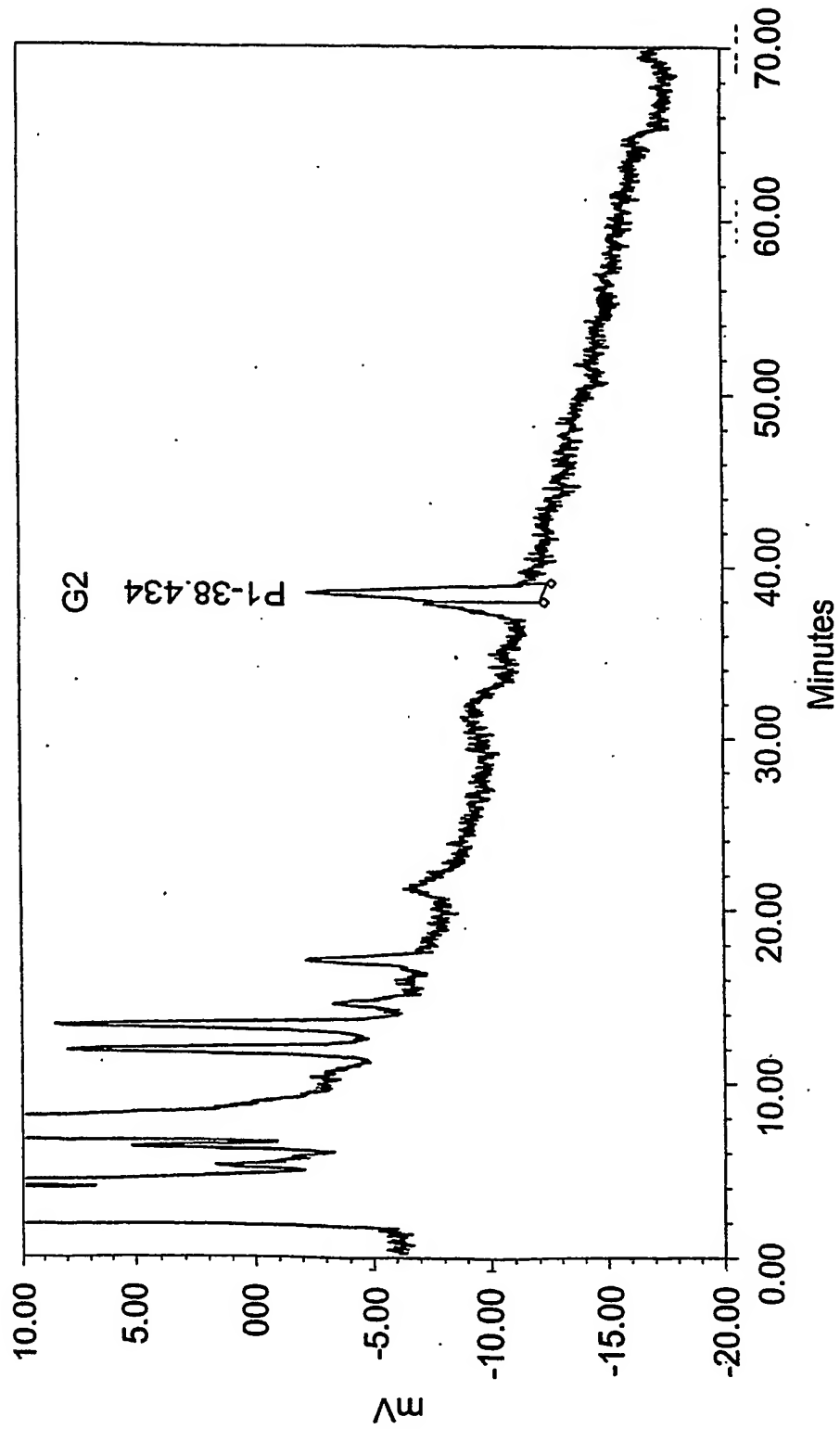


FIG. 104A

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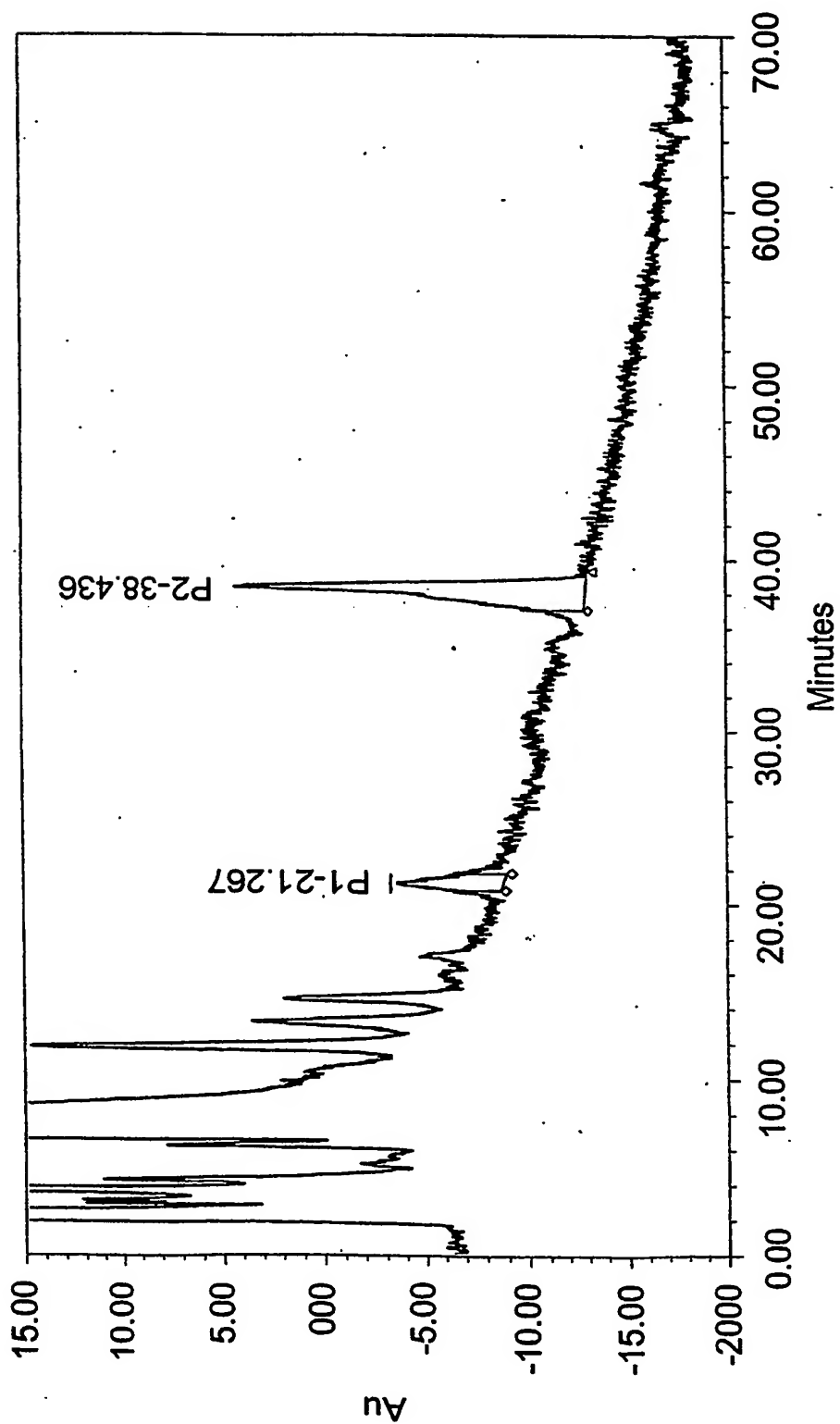


FIG. 104B

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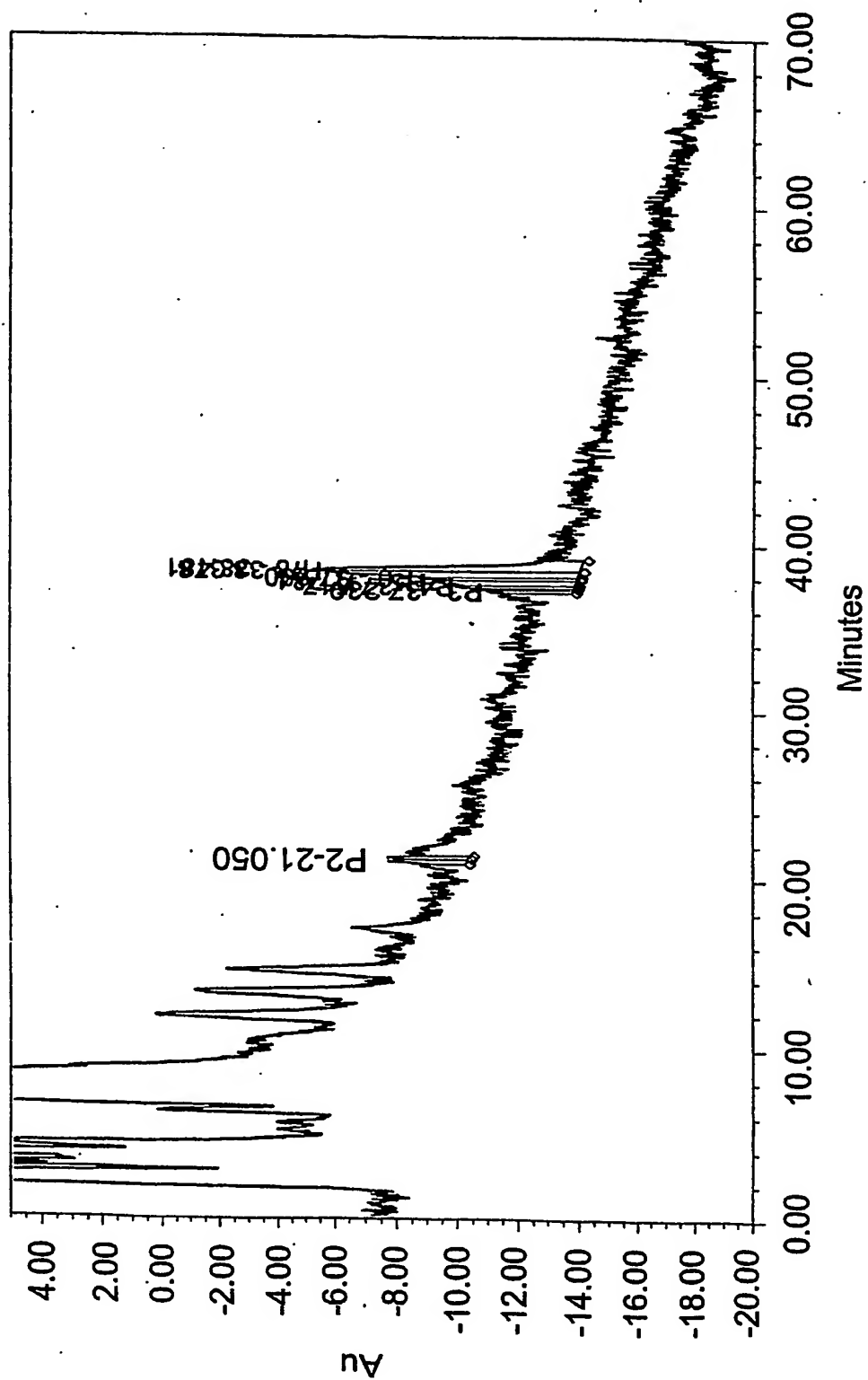


FIG. 104C

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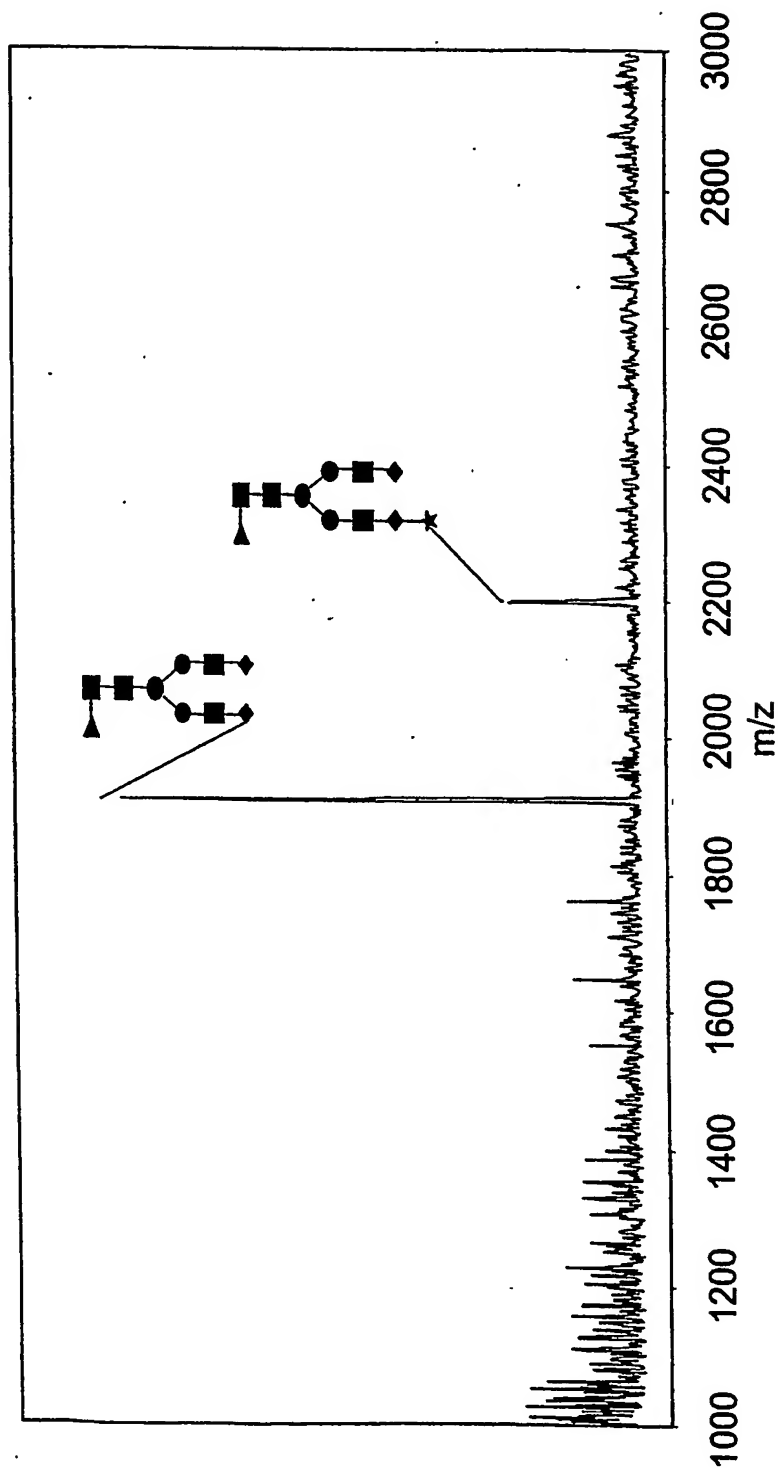


FIG. 105A



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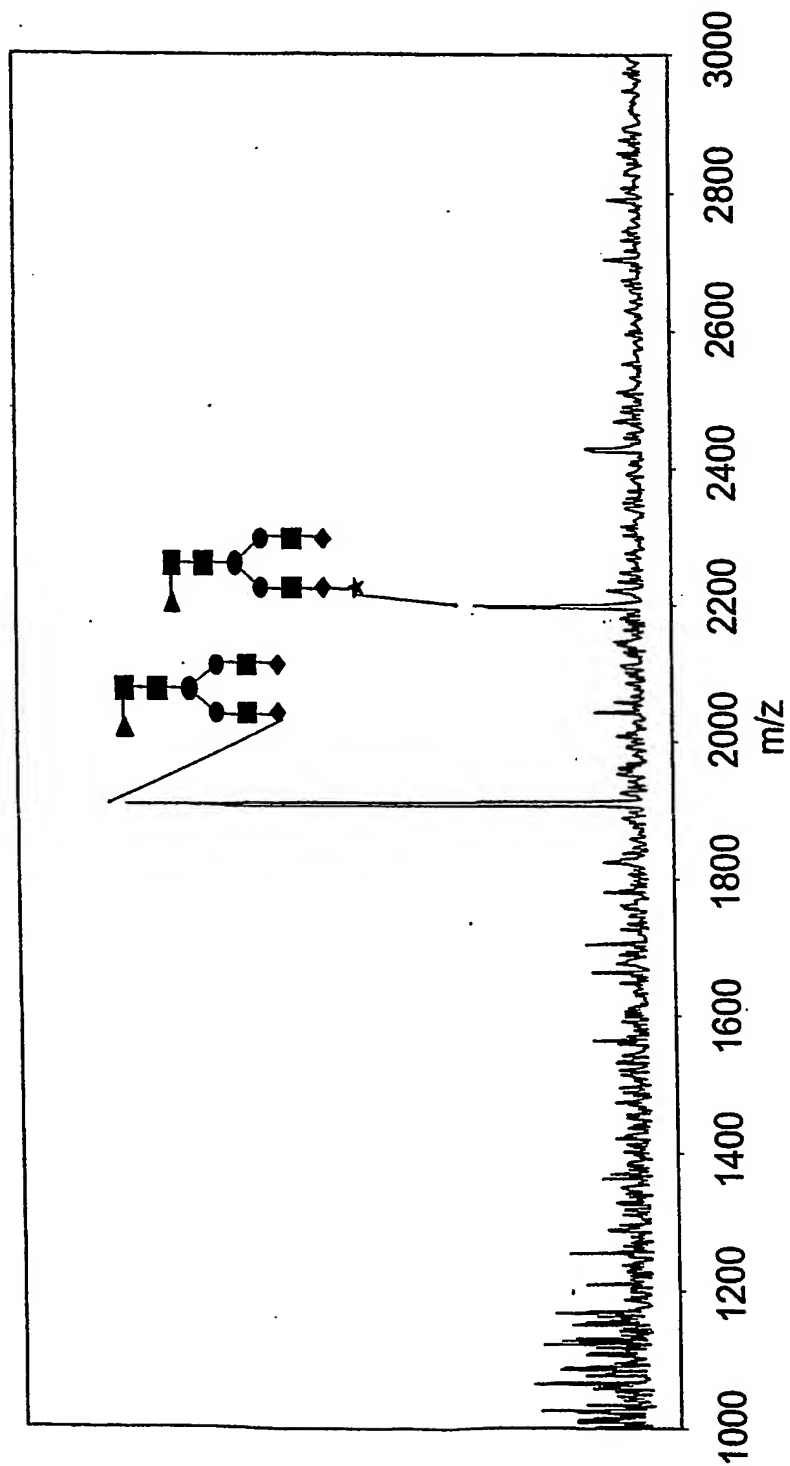


FIG. 105B

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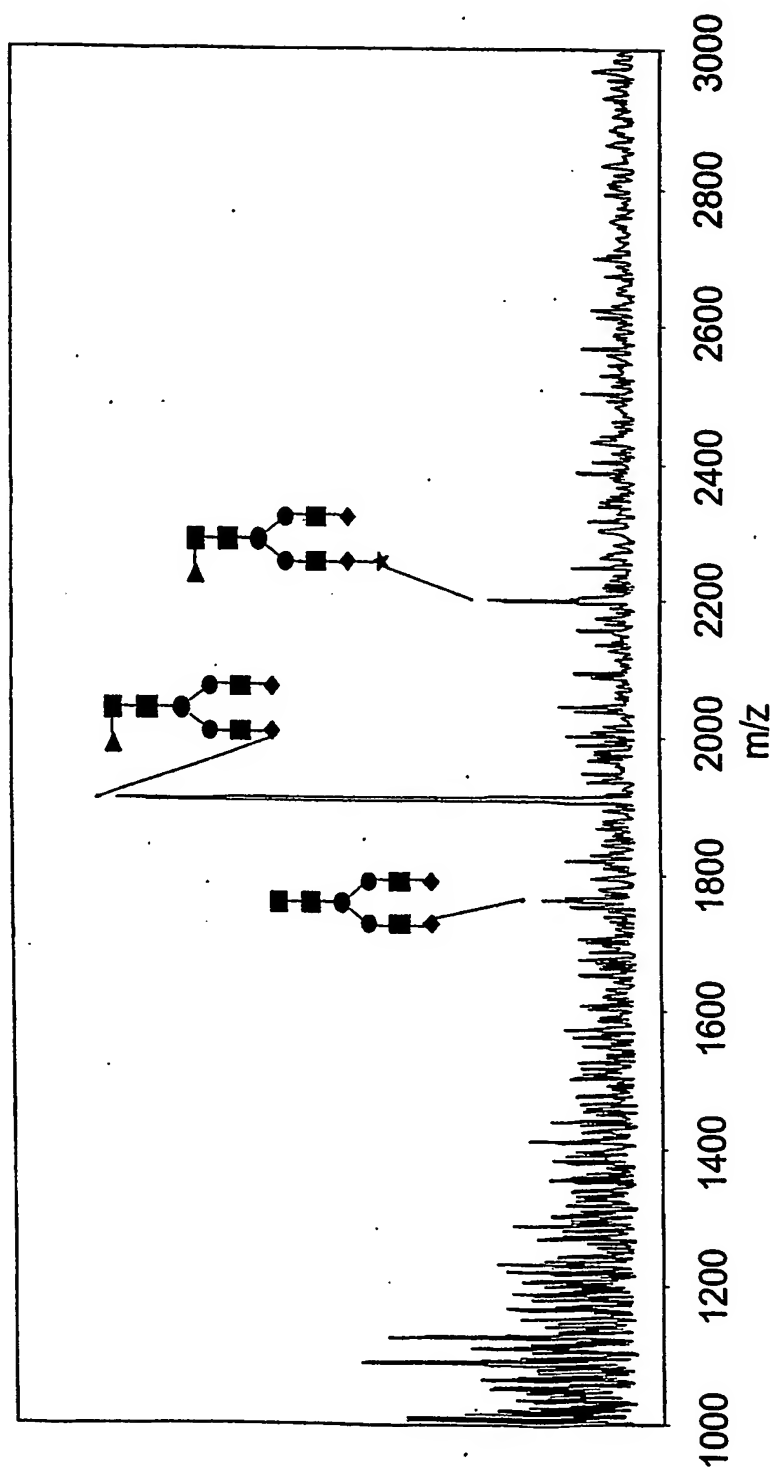


FIG. 105C

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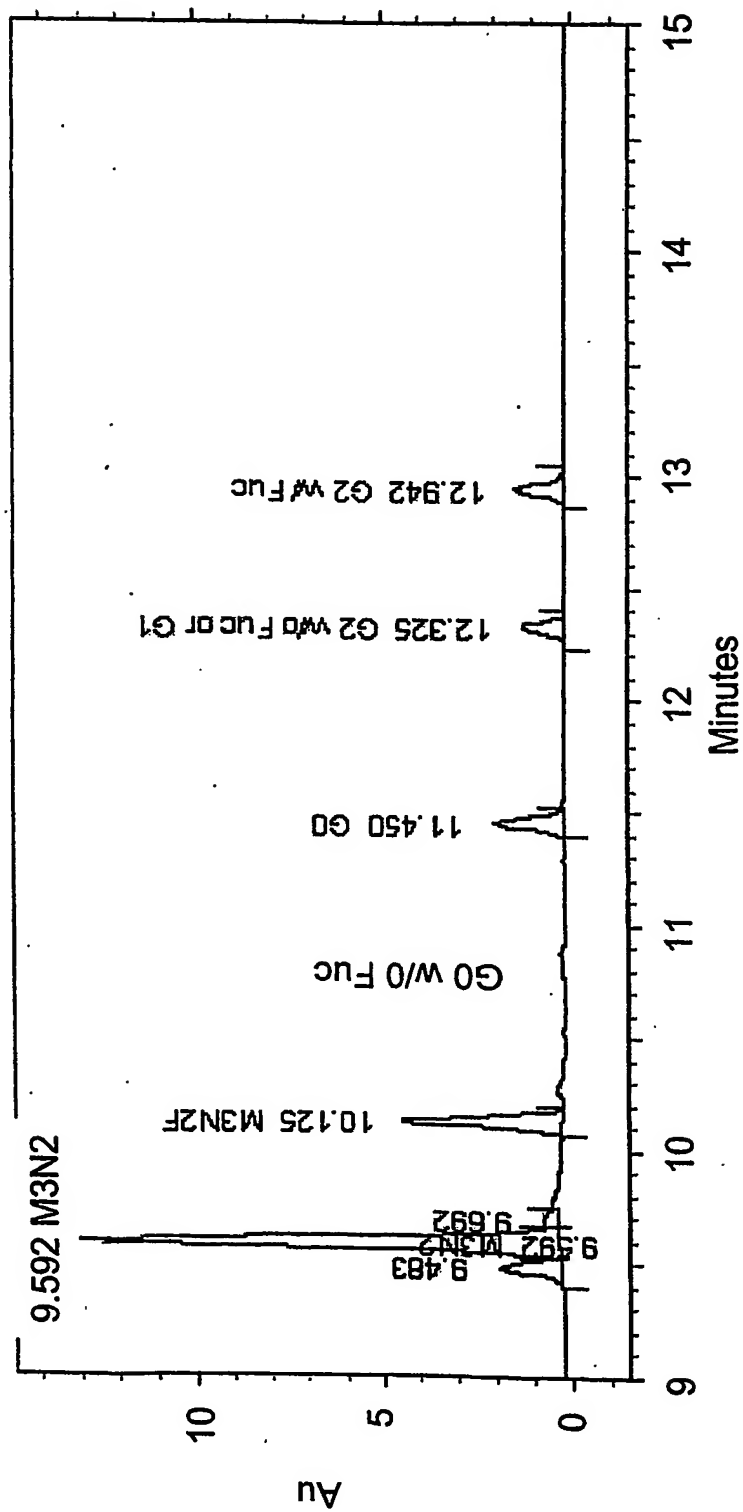


FIG. 106A

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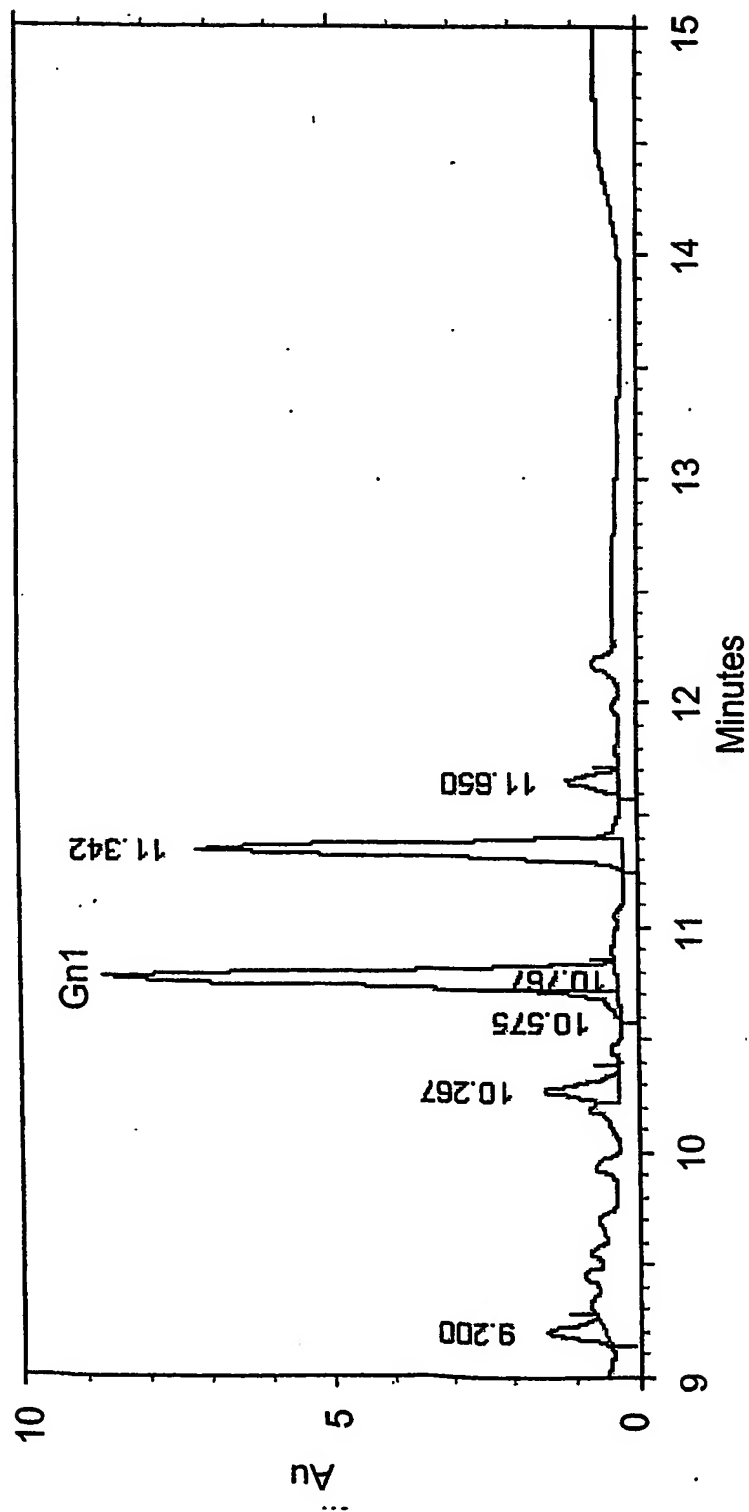


FIG. 106B

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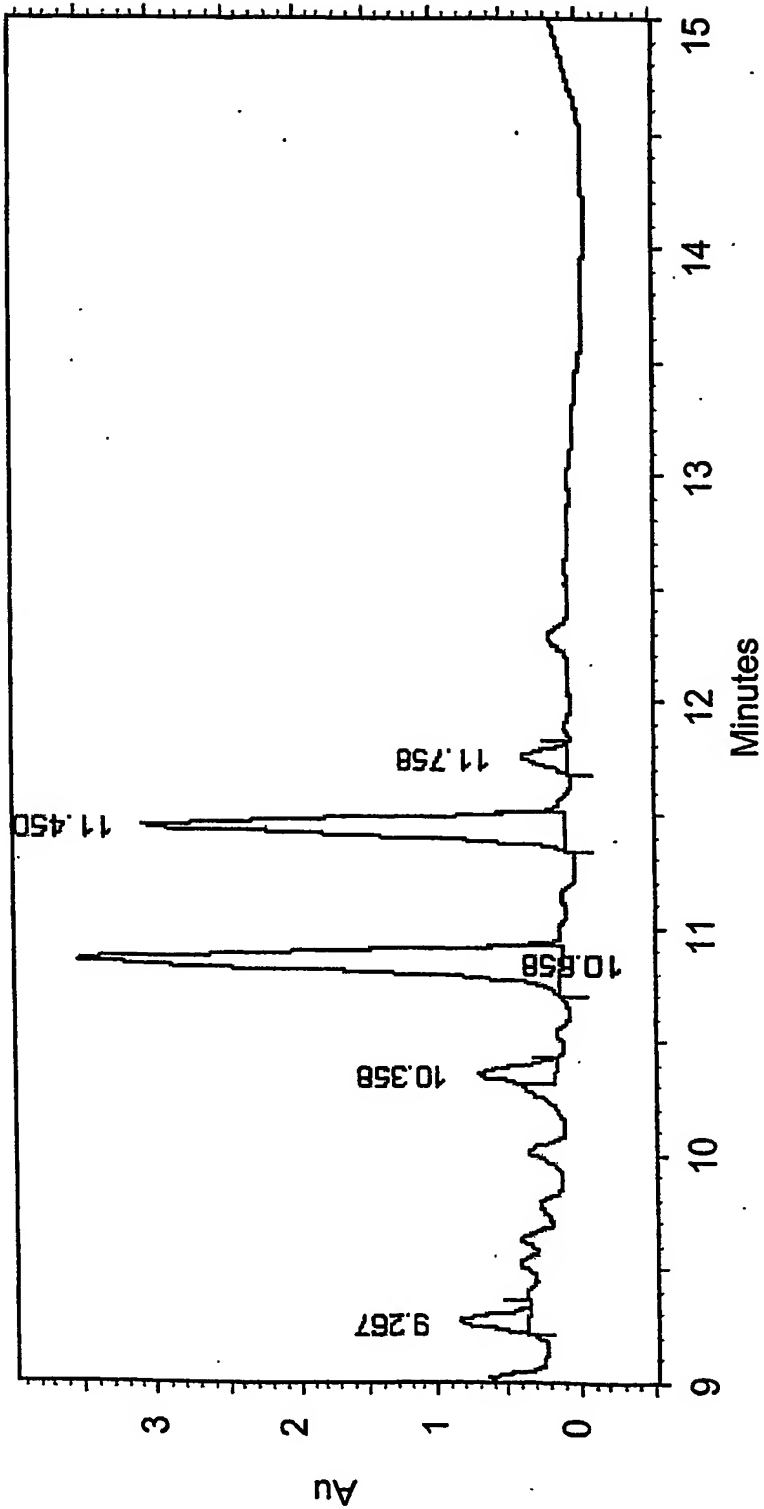


FIG. 106C

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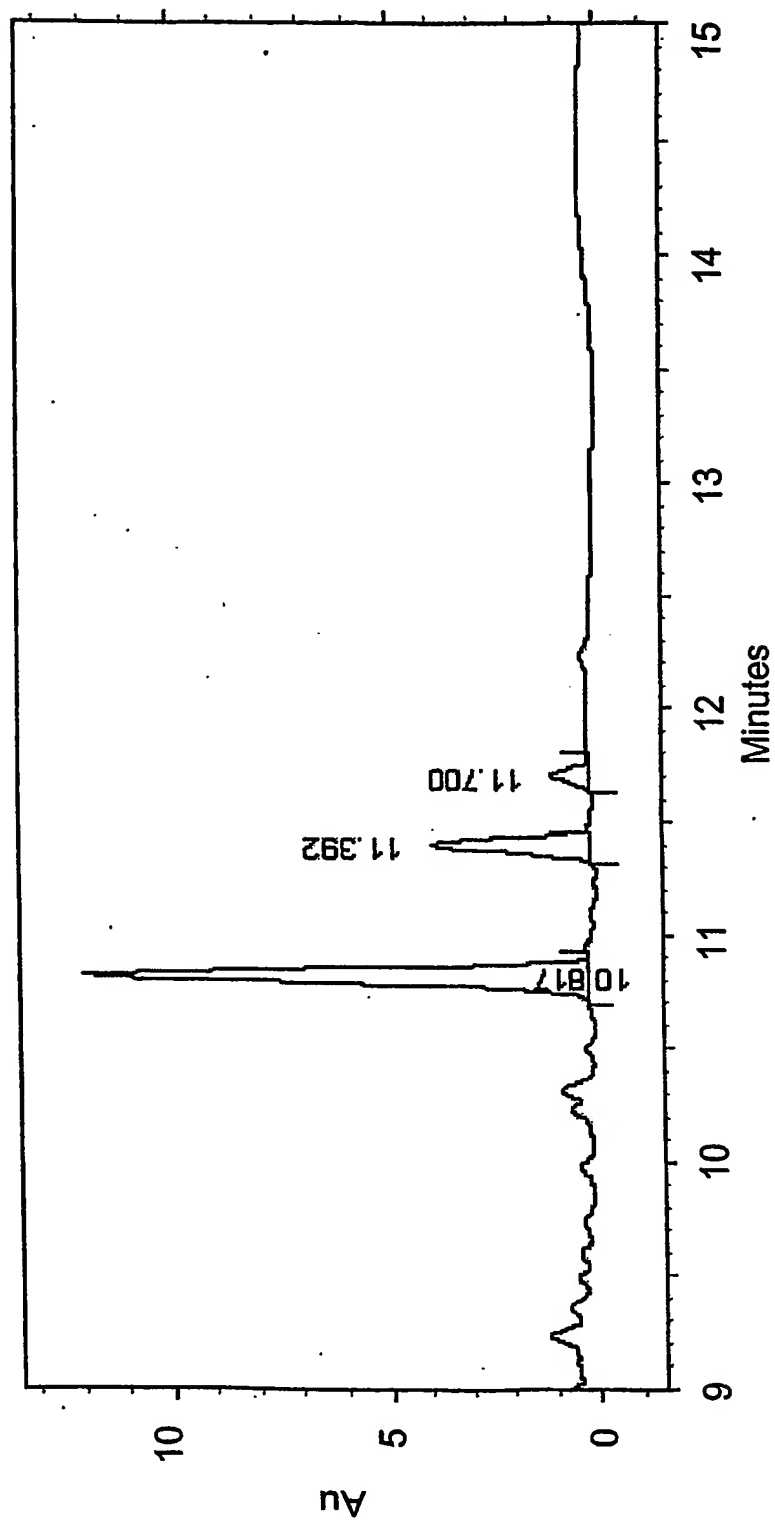


FIG. 106D

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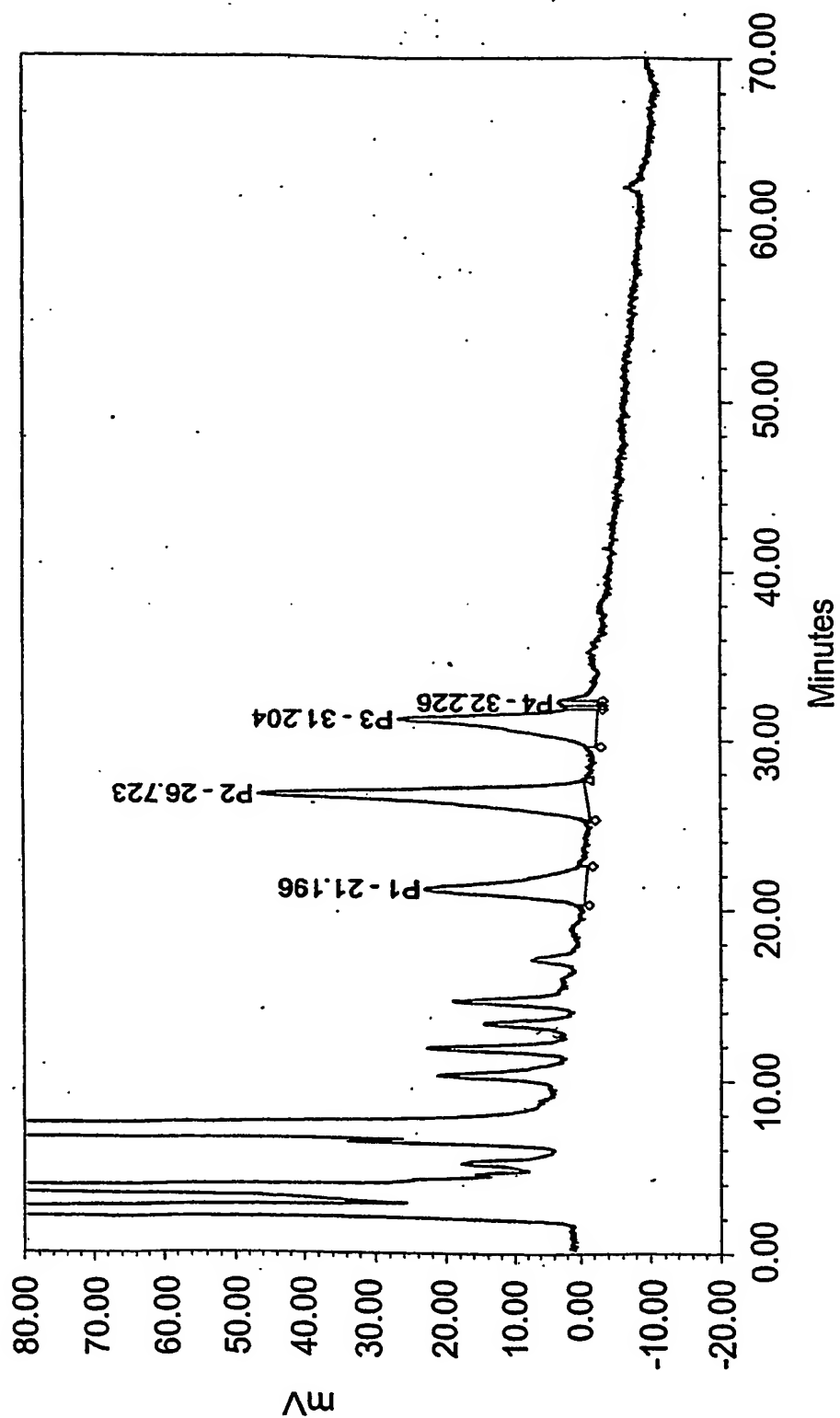


FIG. 107A

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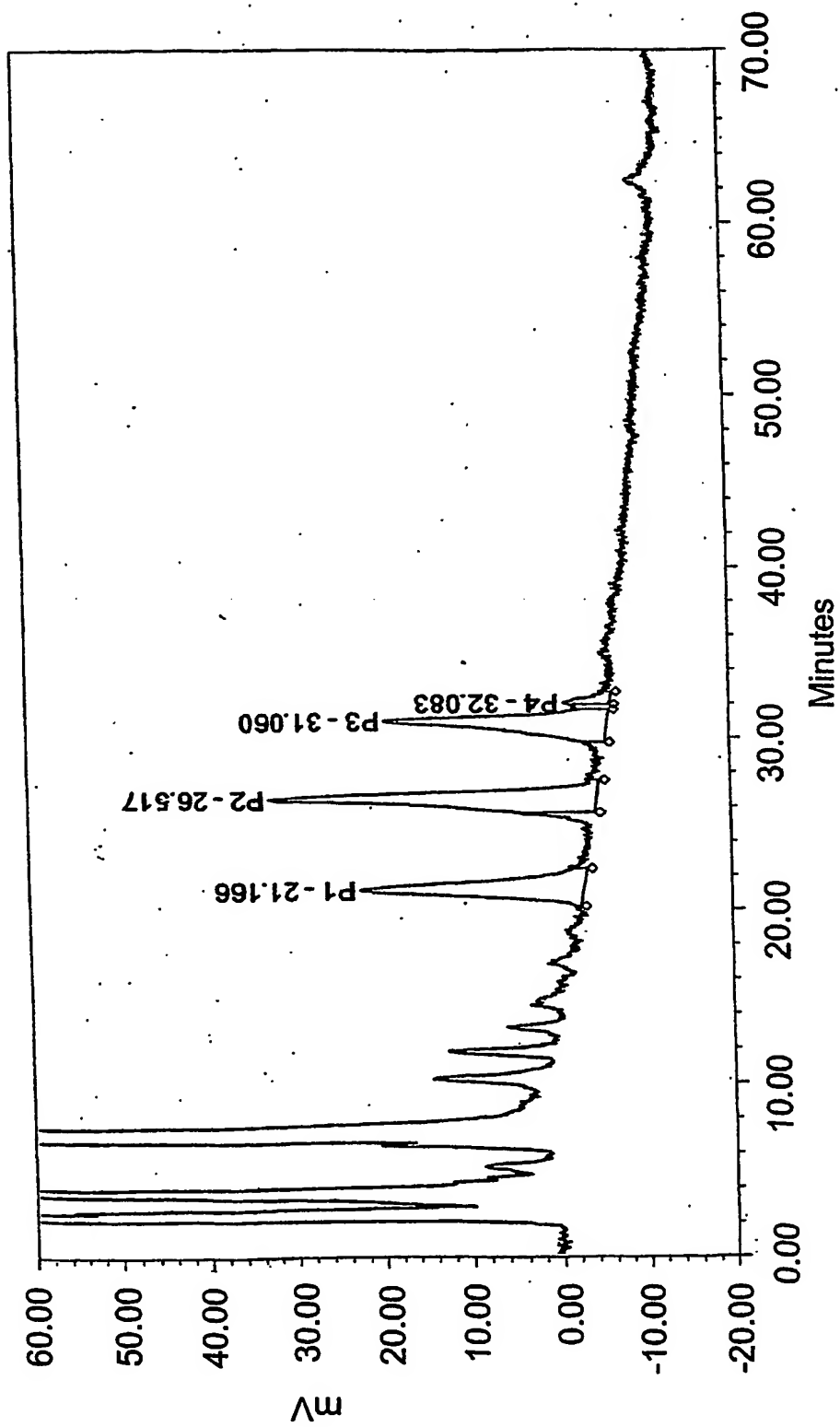


FIG. 107B



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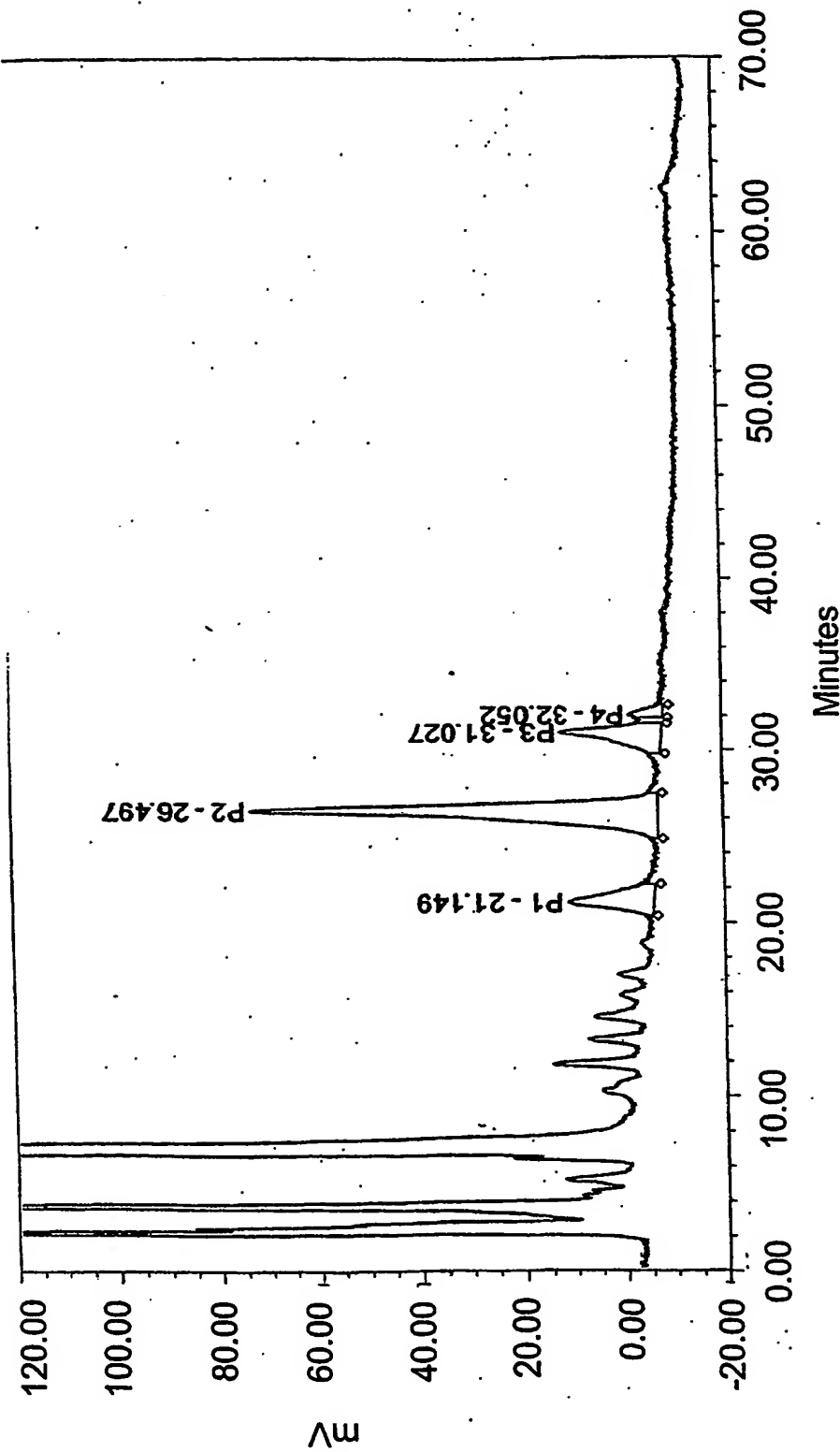


FIG. 107C

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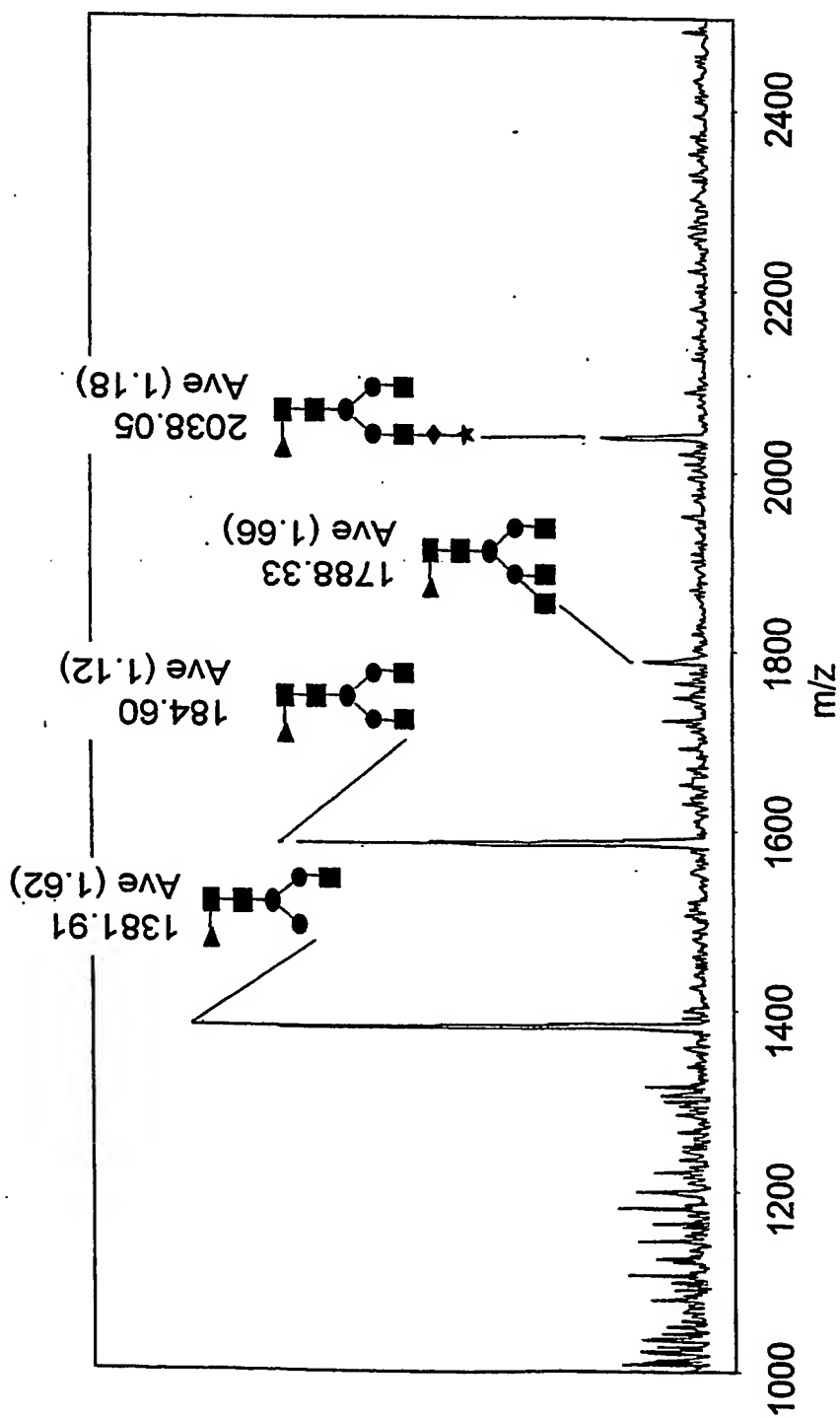


FIG. 108A

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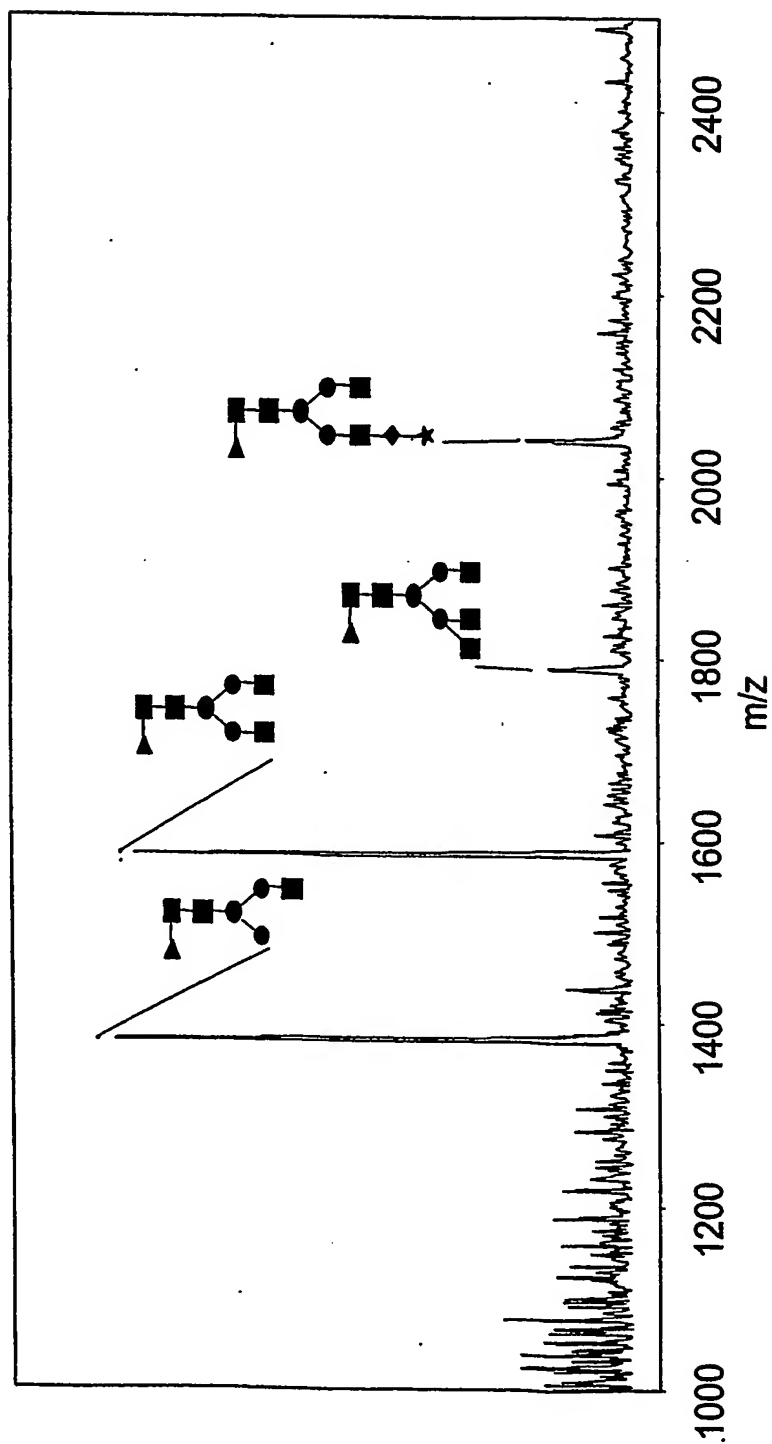


FIG. 108B

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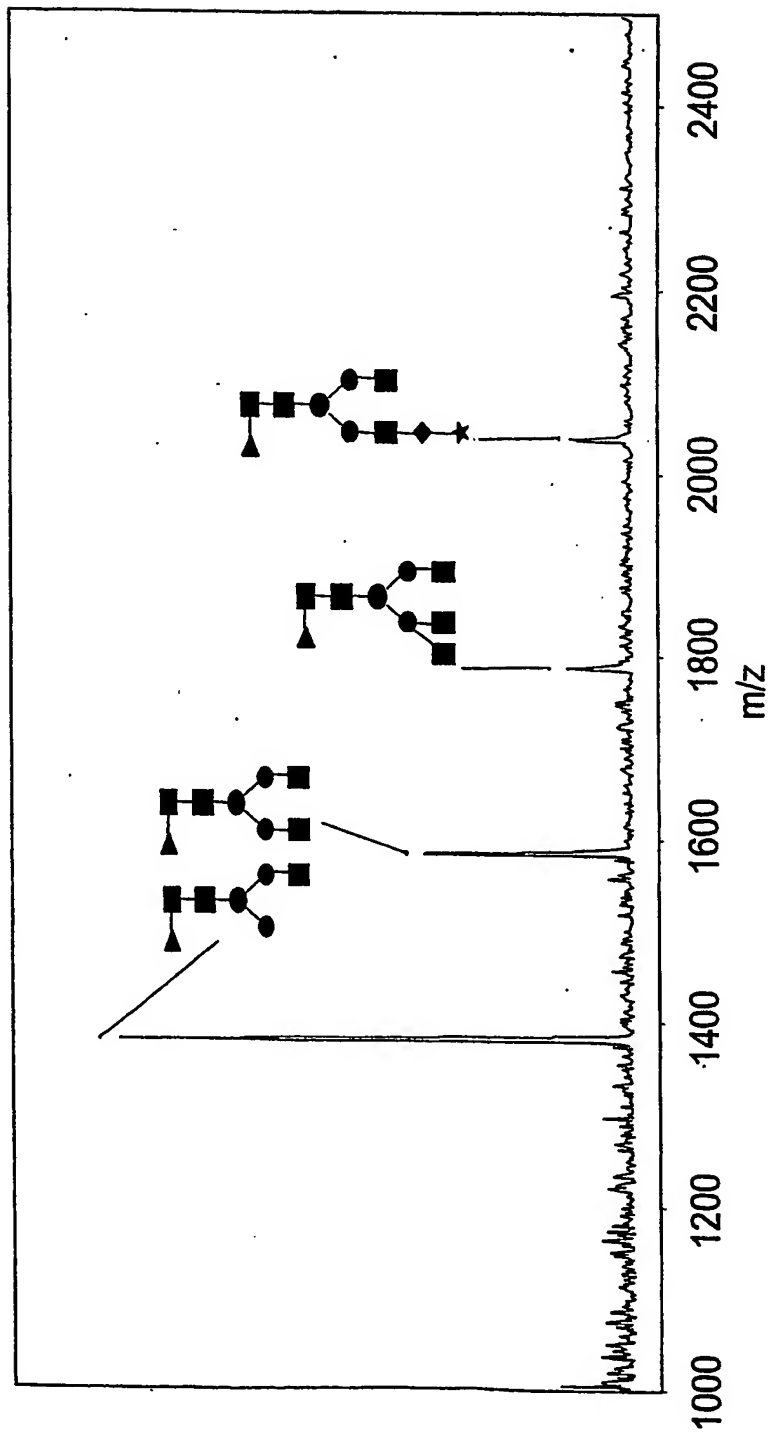


FIG. 108C

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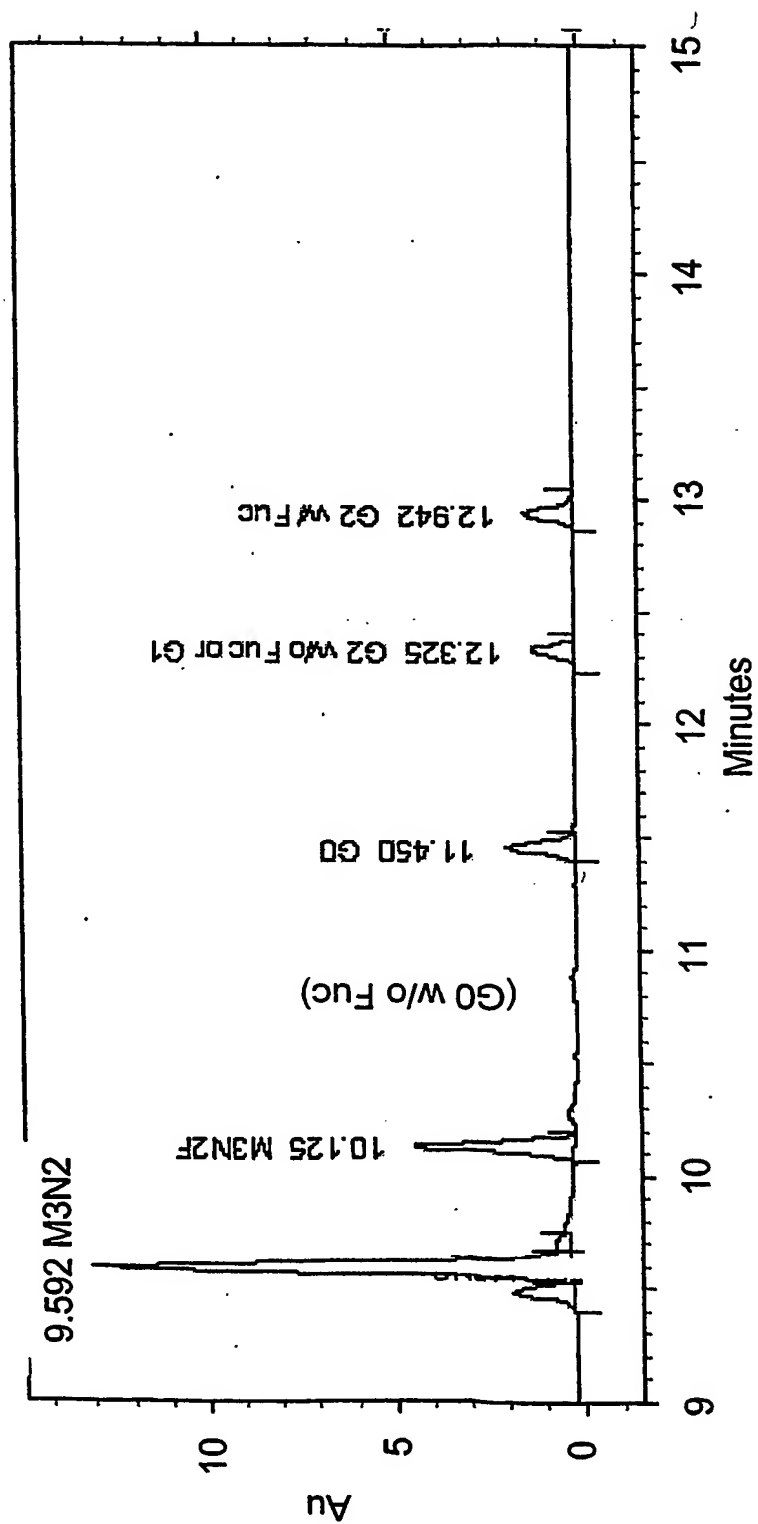


FIG. 109A

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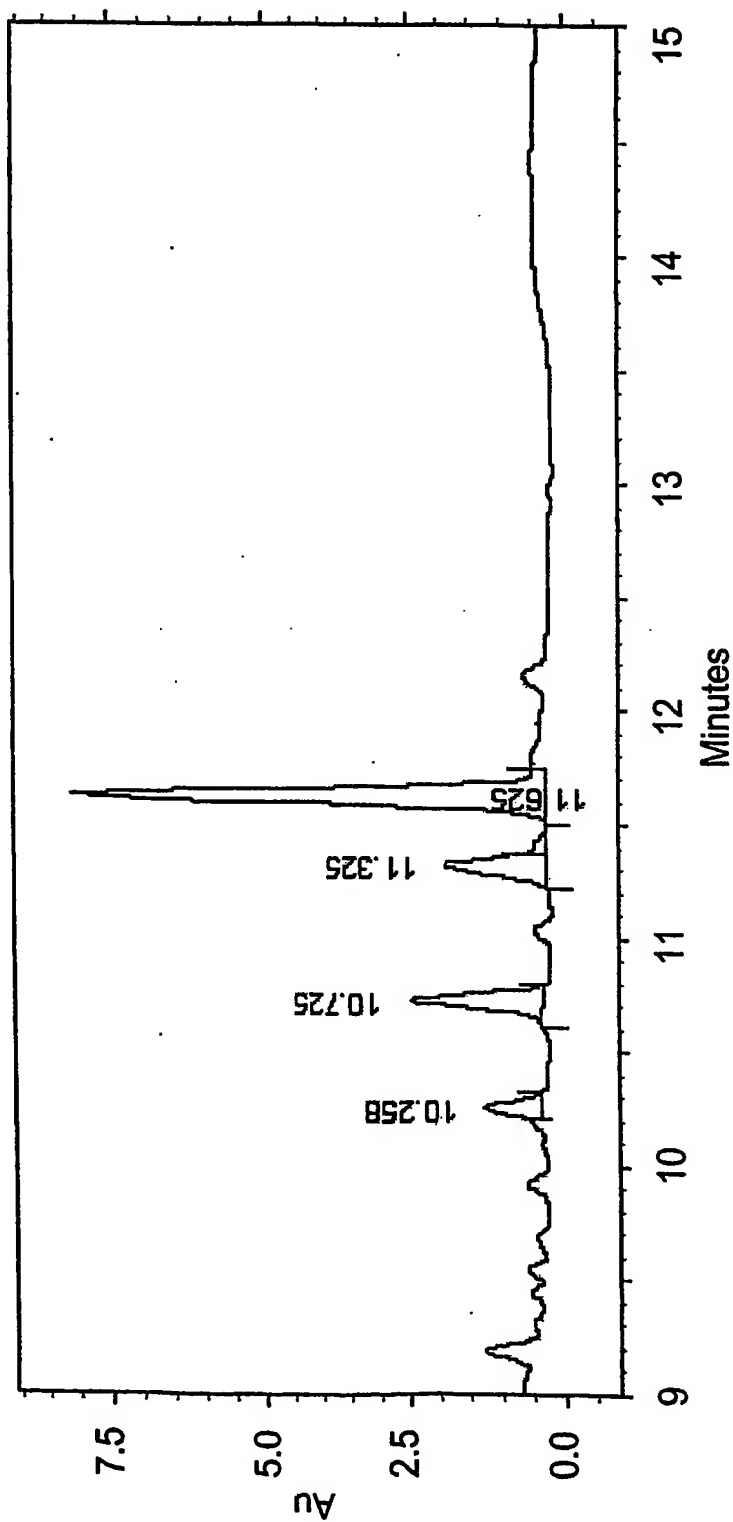


FIG. 109B

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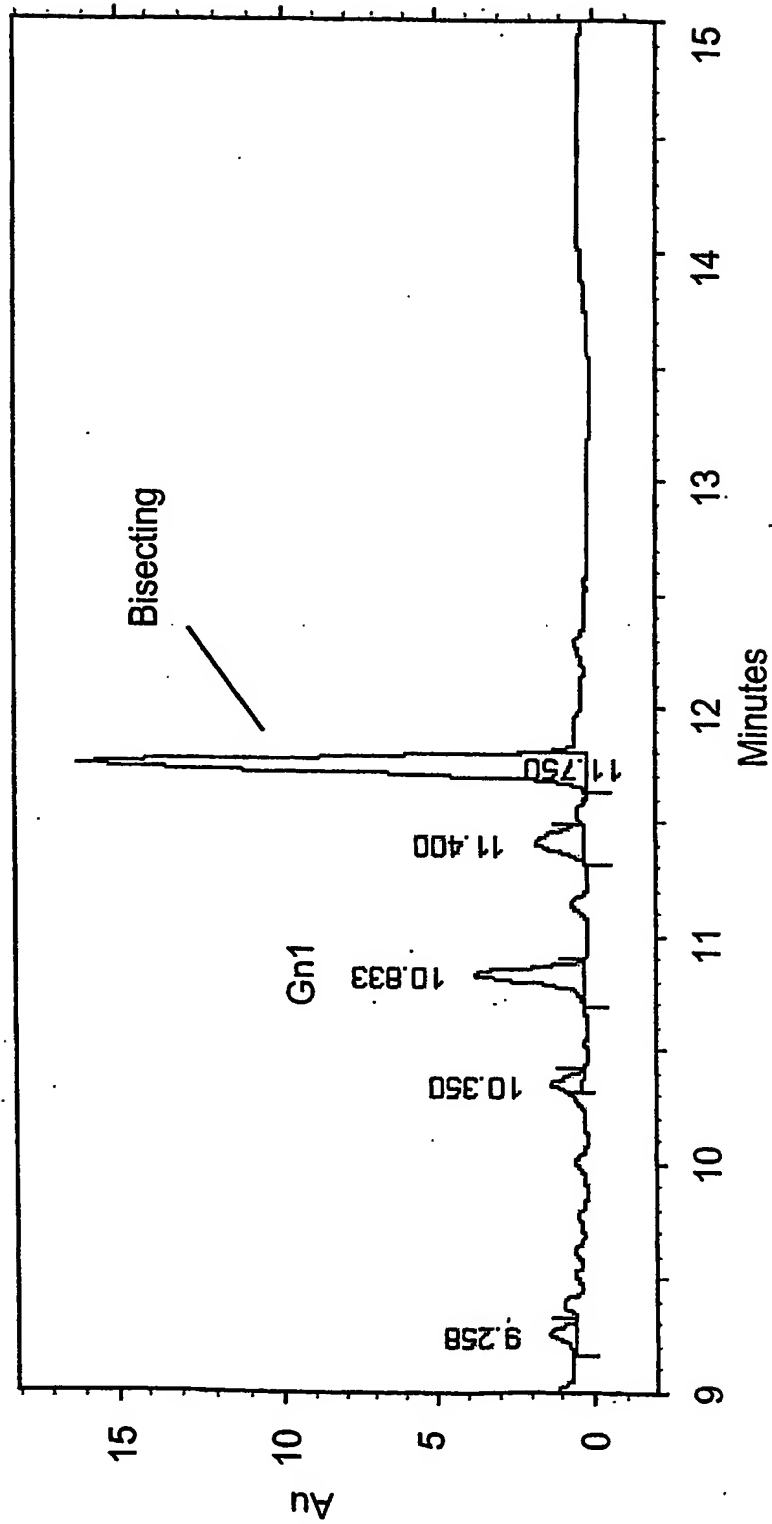


FIG. 109C

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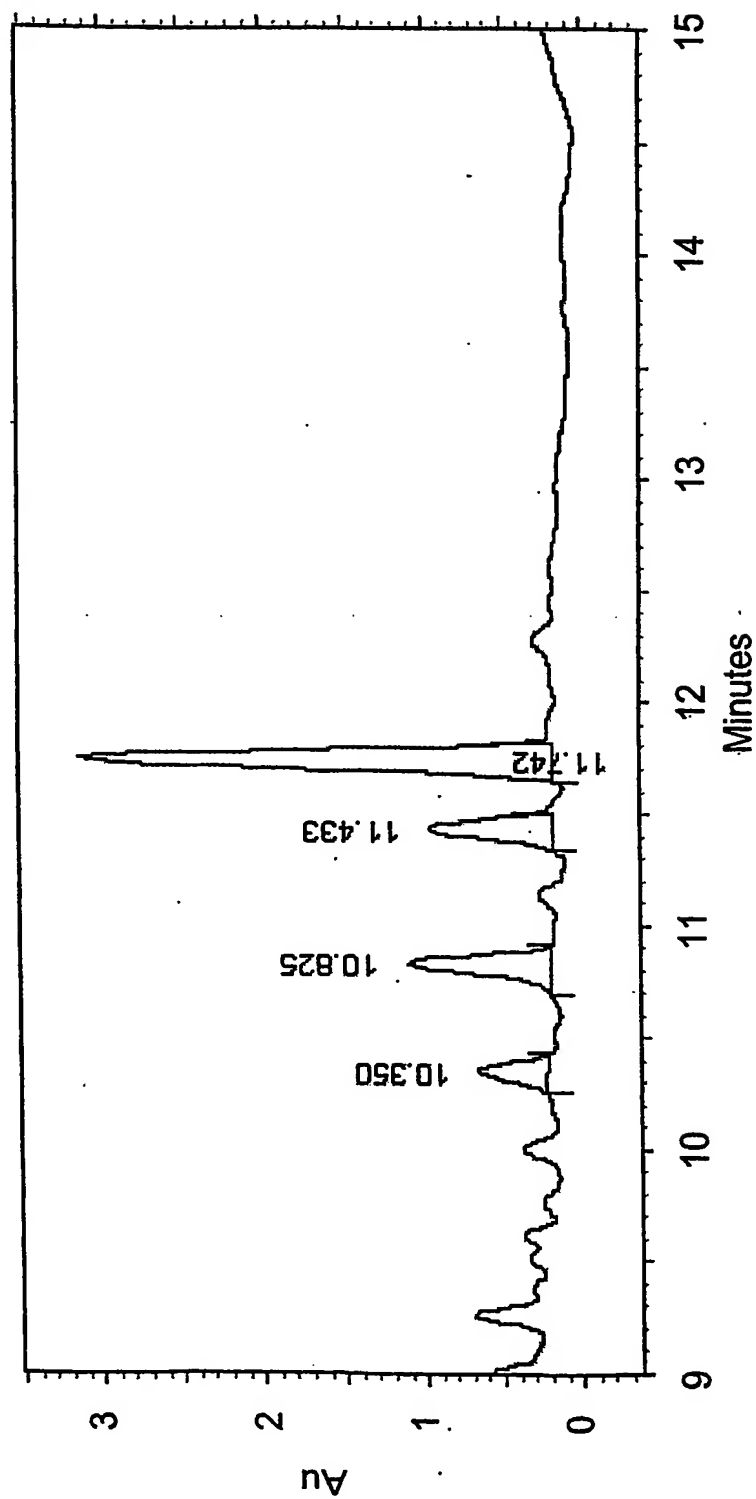


FIG. 109D



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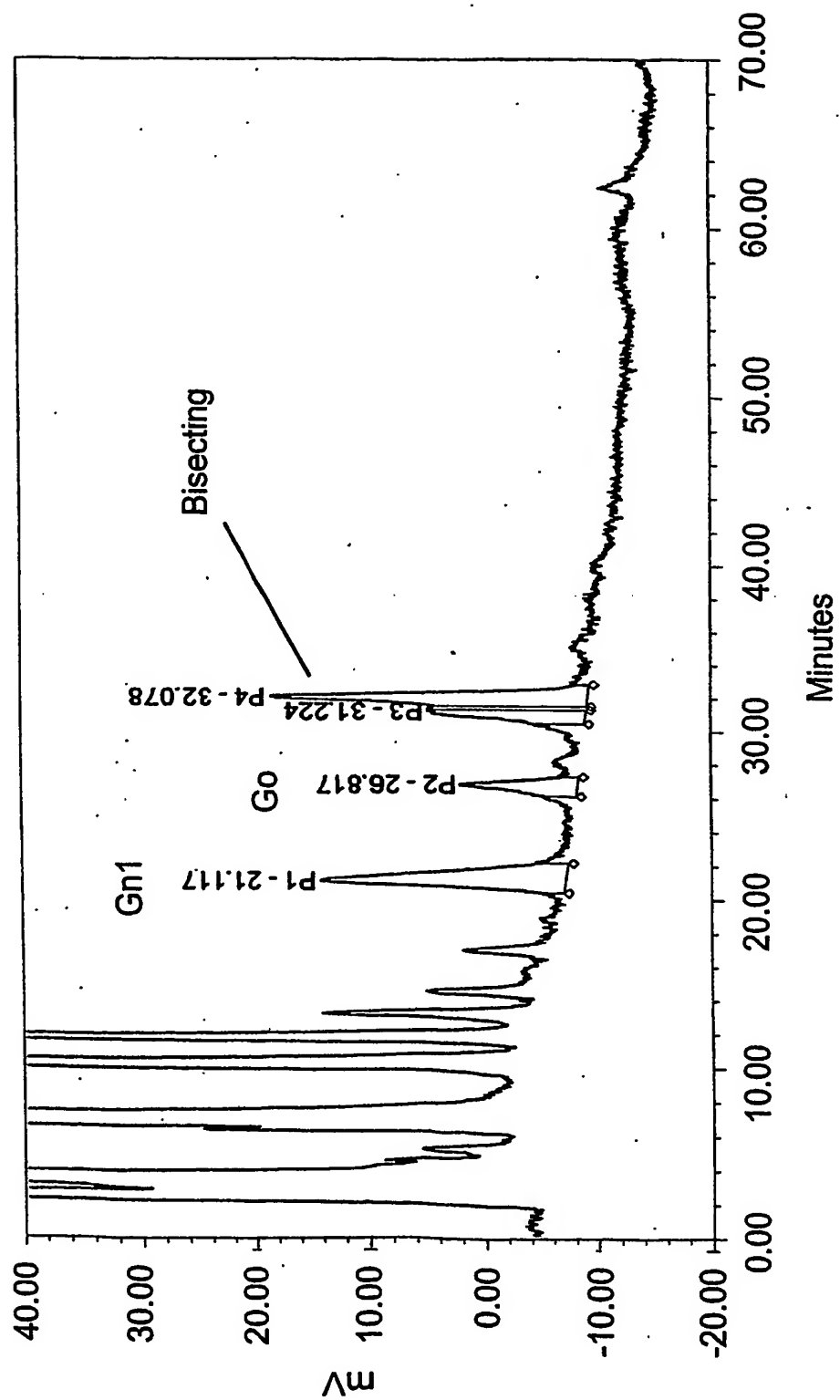


FIG. 110A

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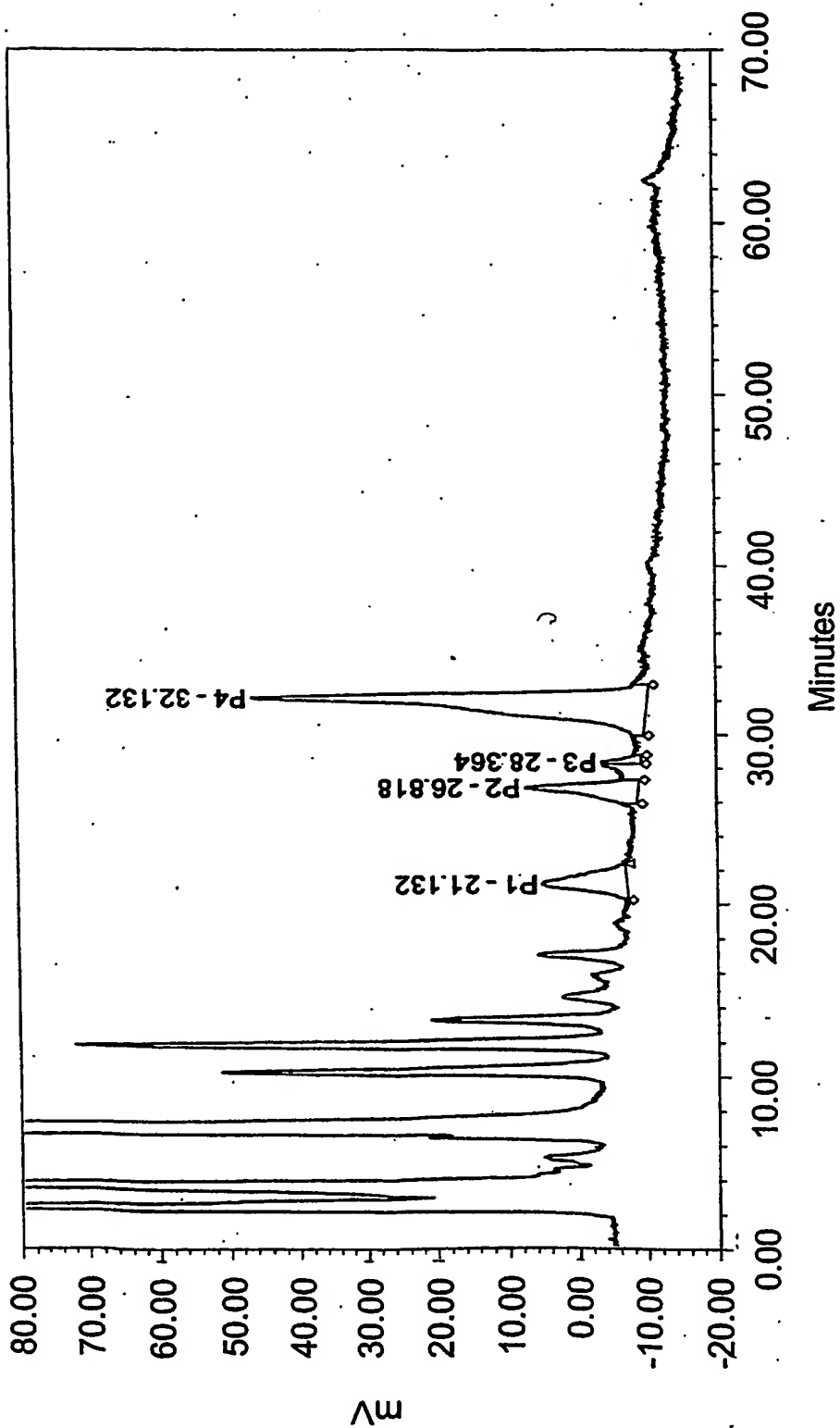


FIG. 110B

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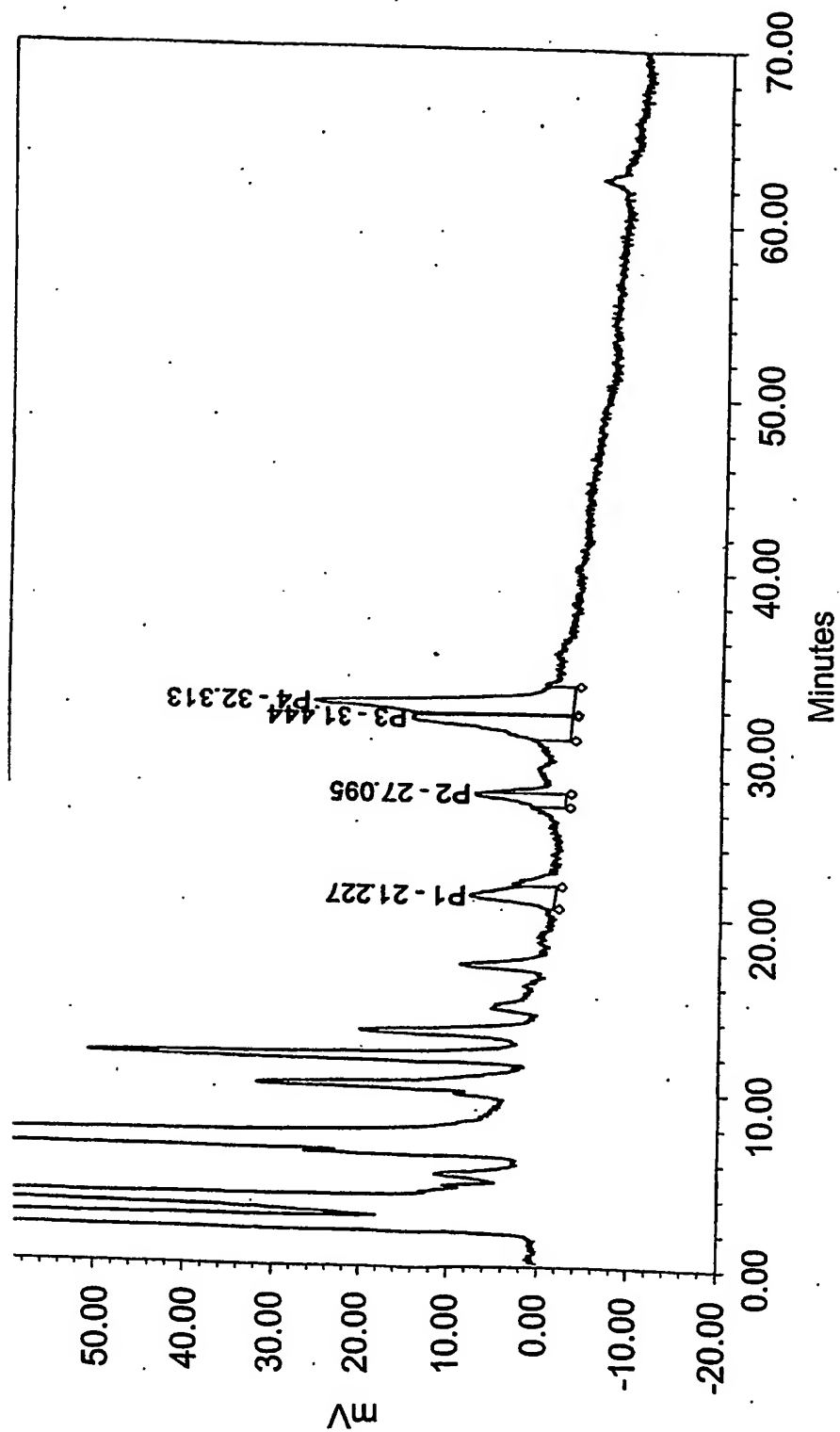


FIG. 110C

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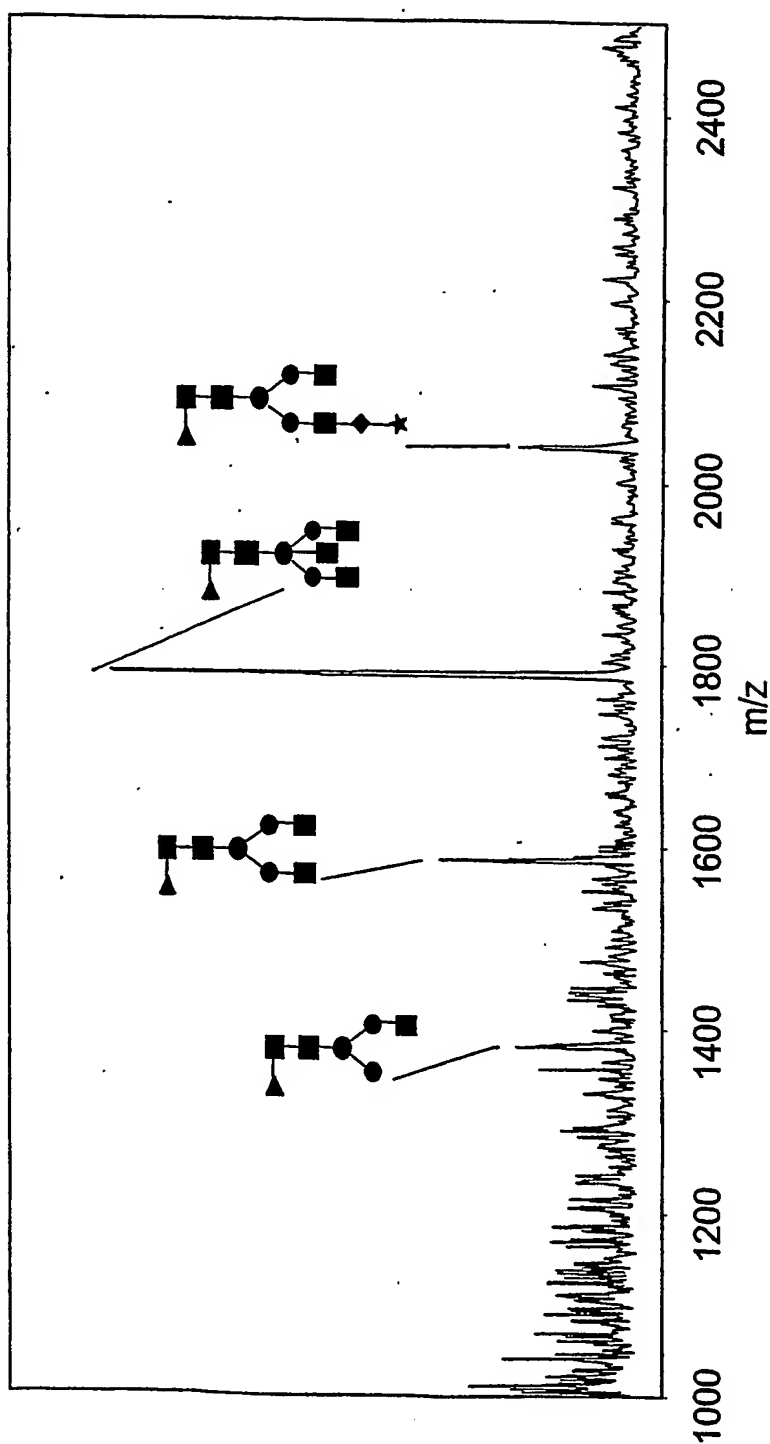


FIG. 111A

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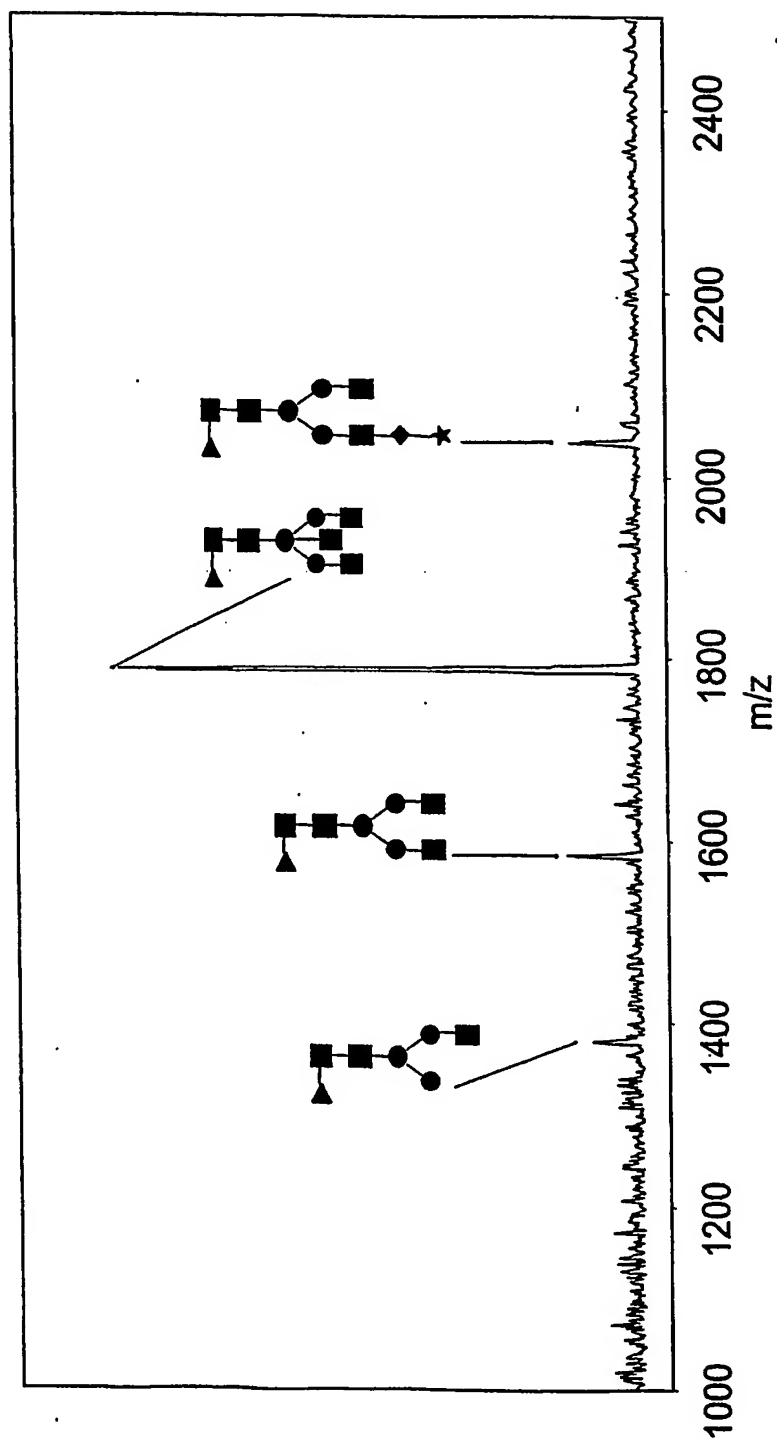


FIG. 111B

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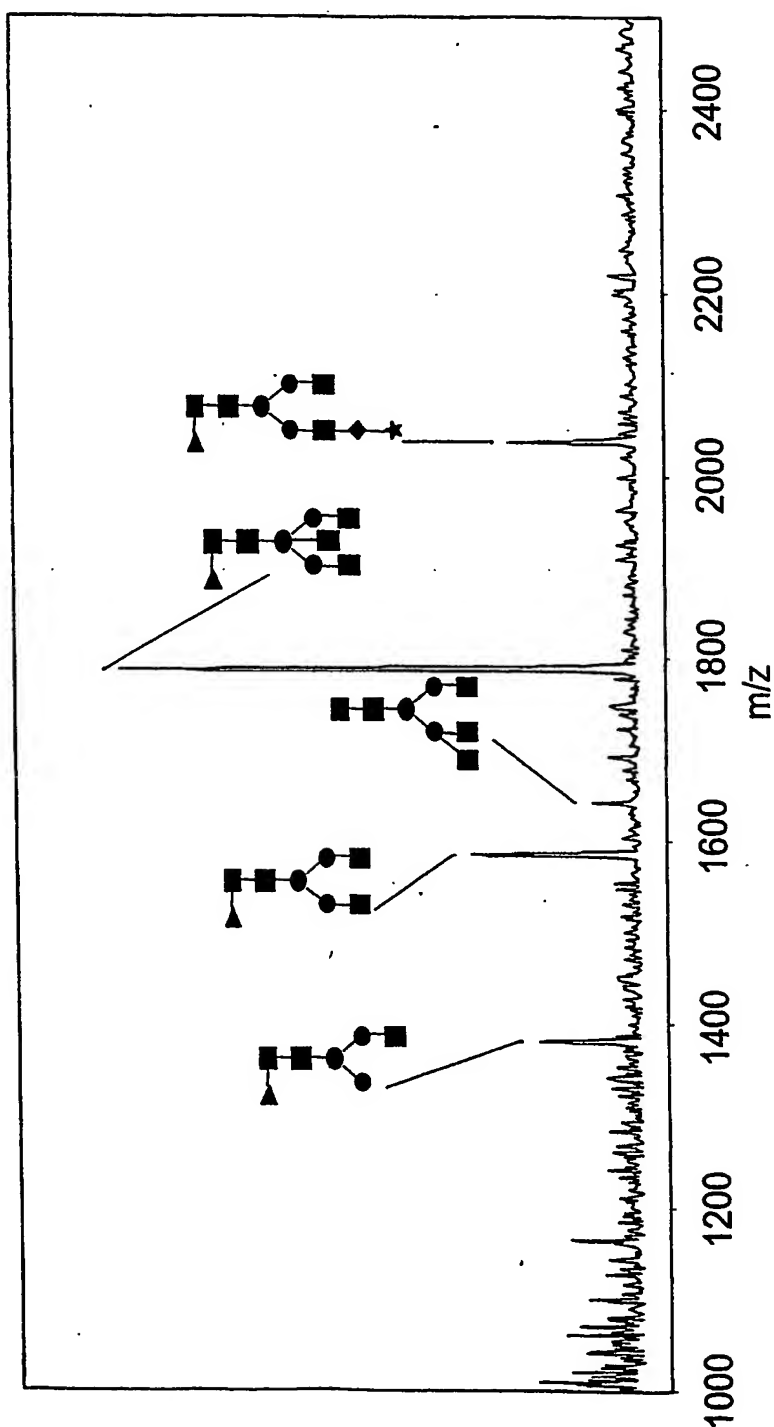


FIG. 111C

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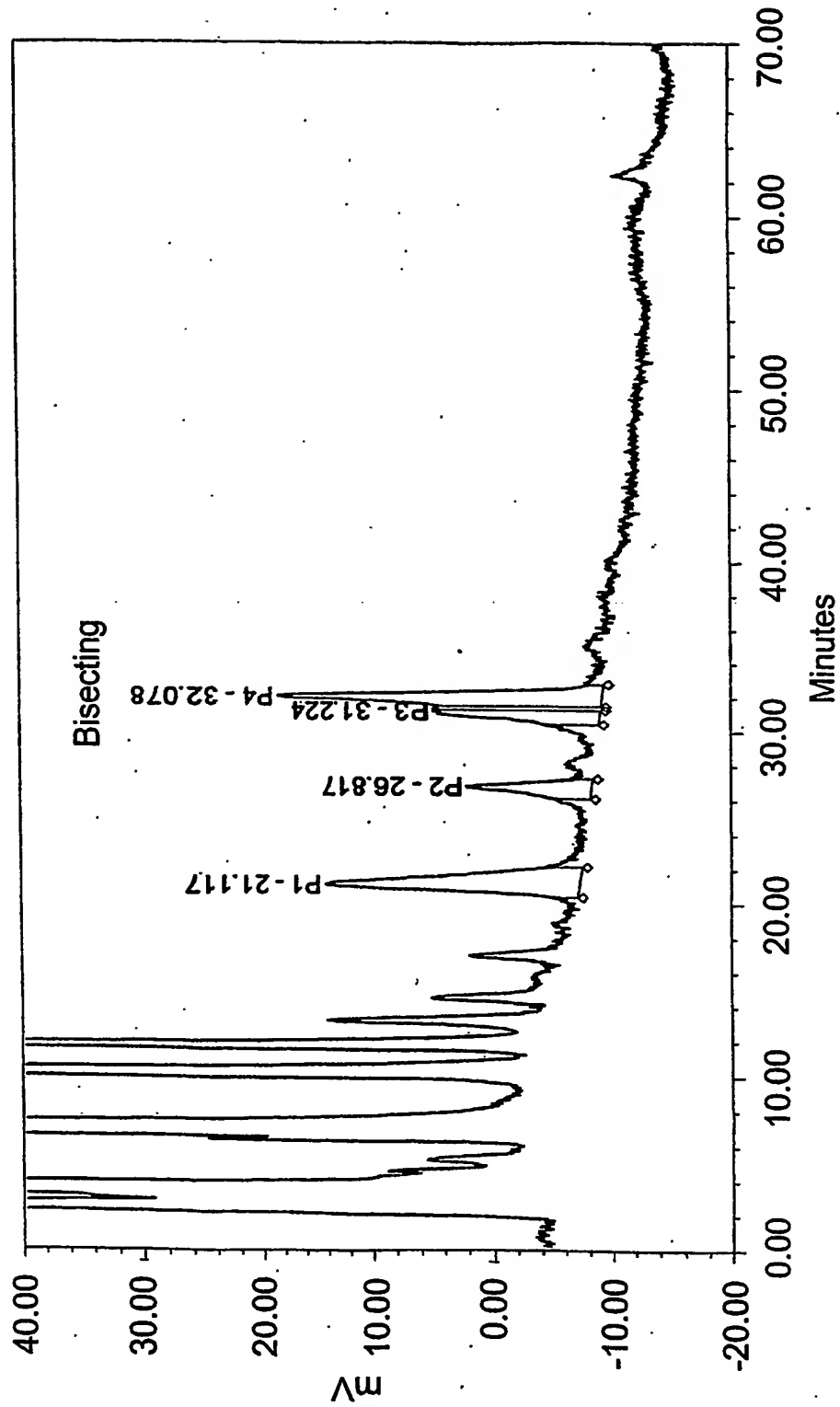


FIG. 112A

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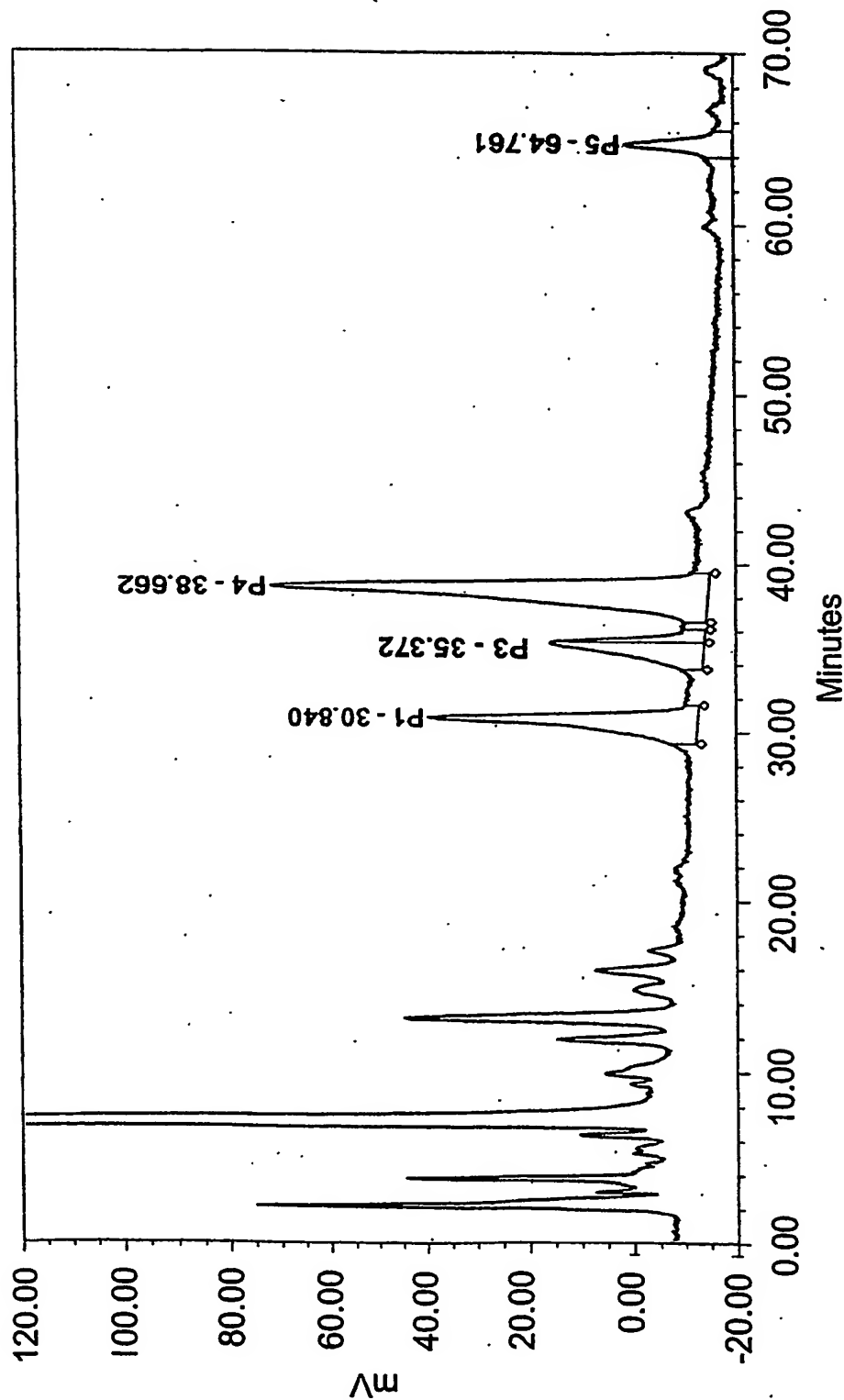


FIG. 112B



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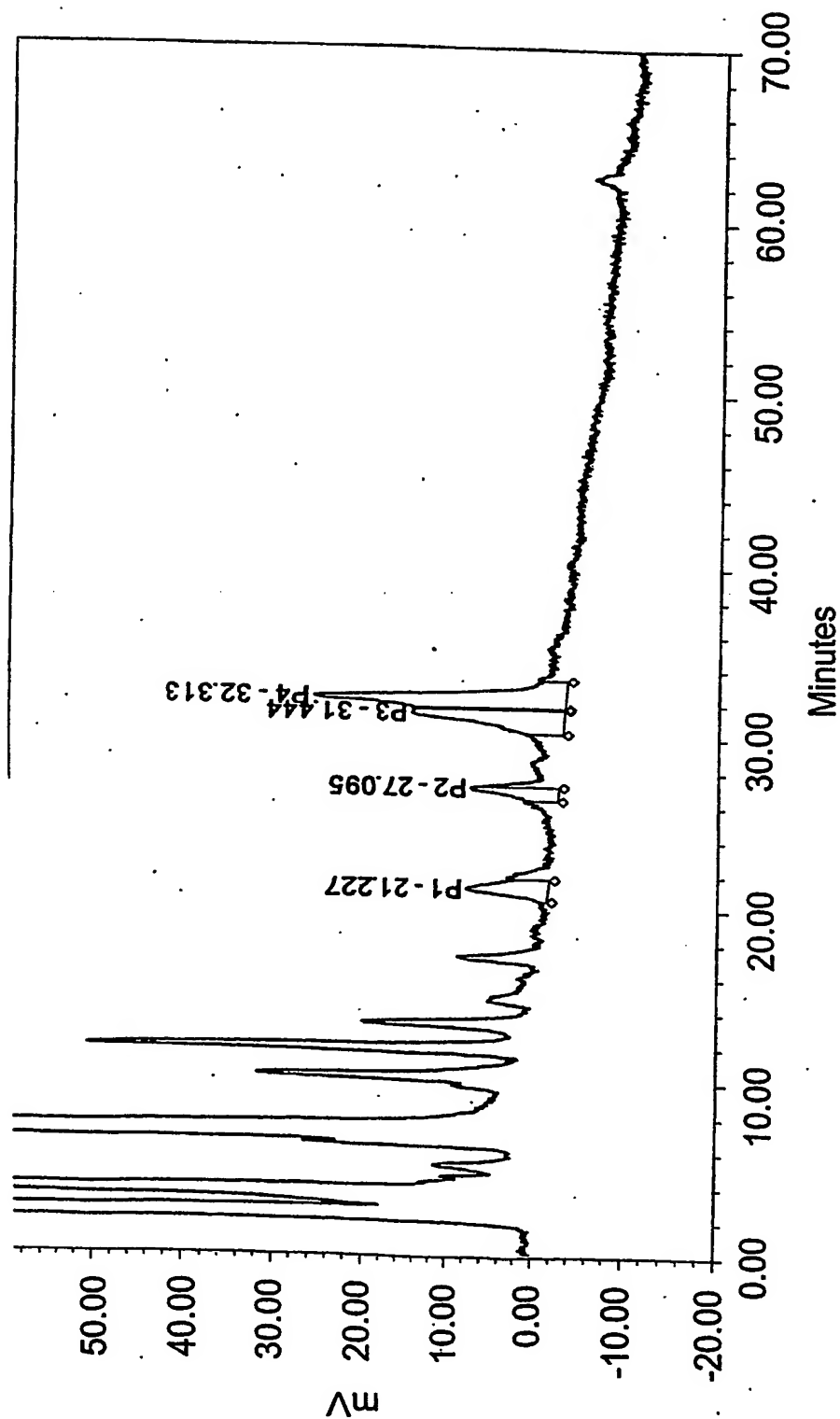


FIG. 112C

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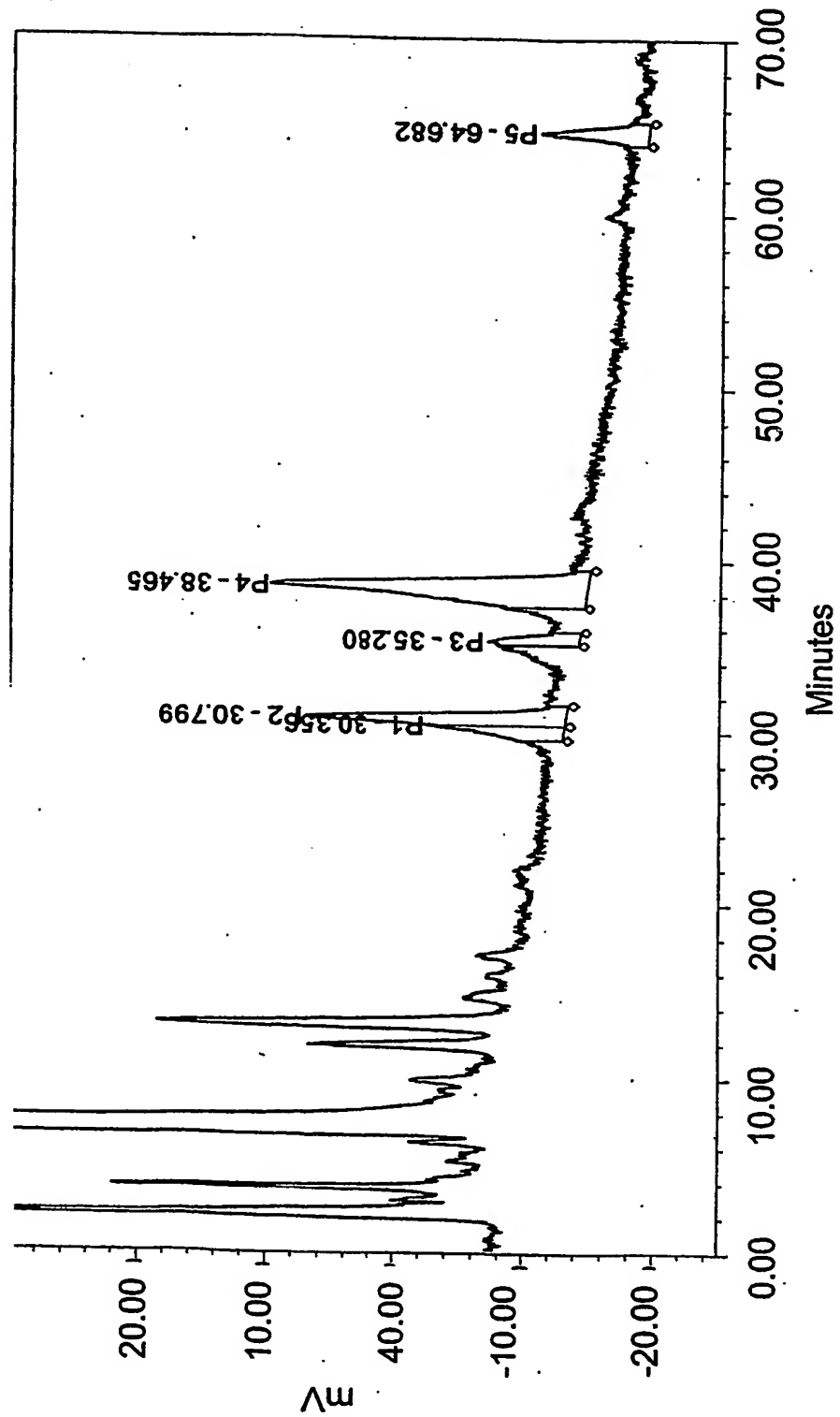


FIG. 112D

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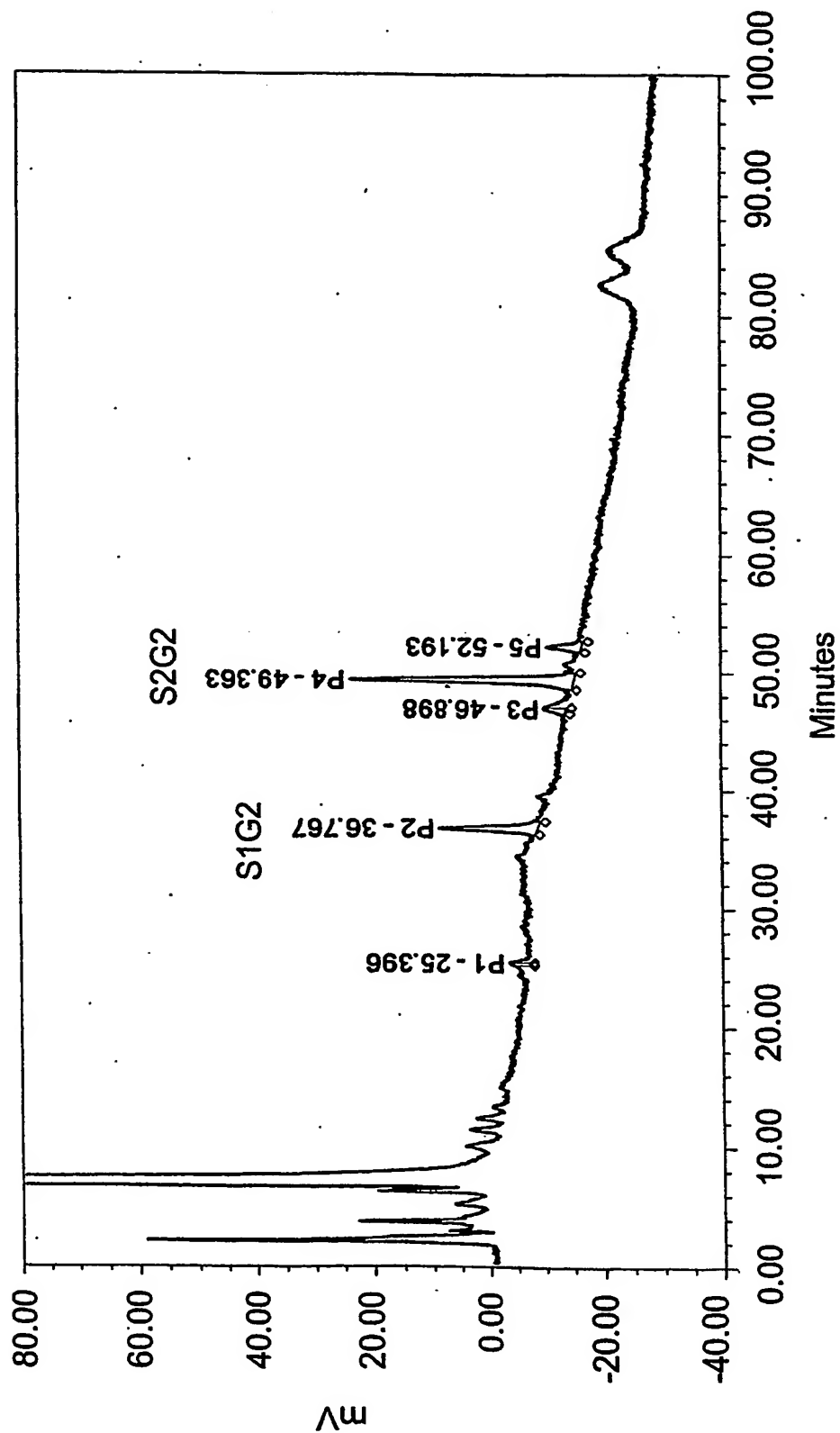


FIG. 113A

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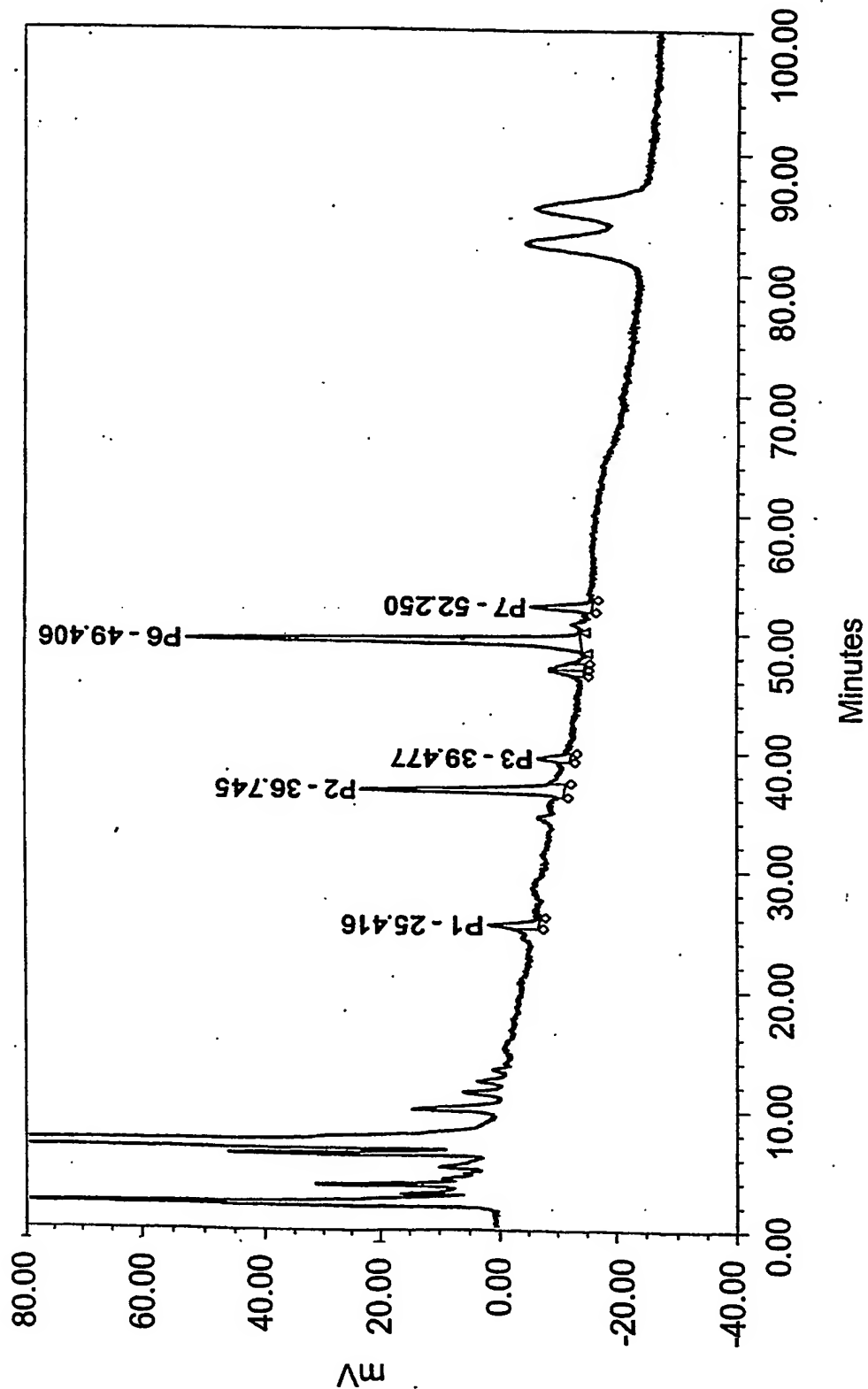


FIG. 113B

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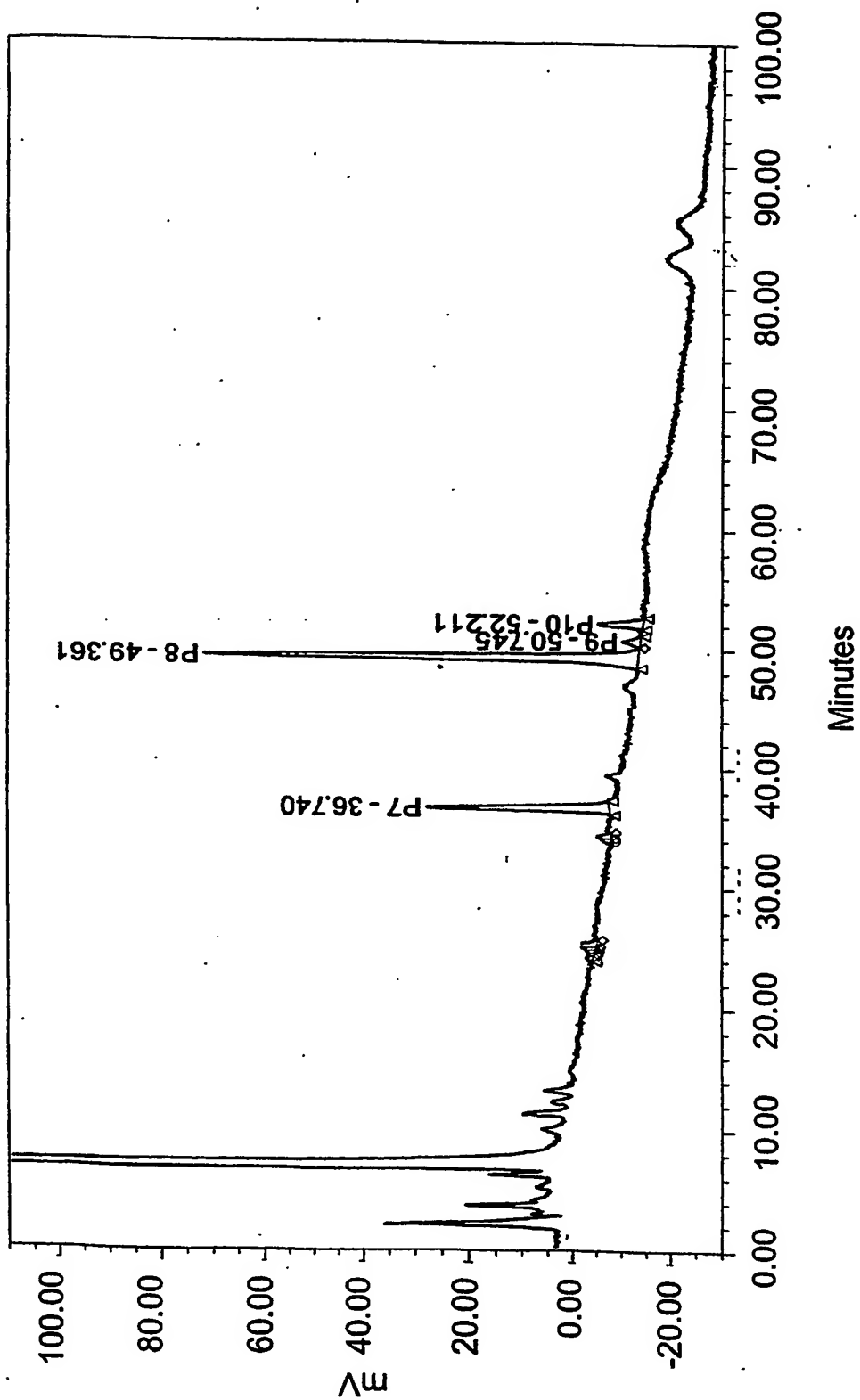


FIG. 113C

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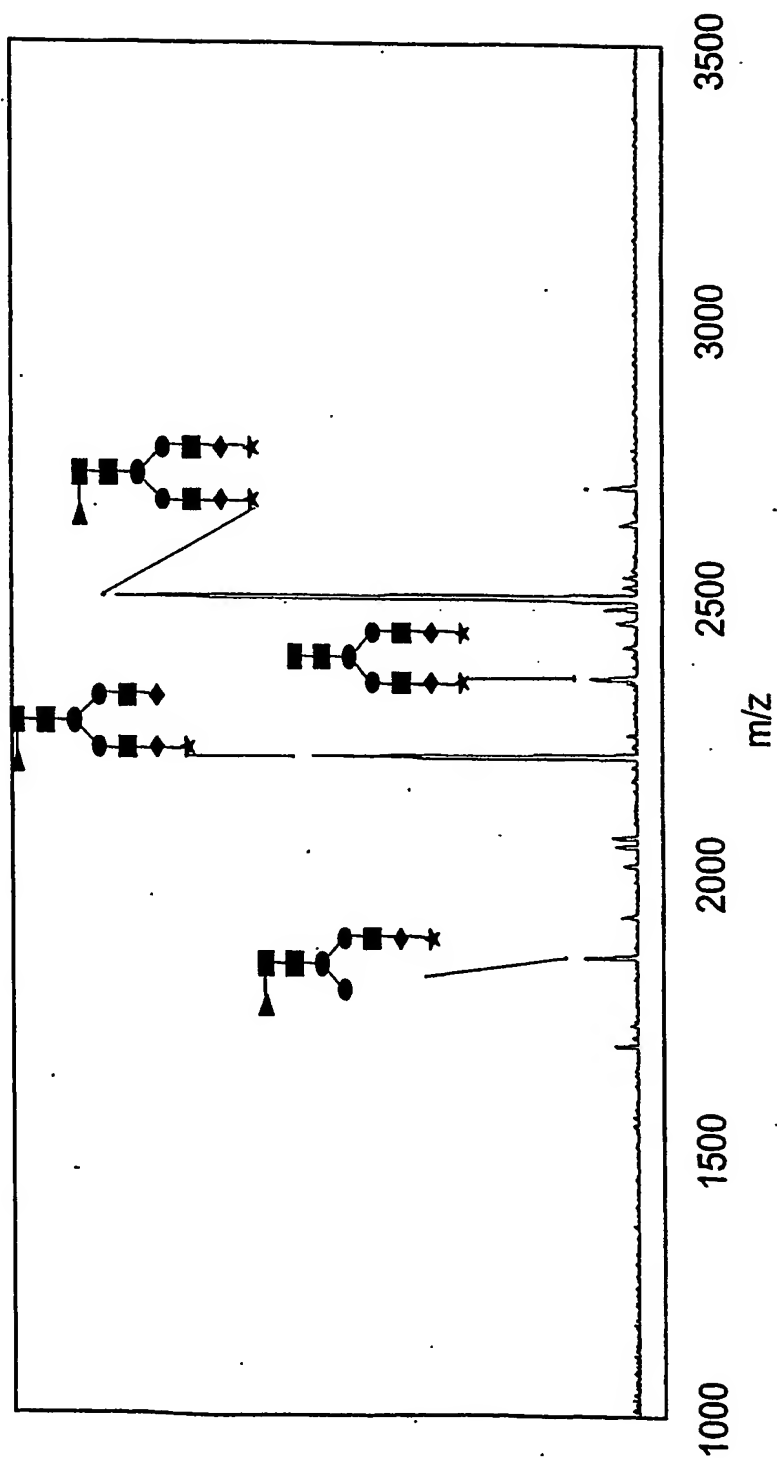


FIG. 114A

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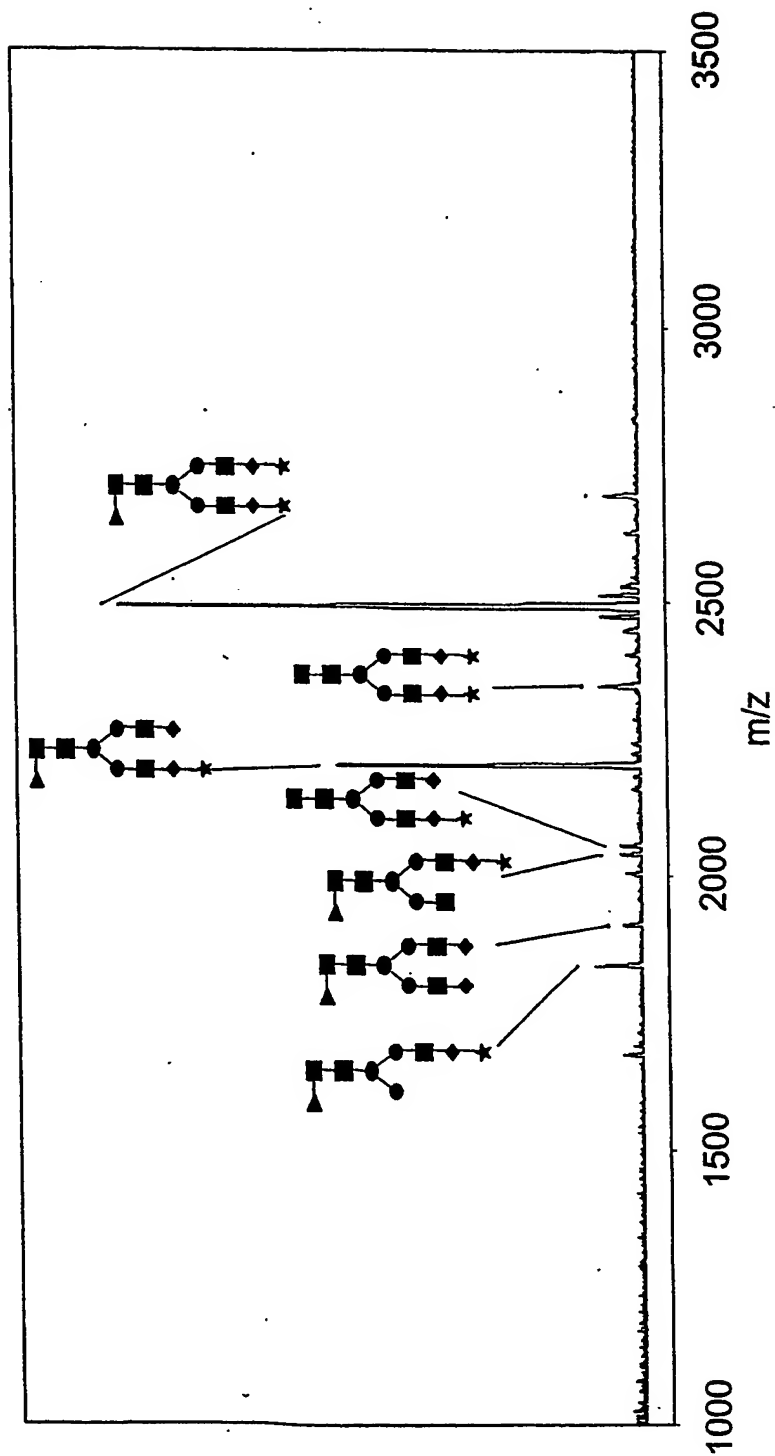


FIG. 114B

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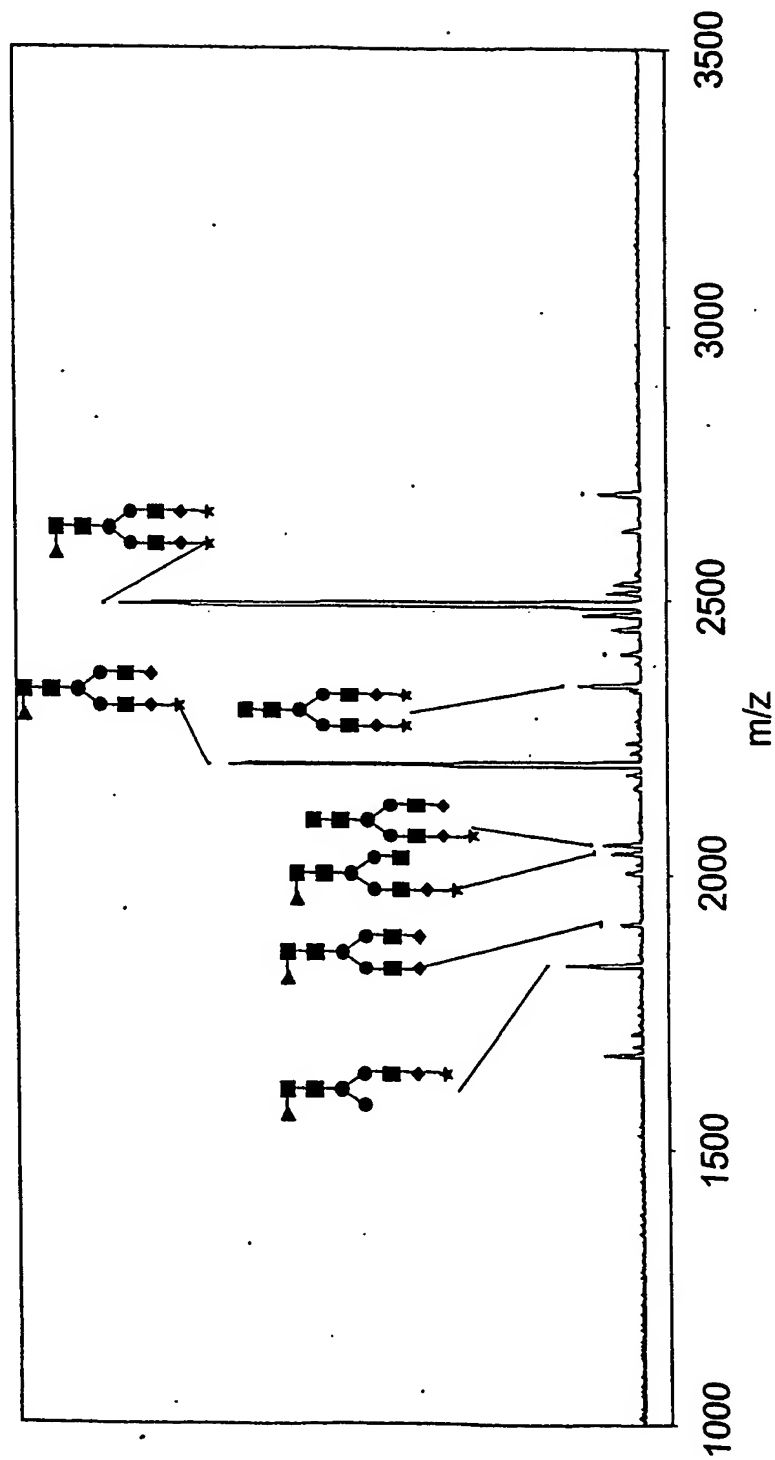


FIG. 114C



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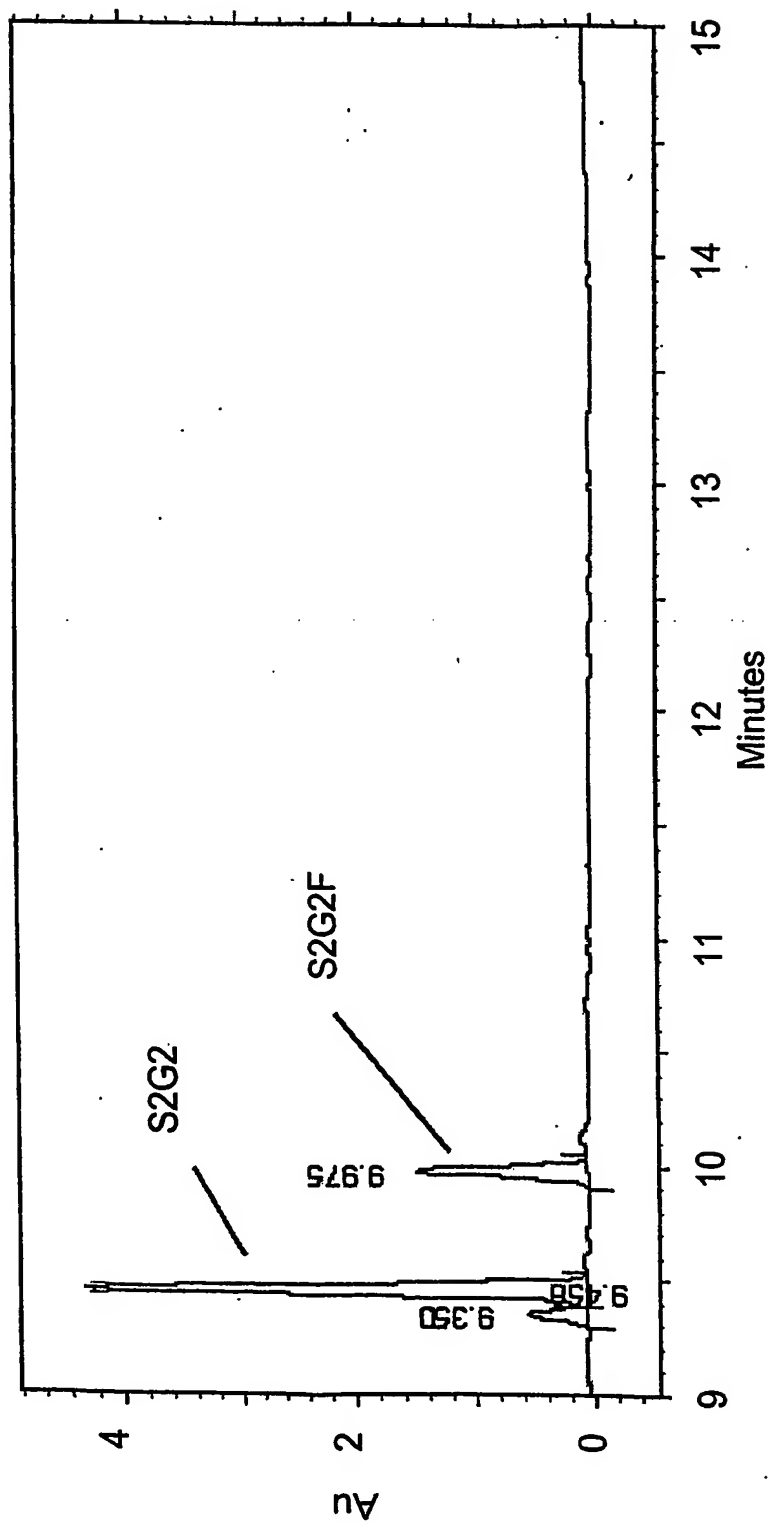


FIG. 115A

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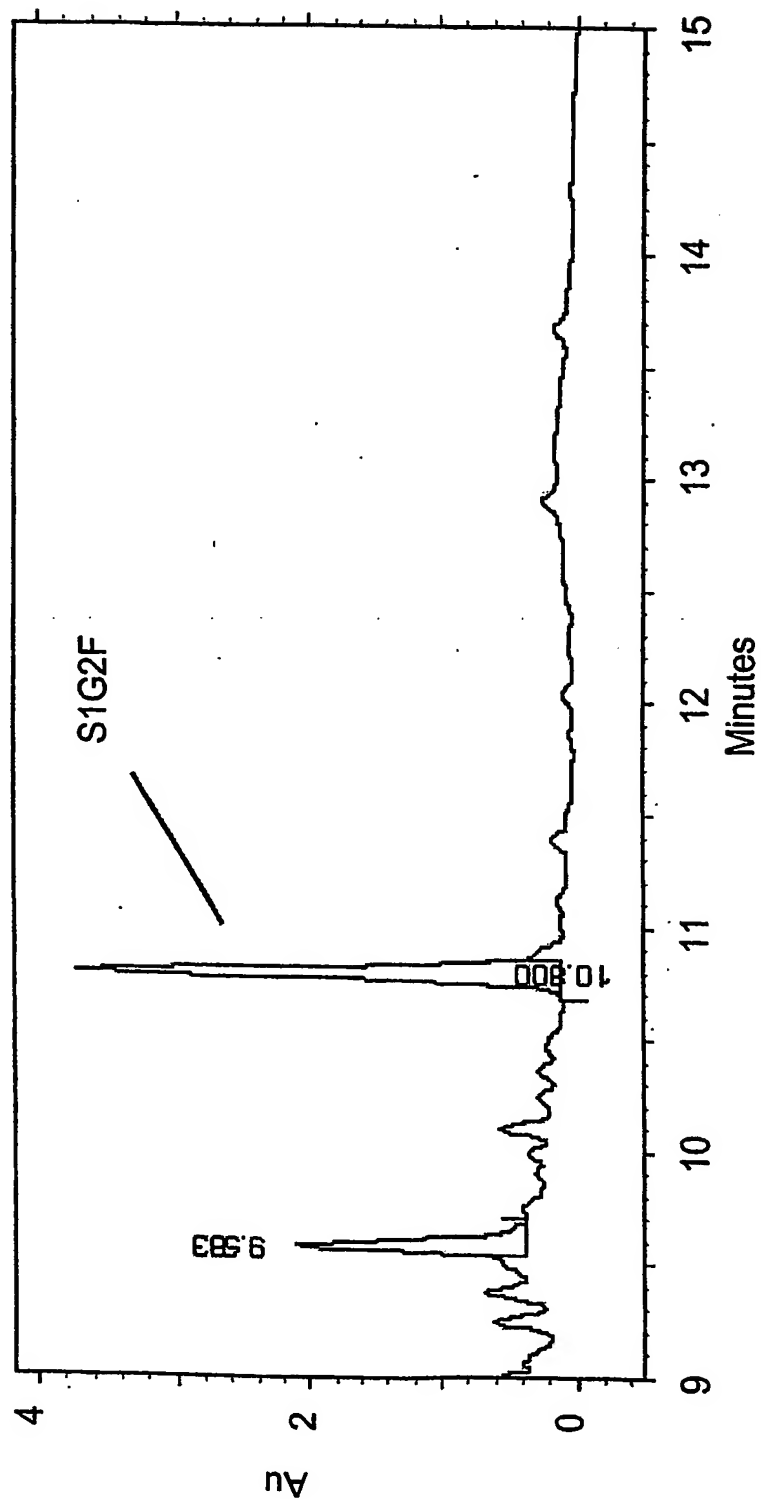


FIG. 115B

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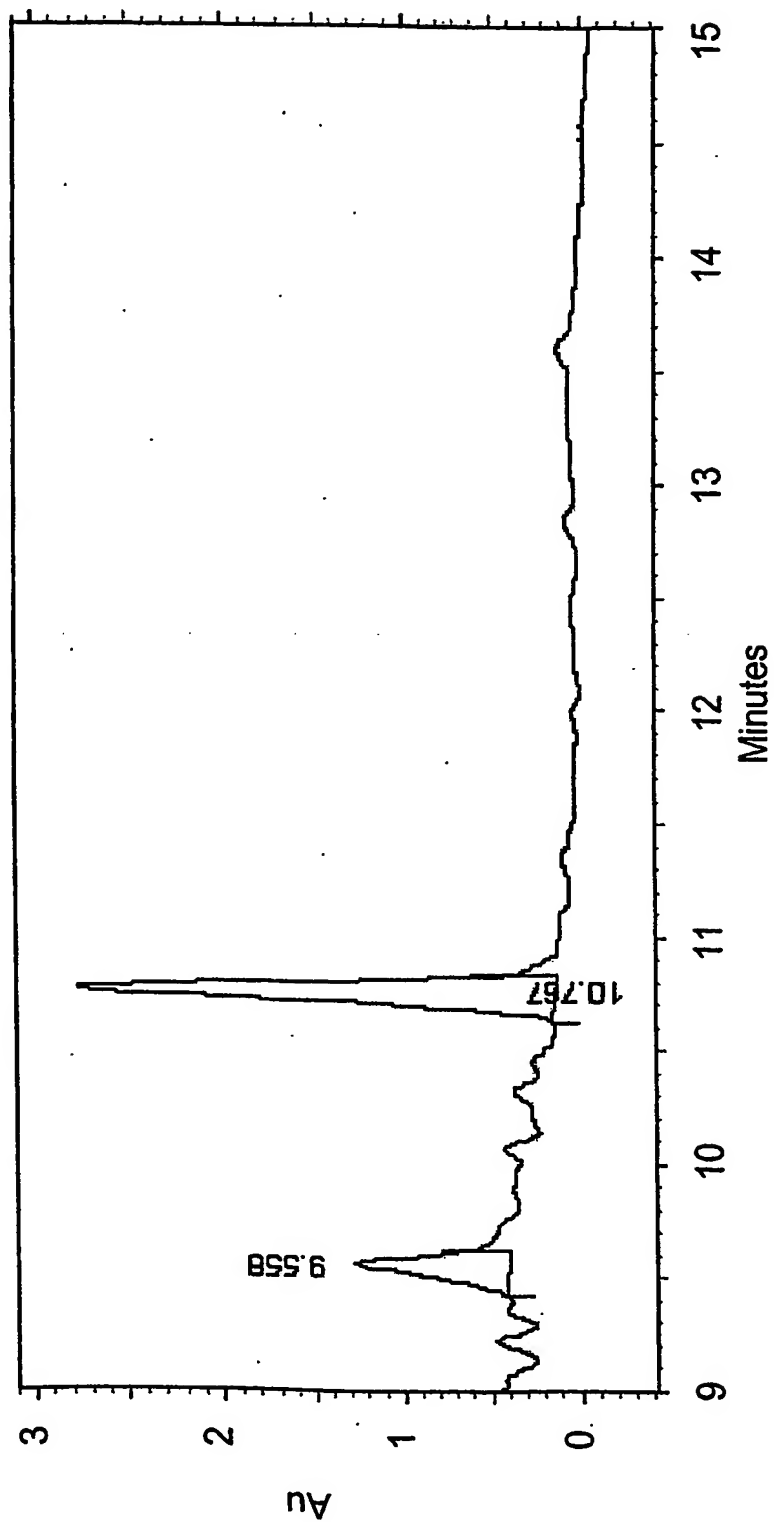


FIG. 115C

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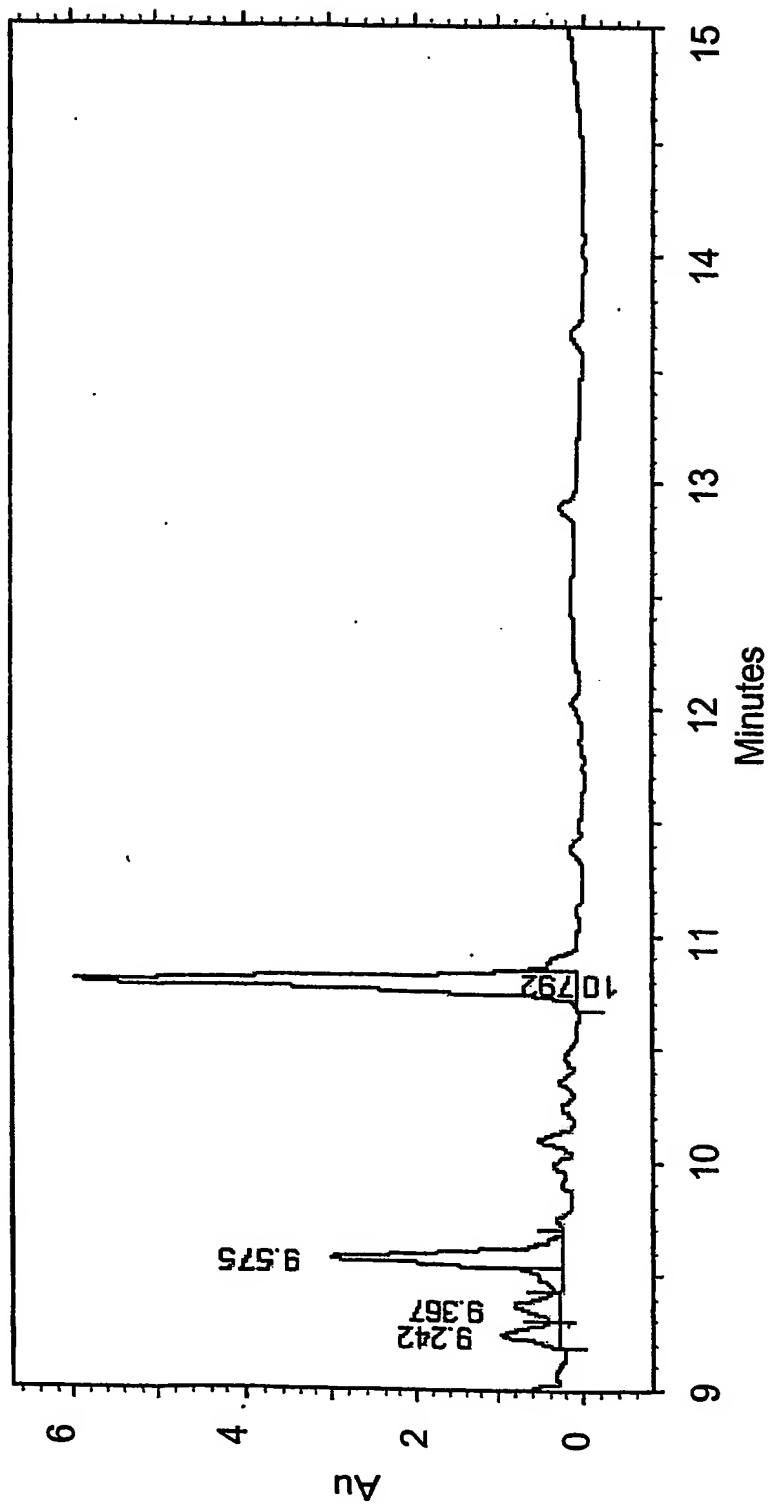


FIG. 115D

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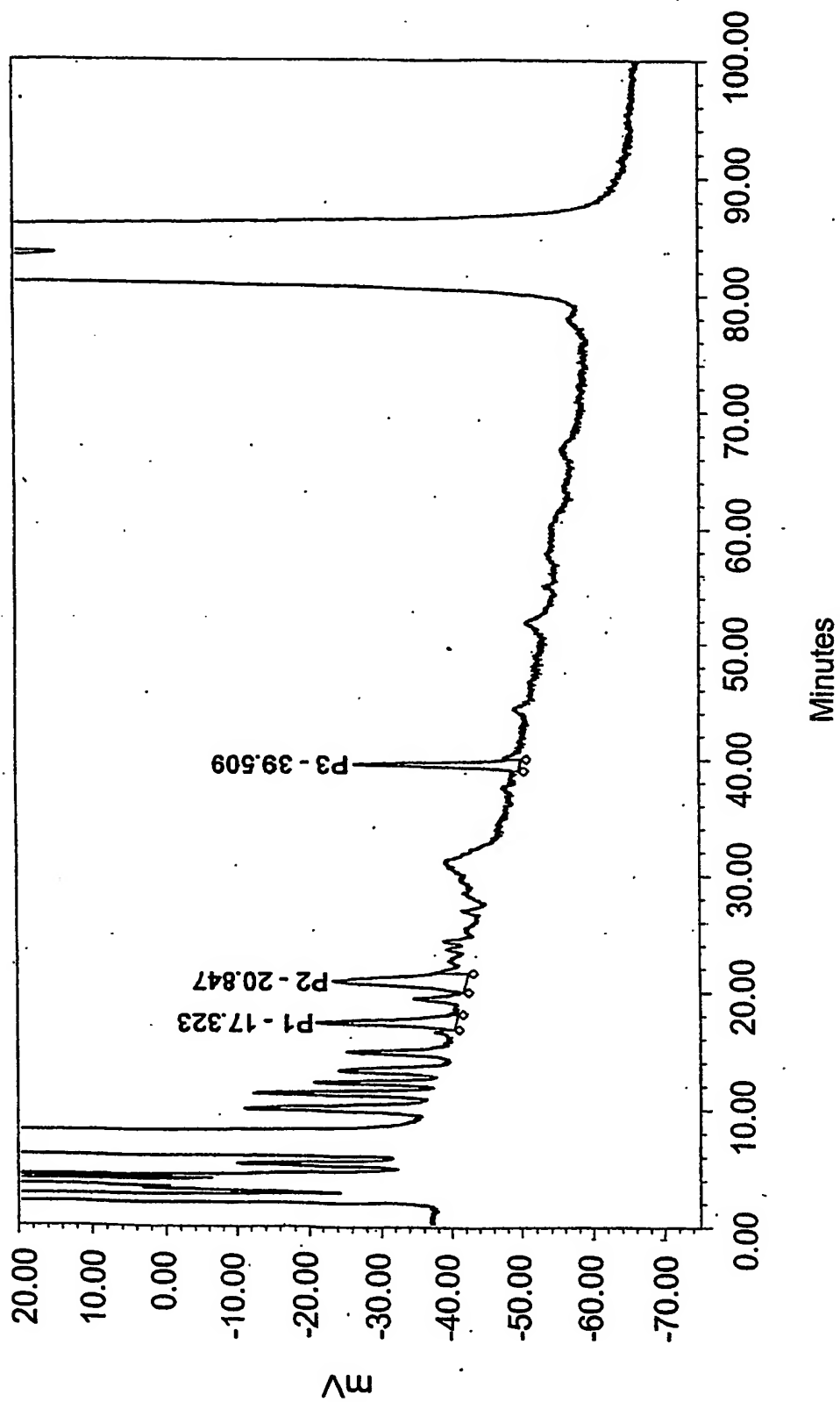


FIG. 116A

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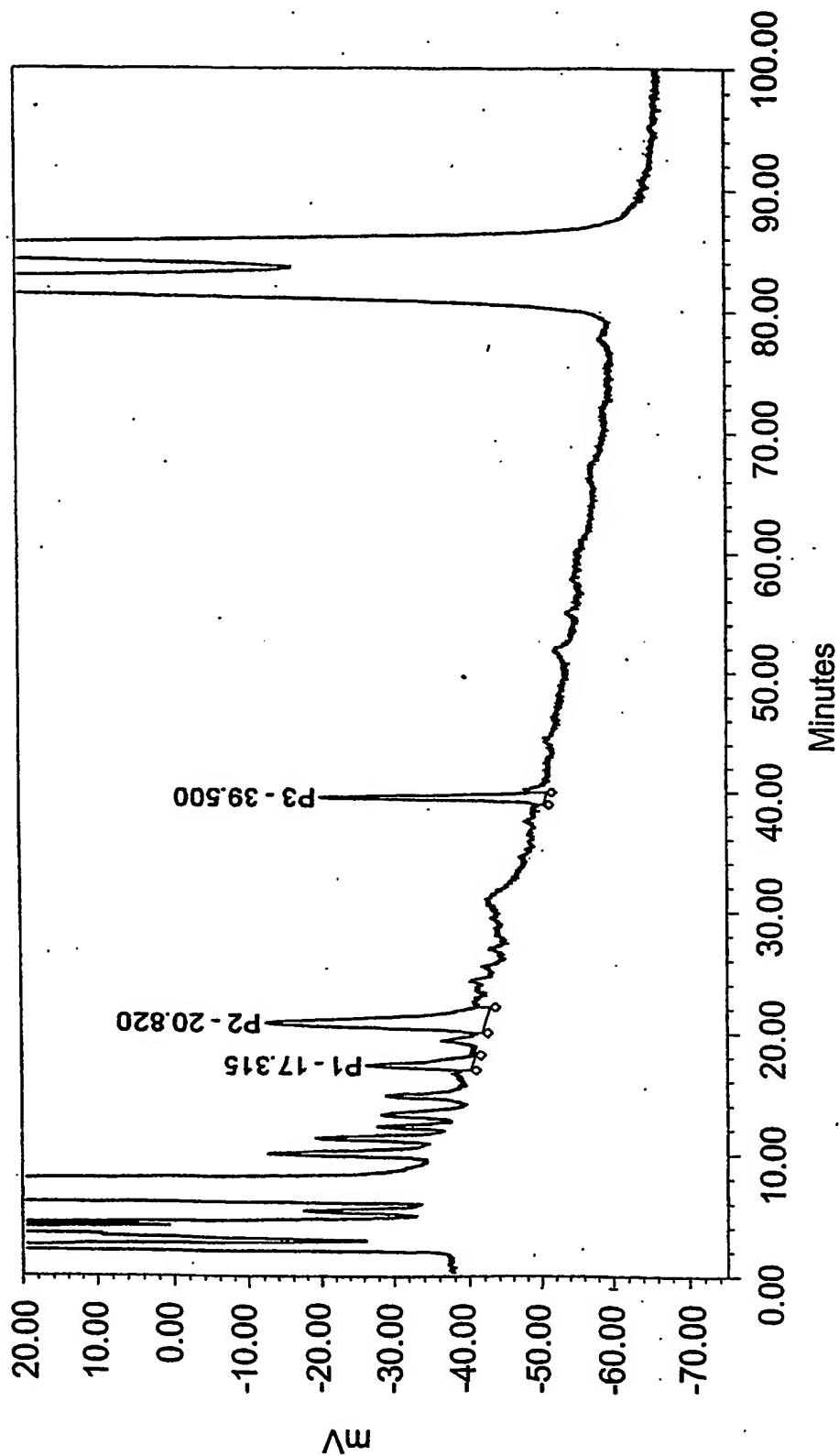


FIG. 116B

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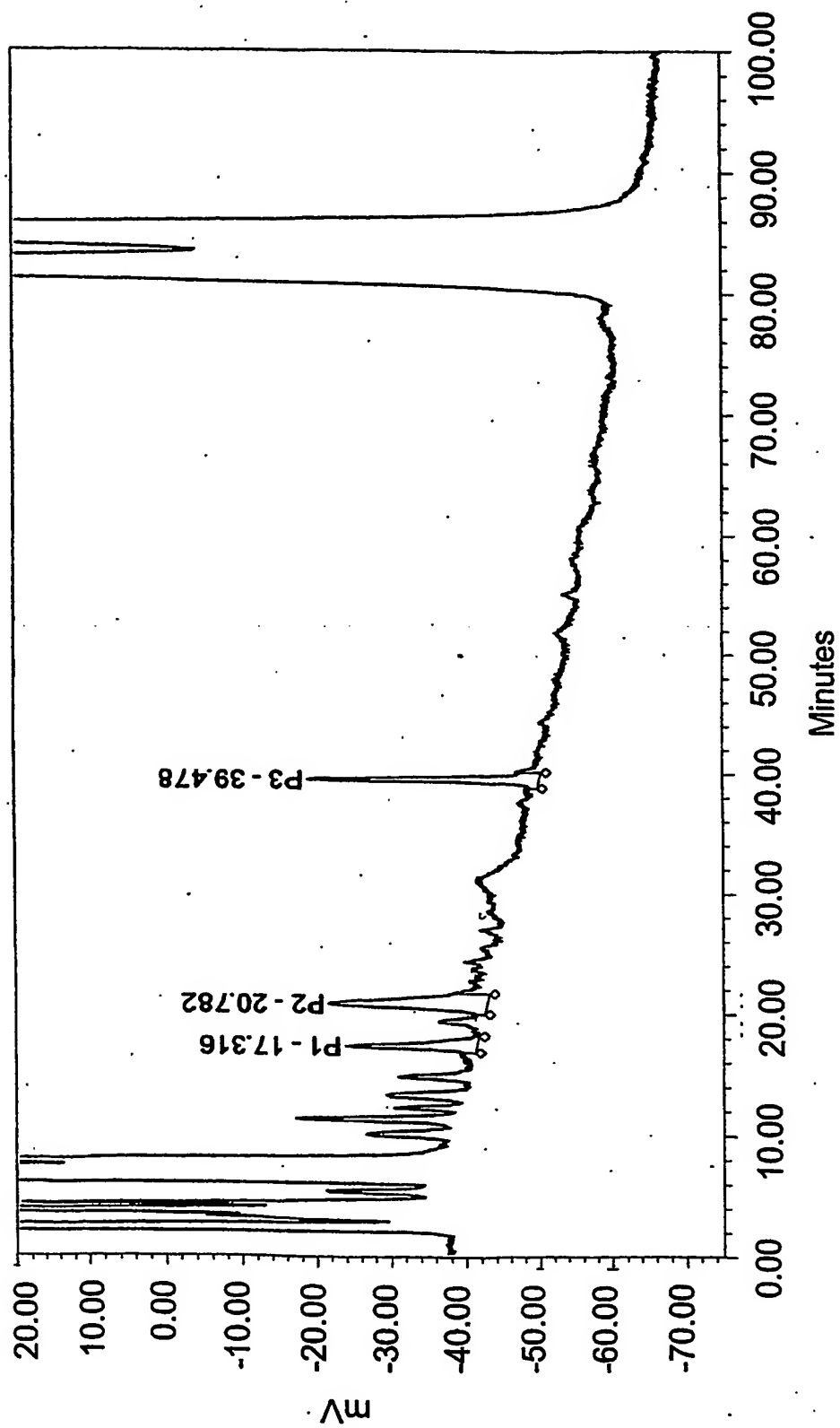


FIG. 116C

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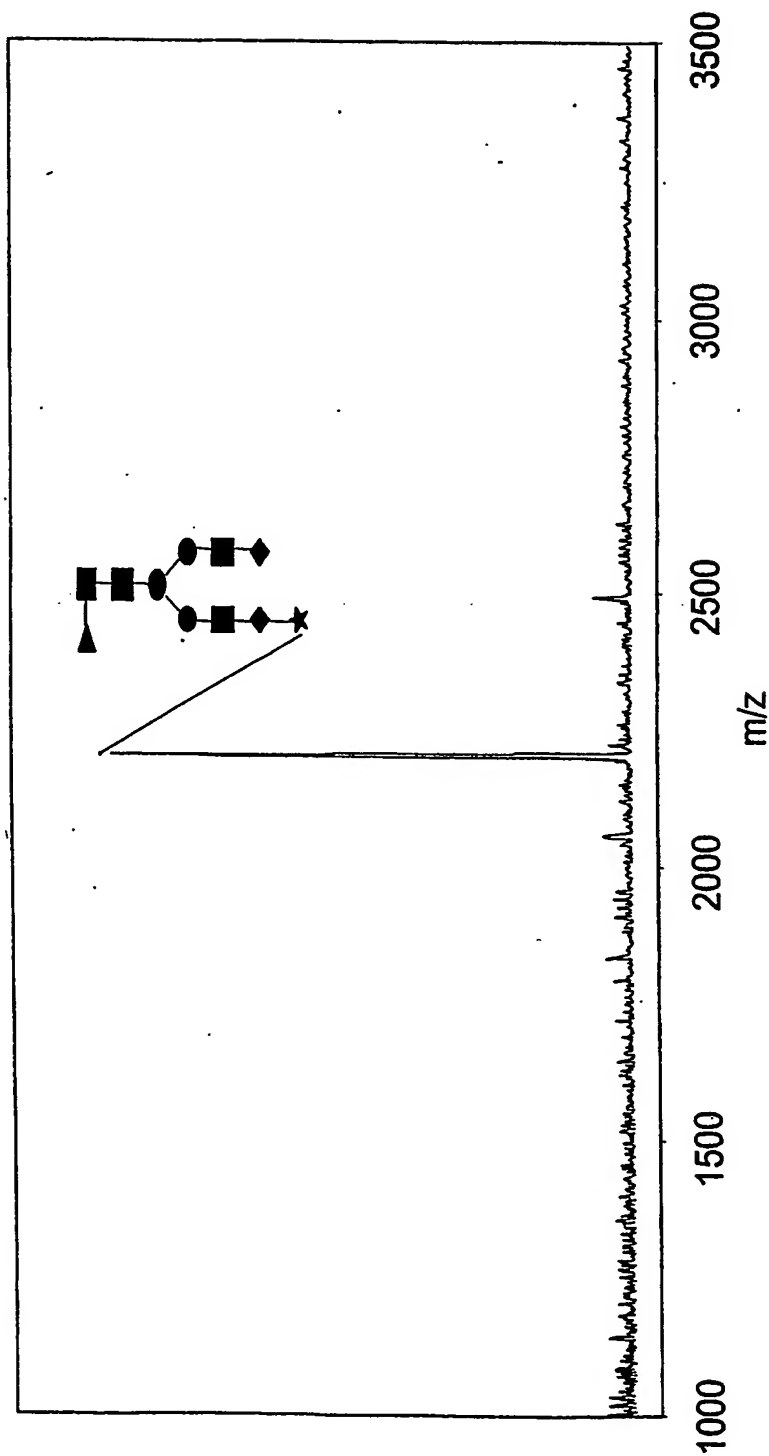


FIG. 117A



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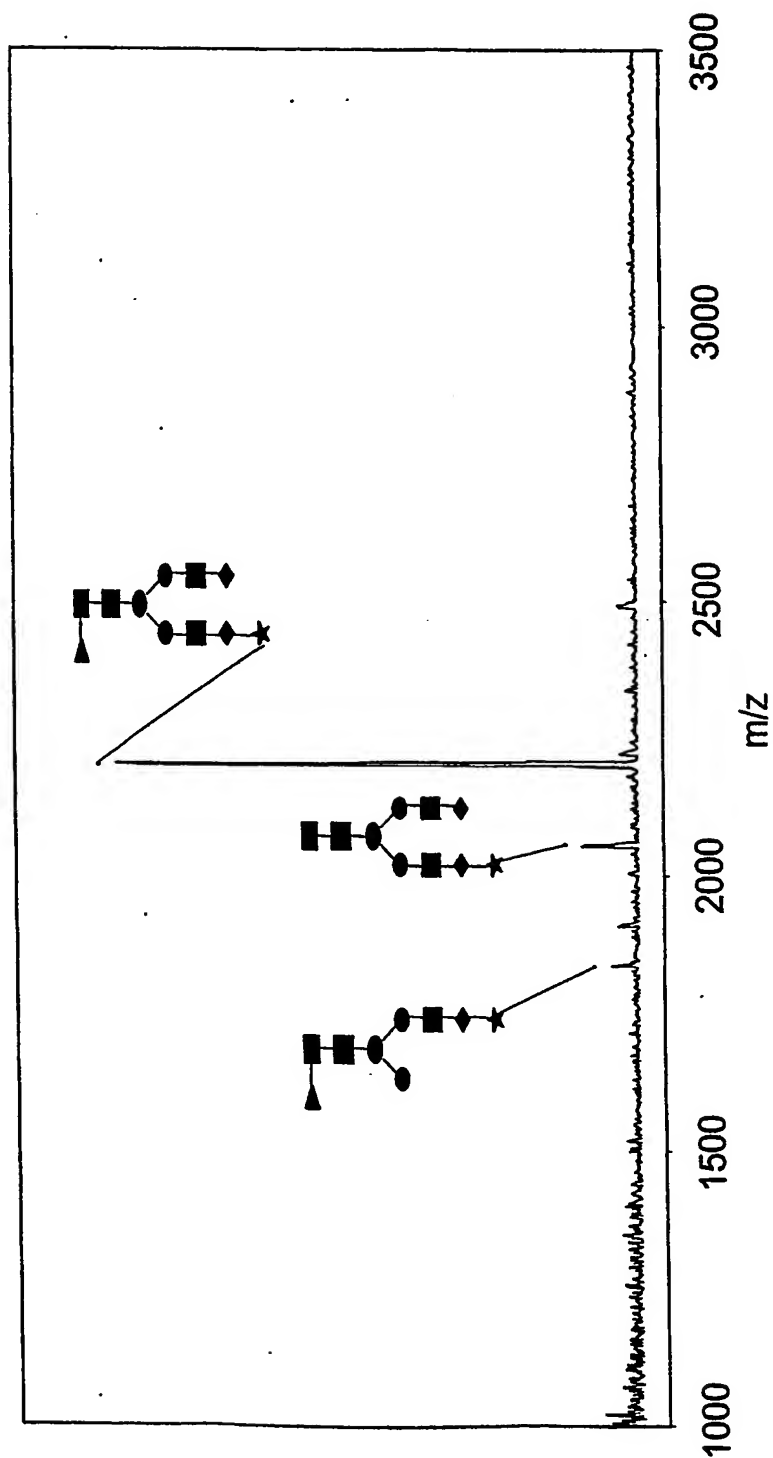


FIG. 117B

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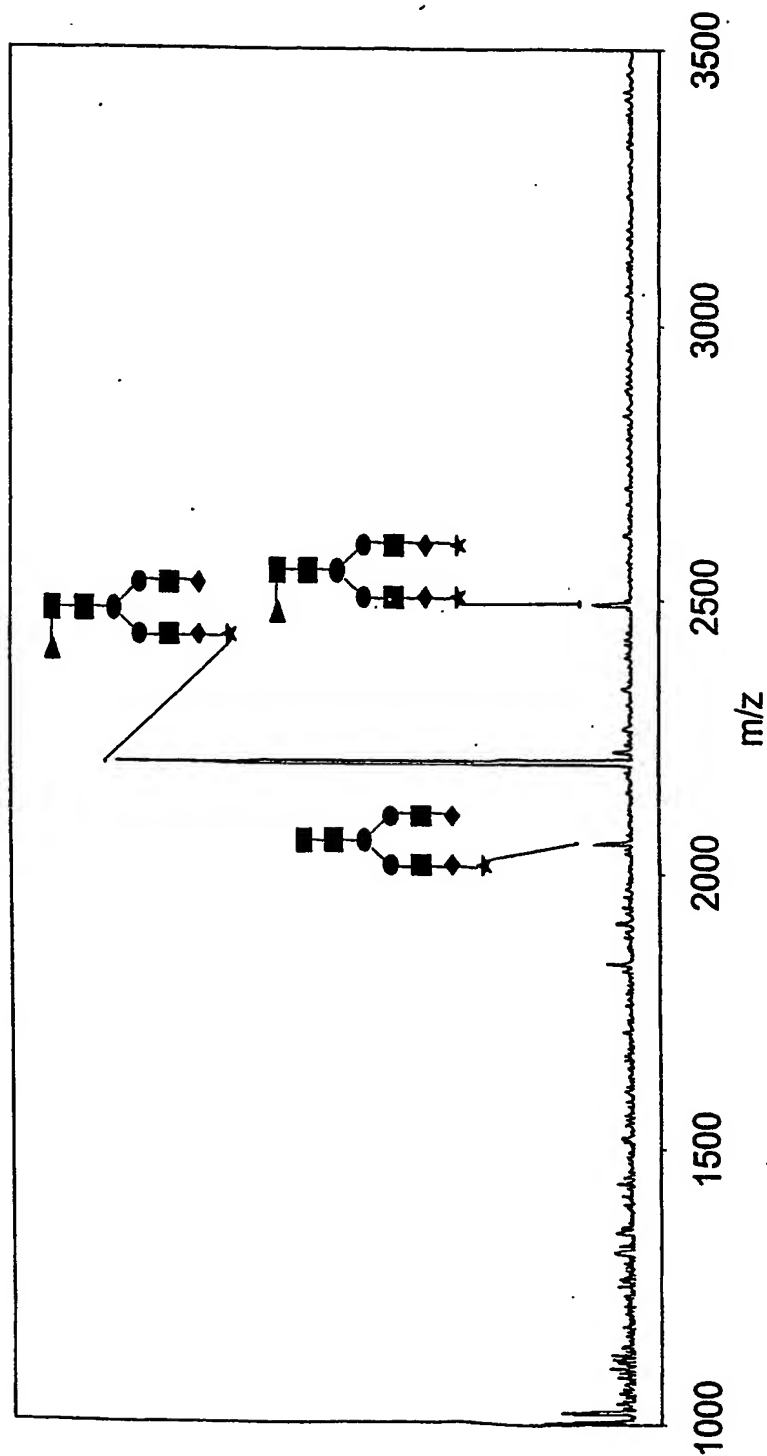
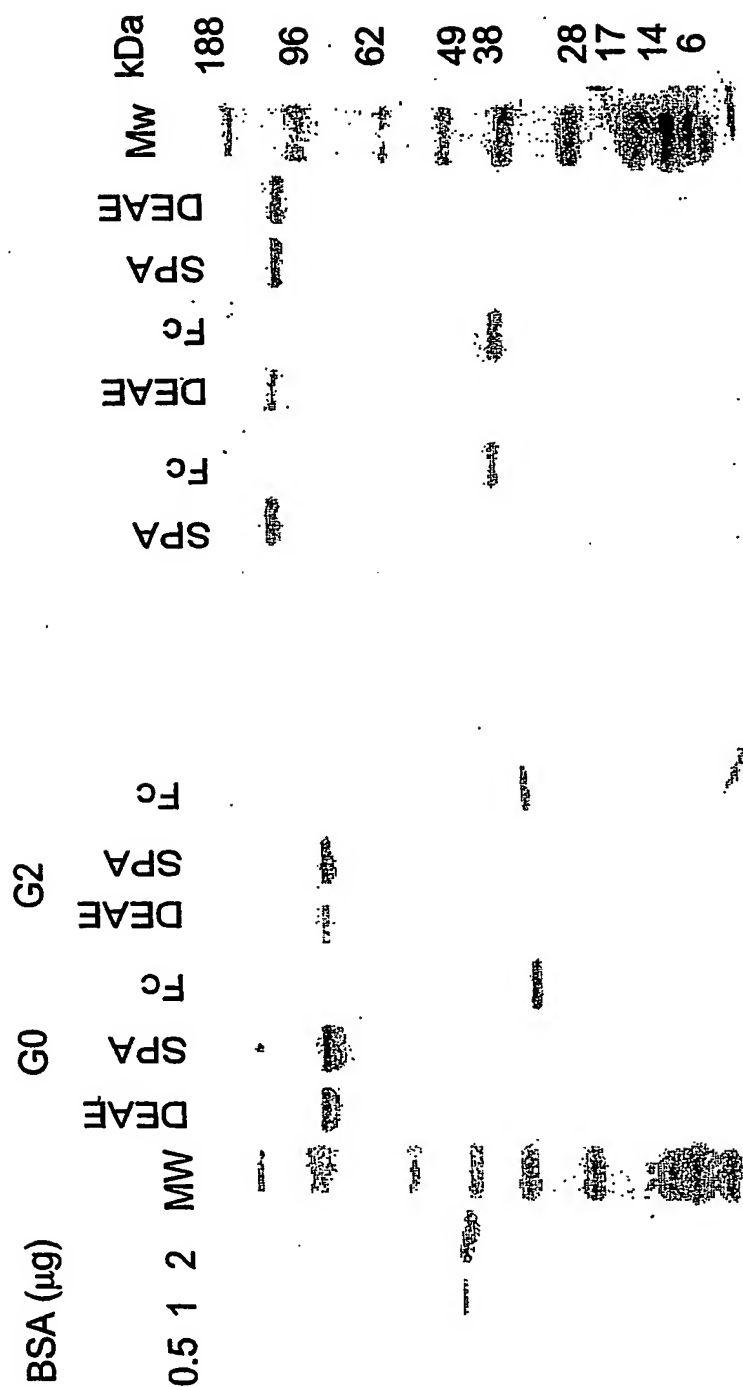


FIG. 117C



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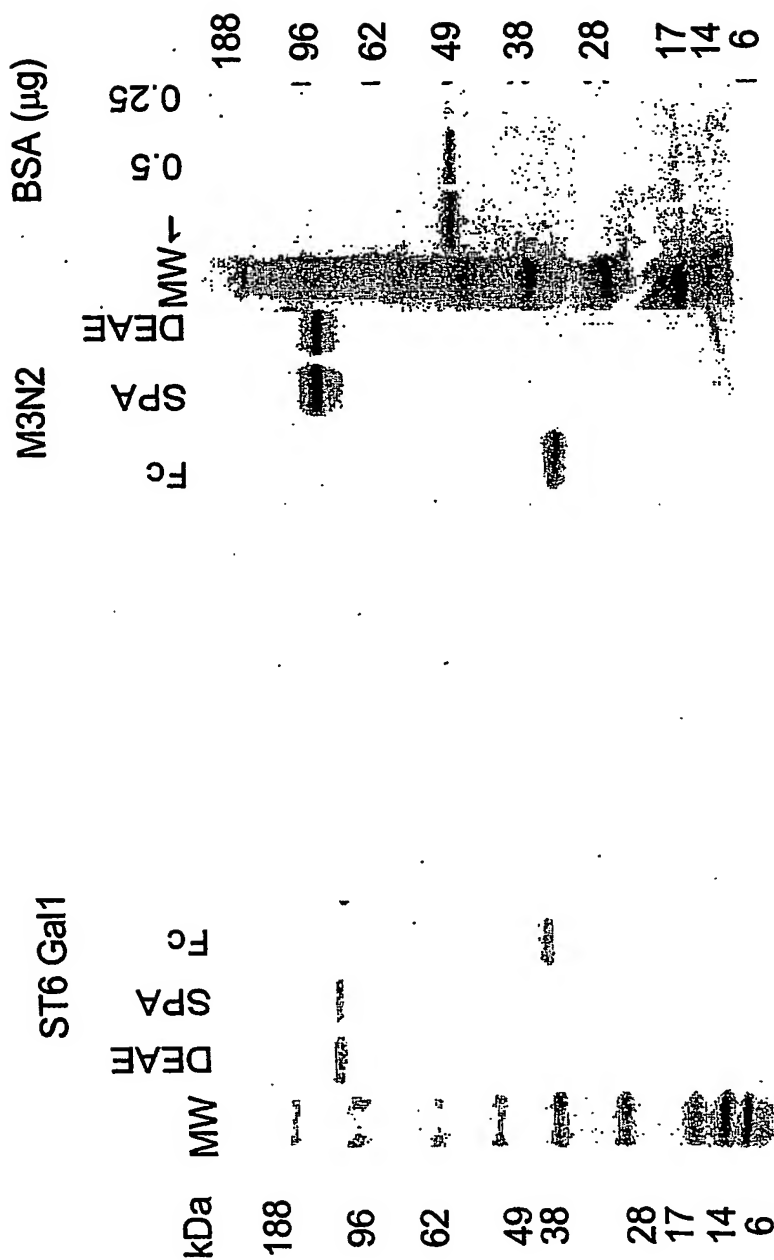


FIG. 118D

FIG. 118C

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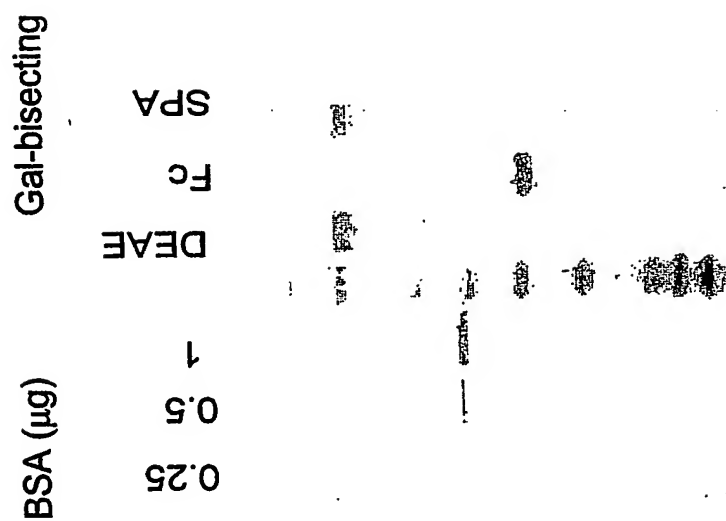


FIG. 118E

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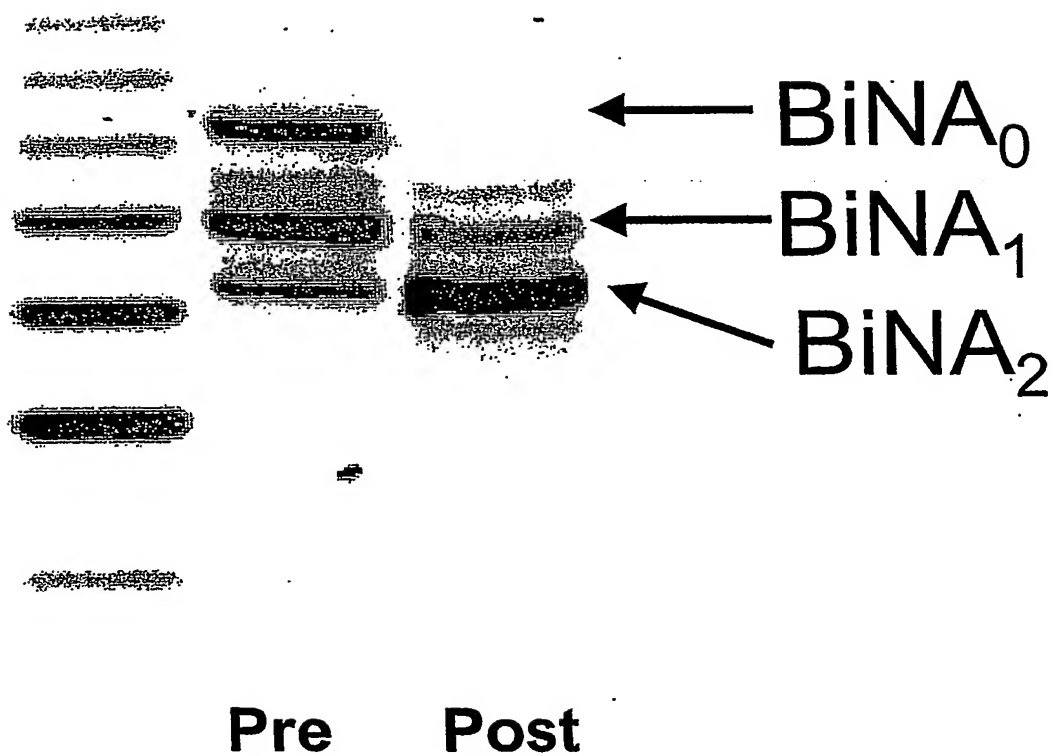


FIG. 119

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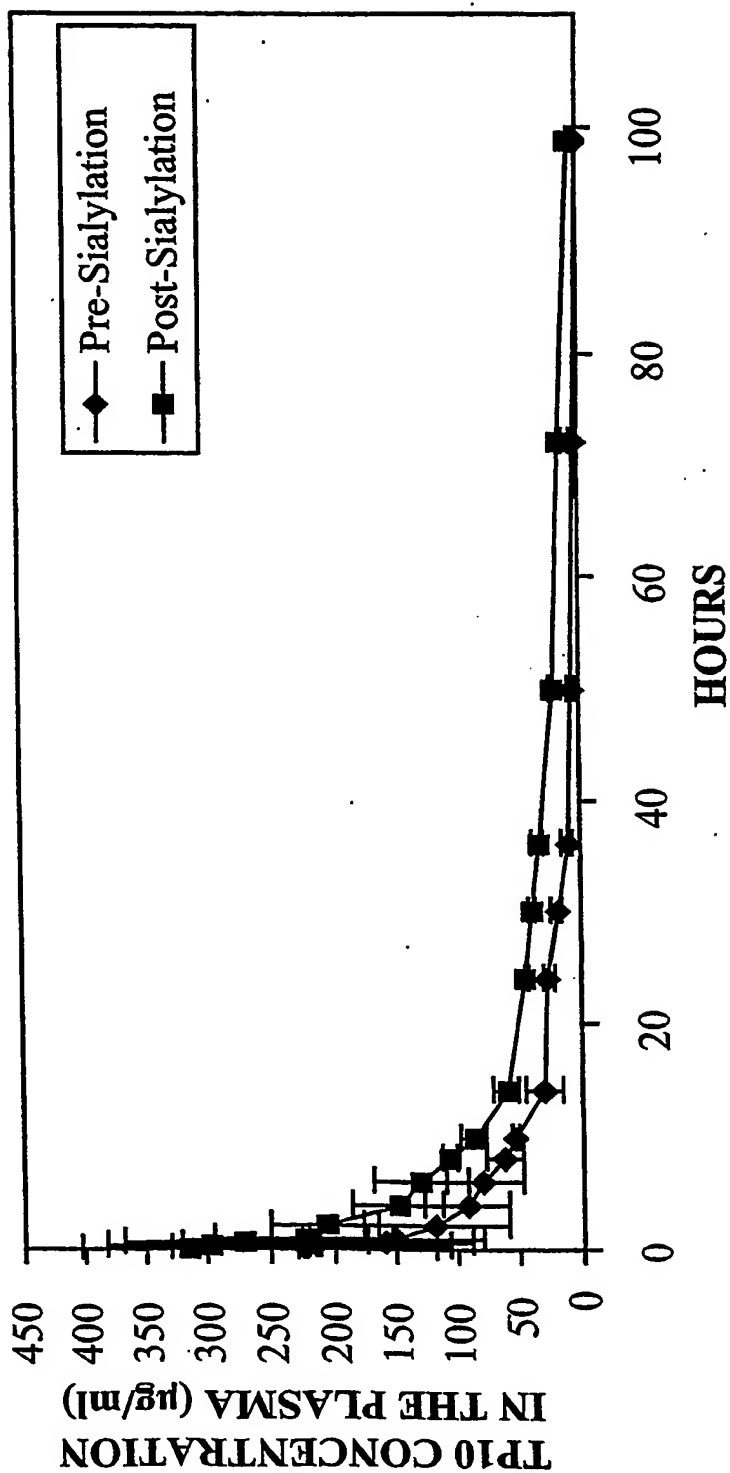


FIG. 120

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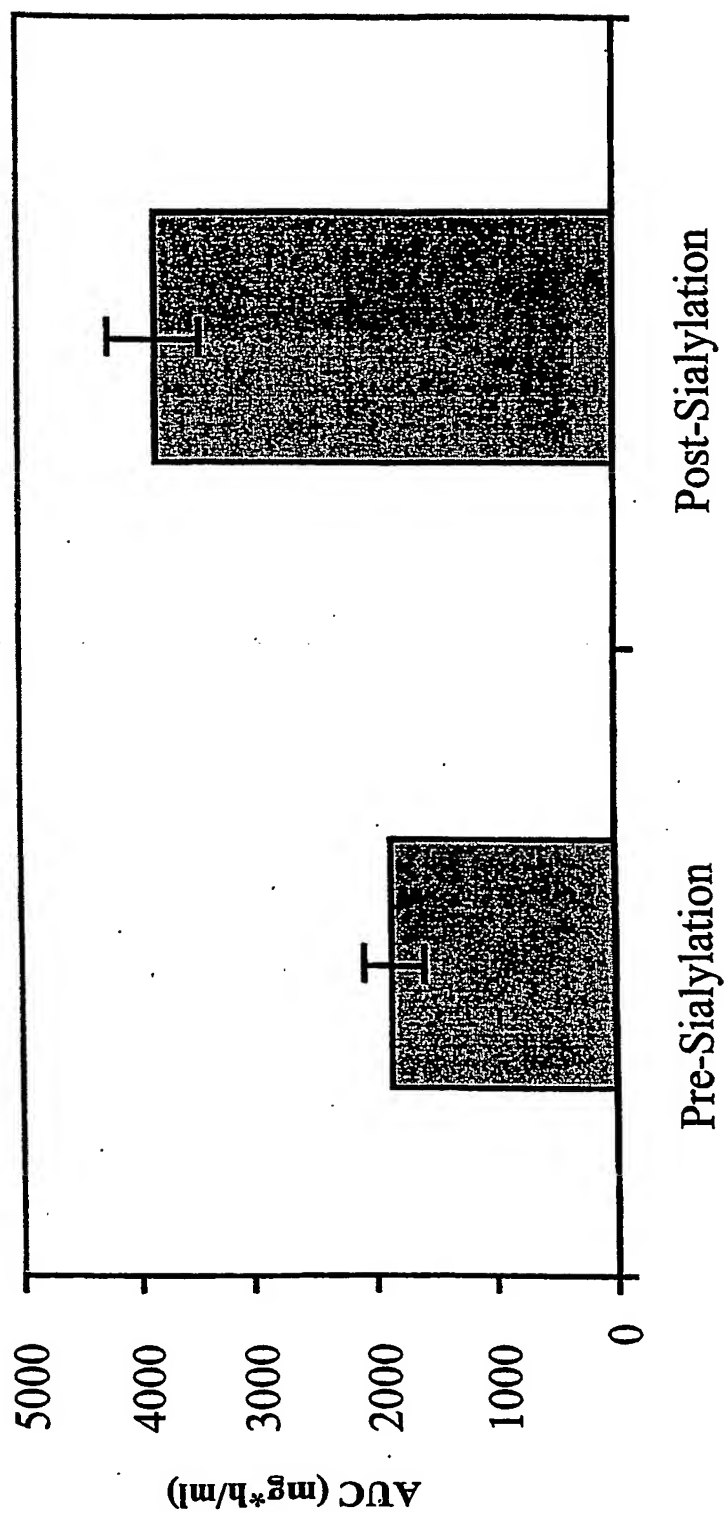


FIG. 121



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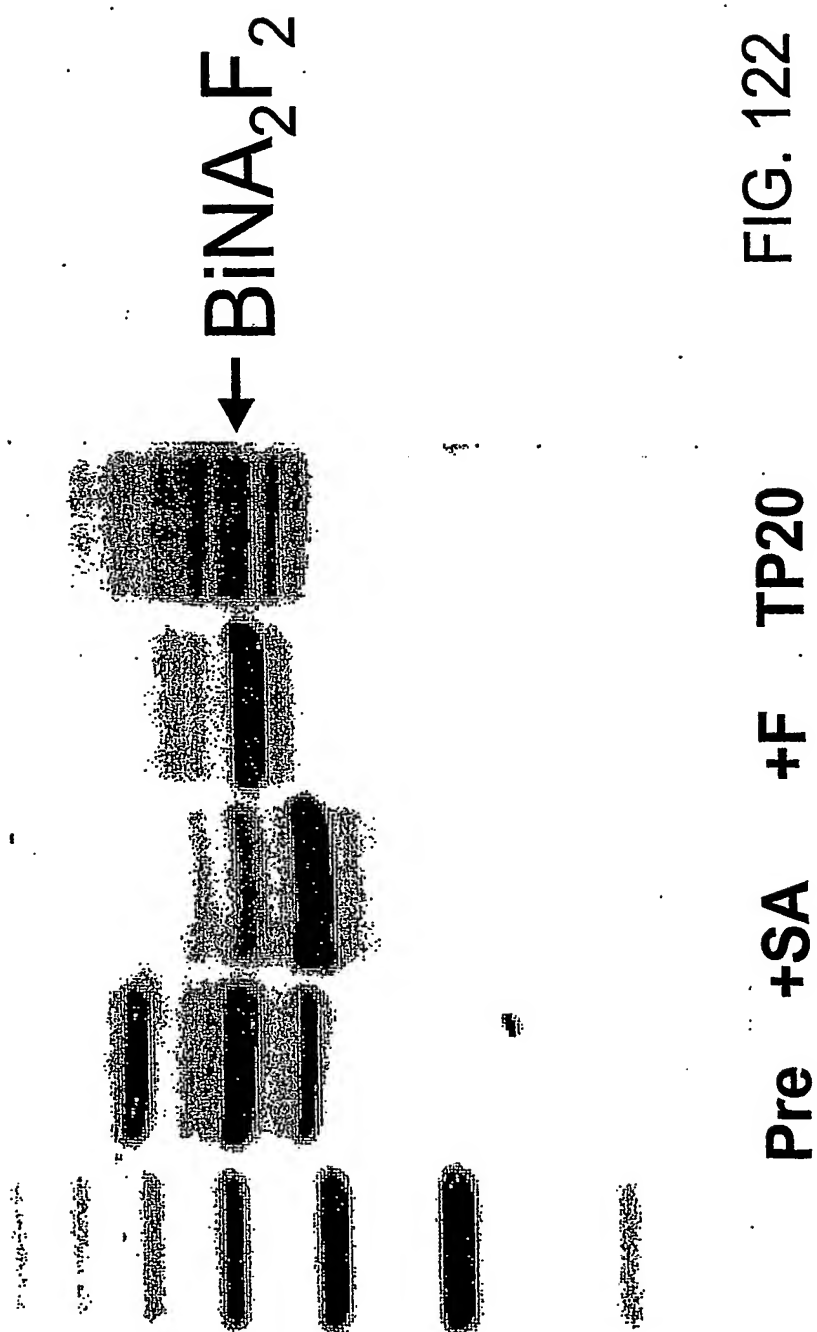


FIG. 122

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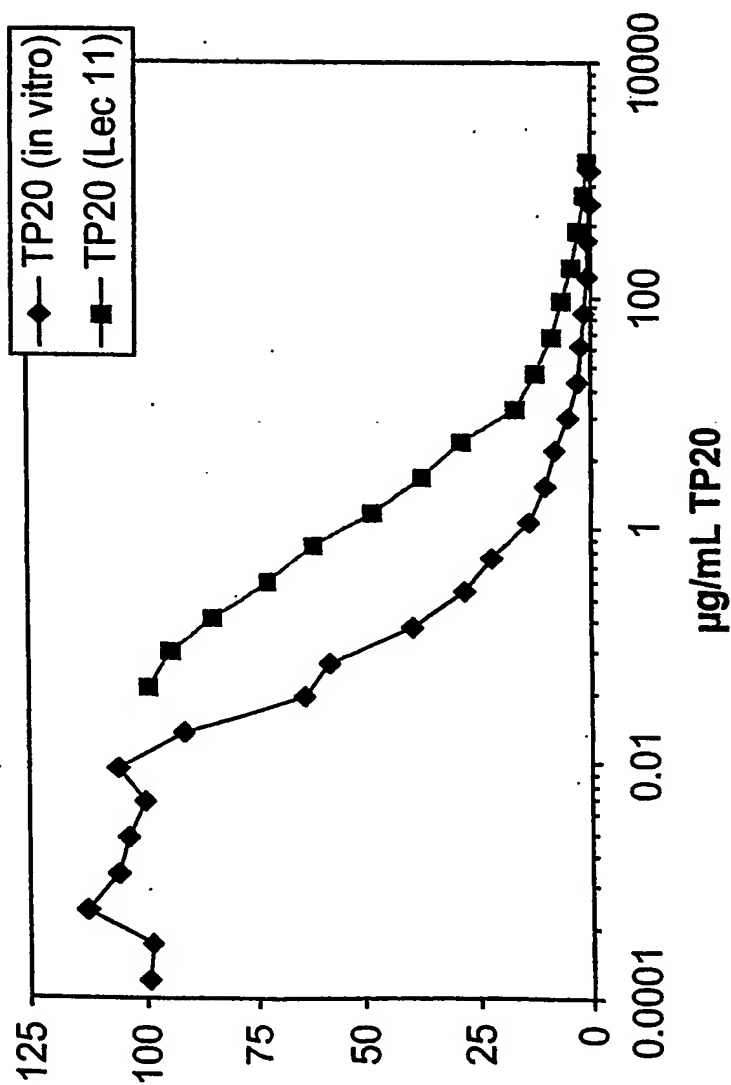


FIG. 123

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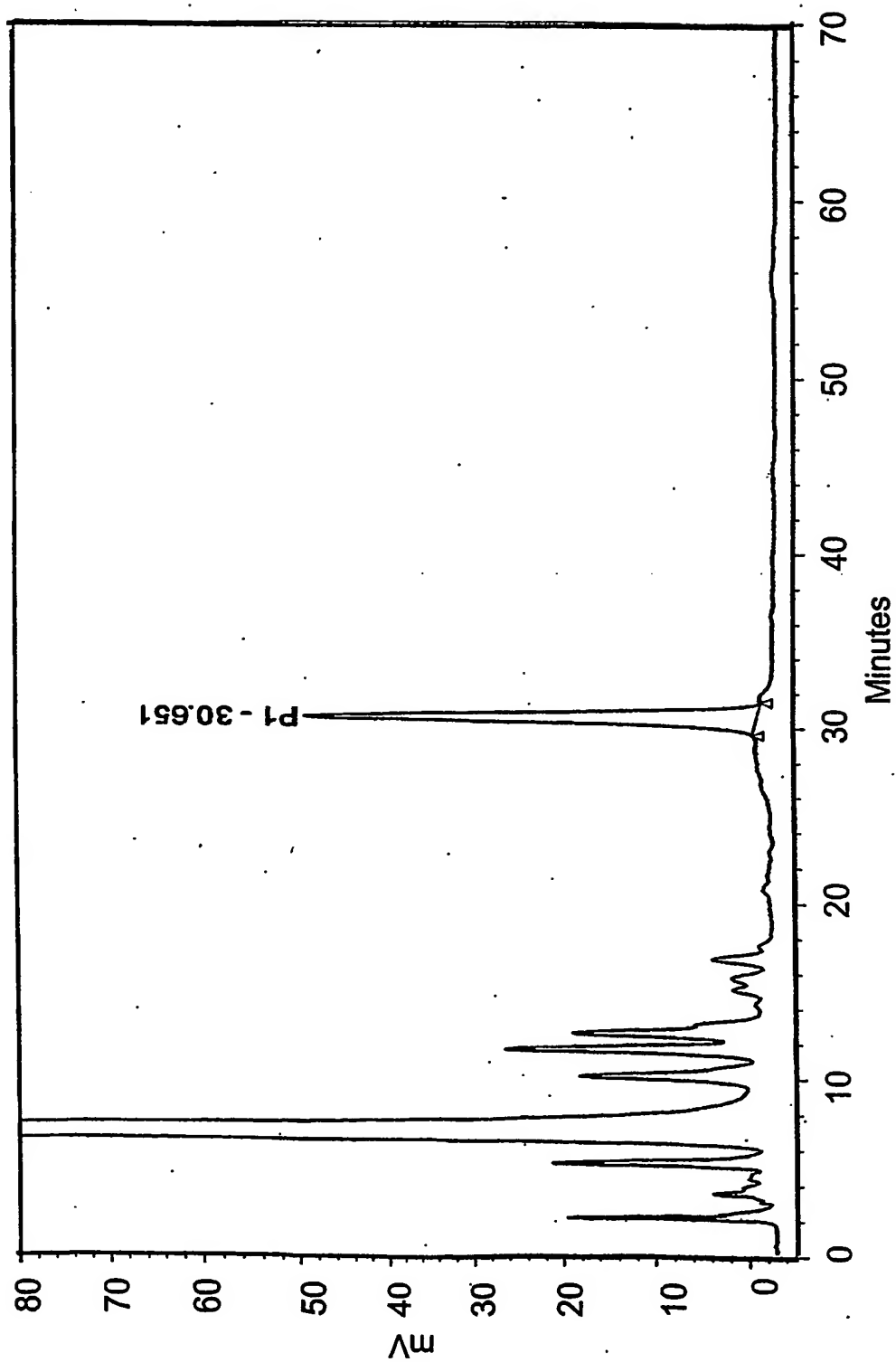


FIG. 124

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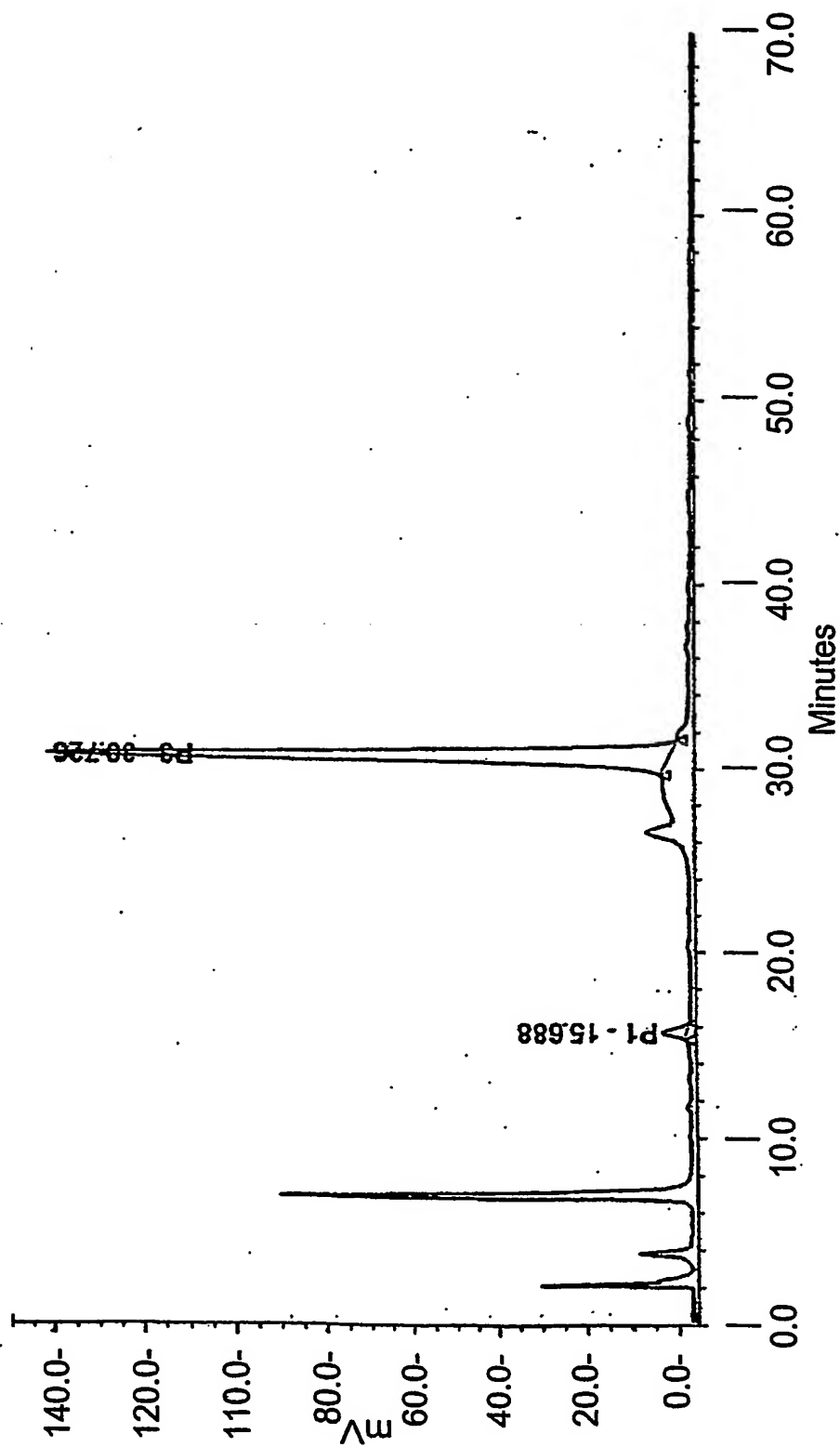


FIG. 125A

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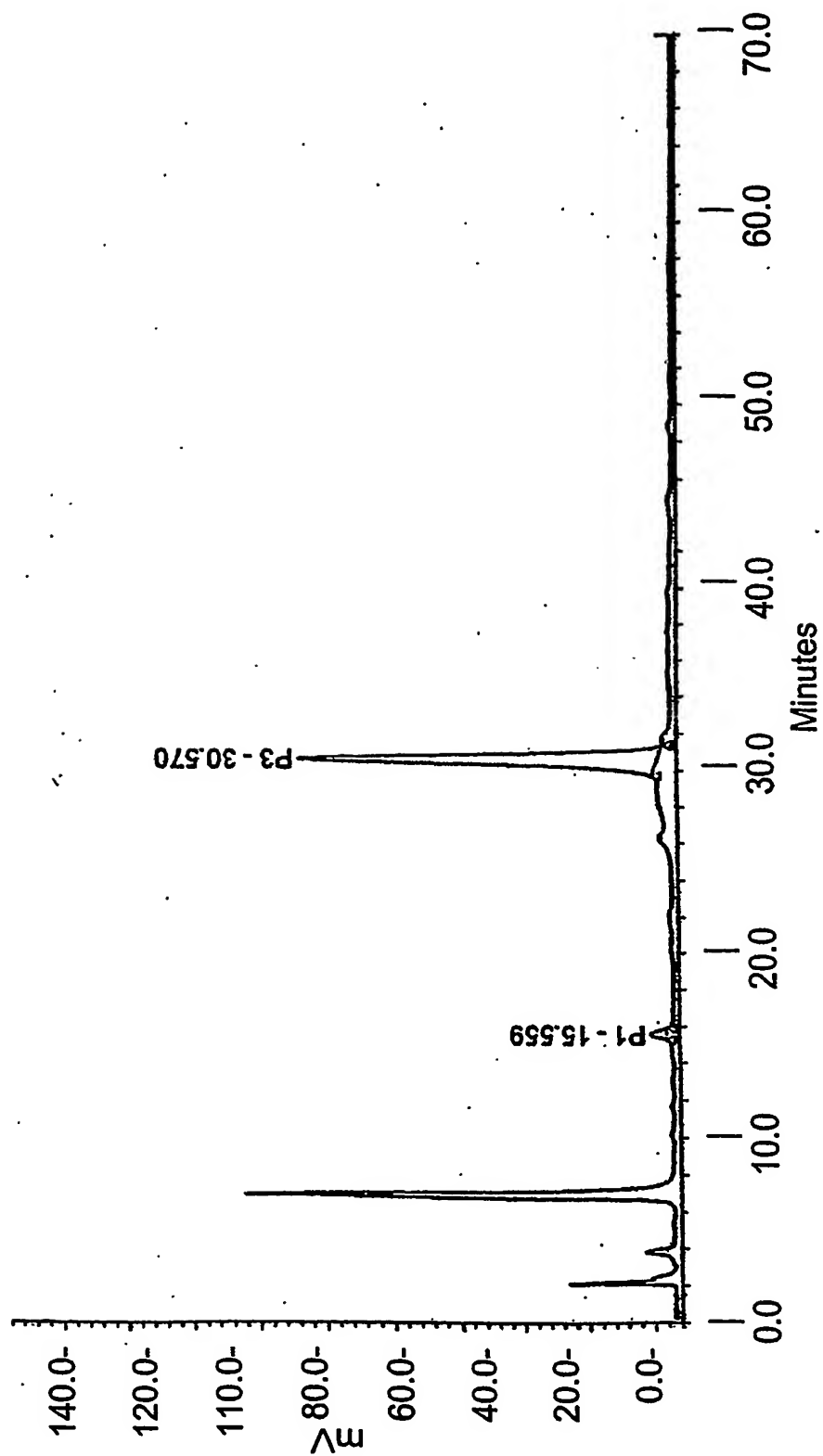


FIG. 125B

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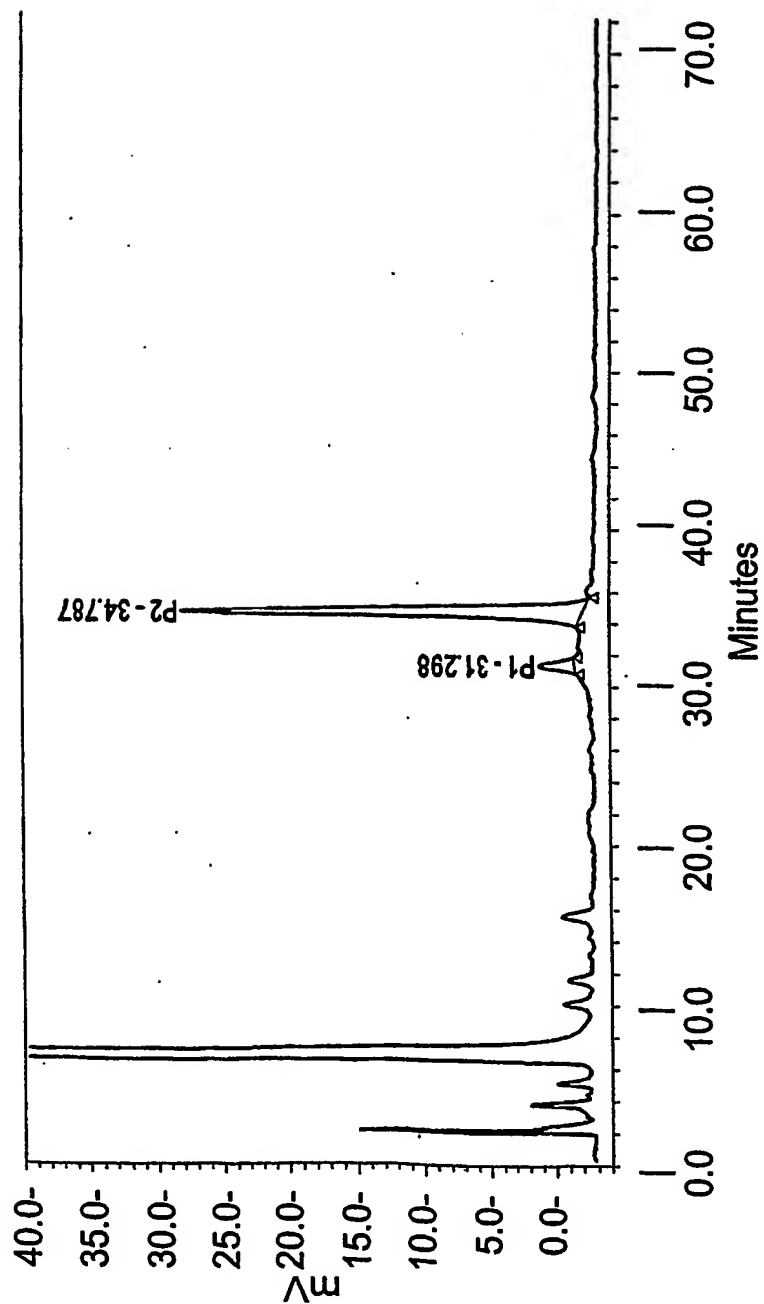


FIG. 126

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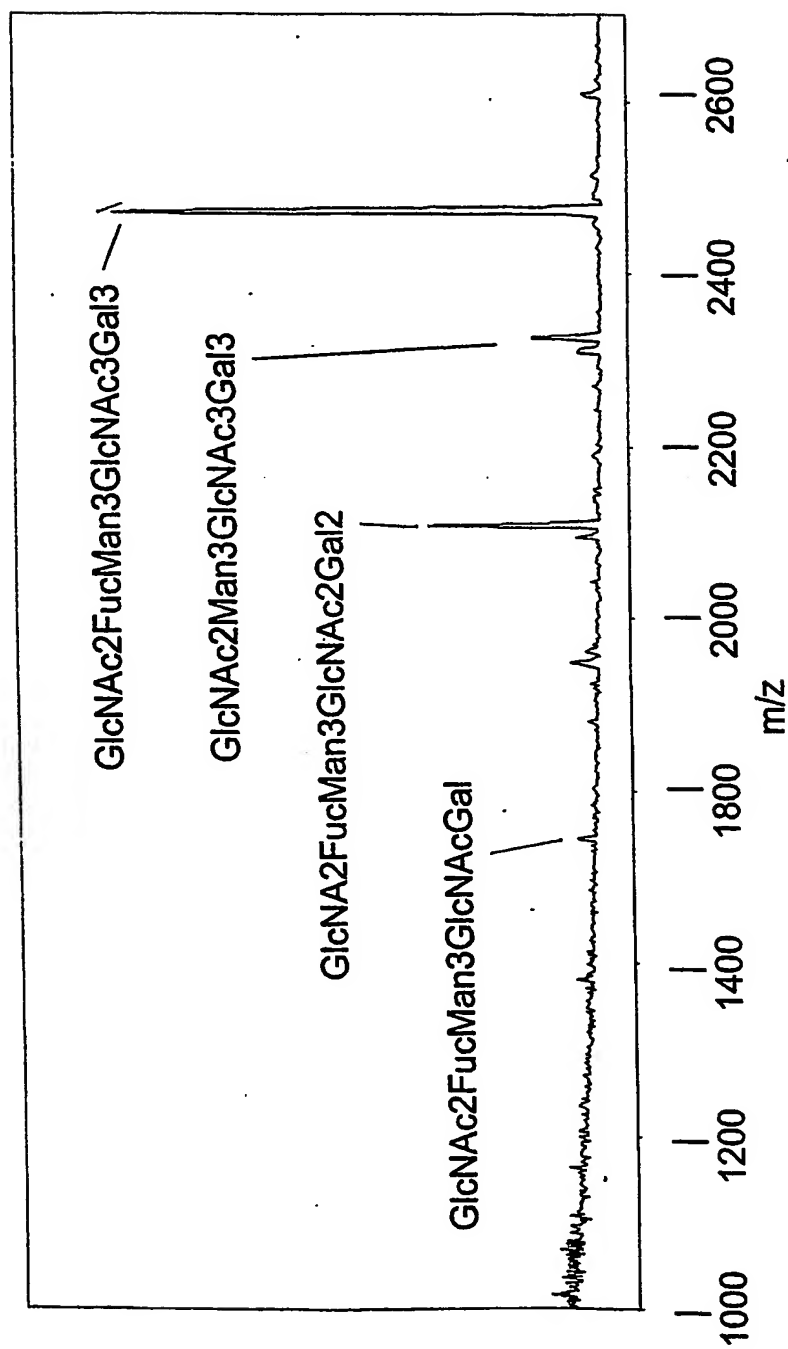


FIG. 127

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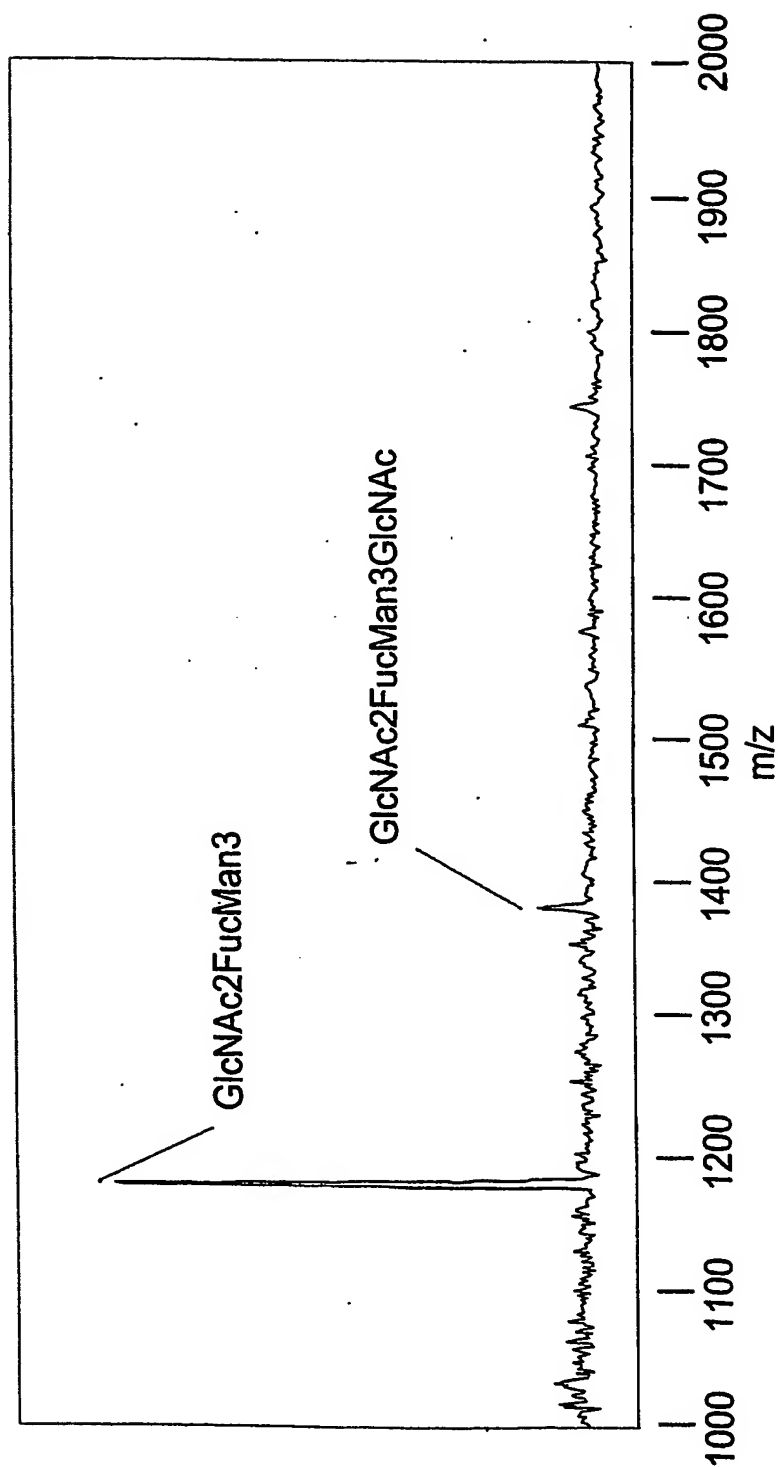


FIG. 128



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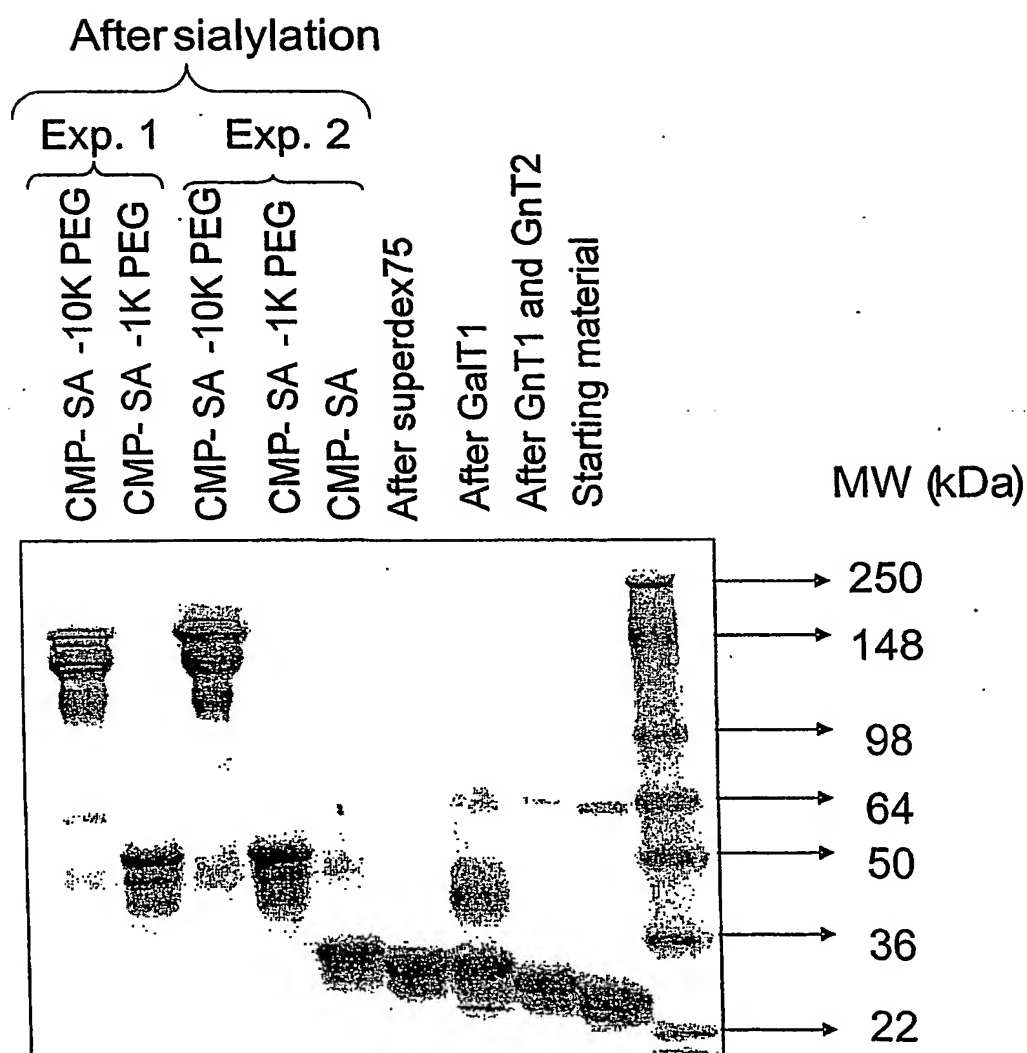


FIG. 129

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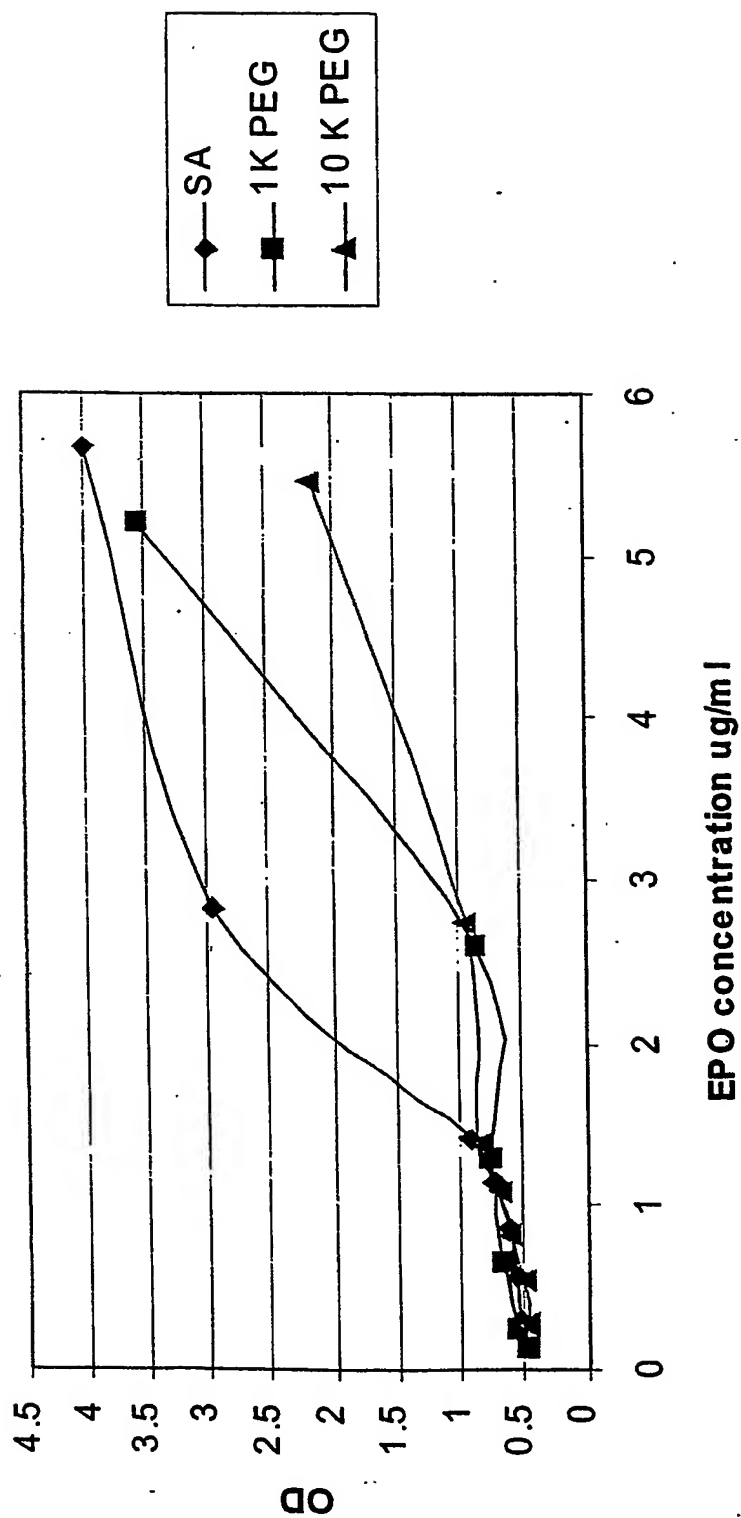
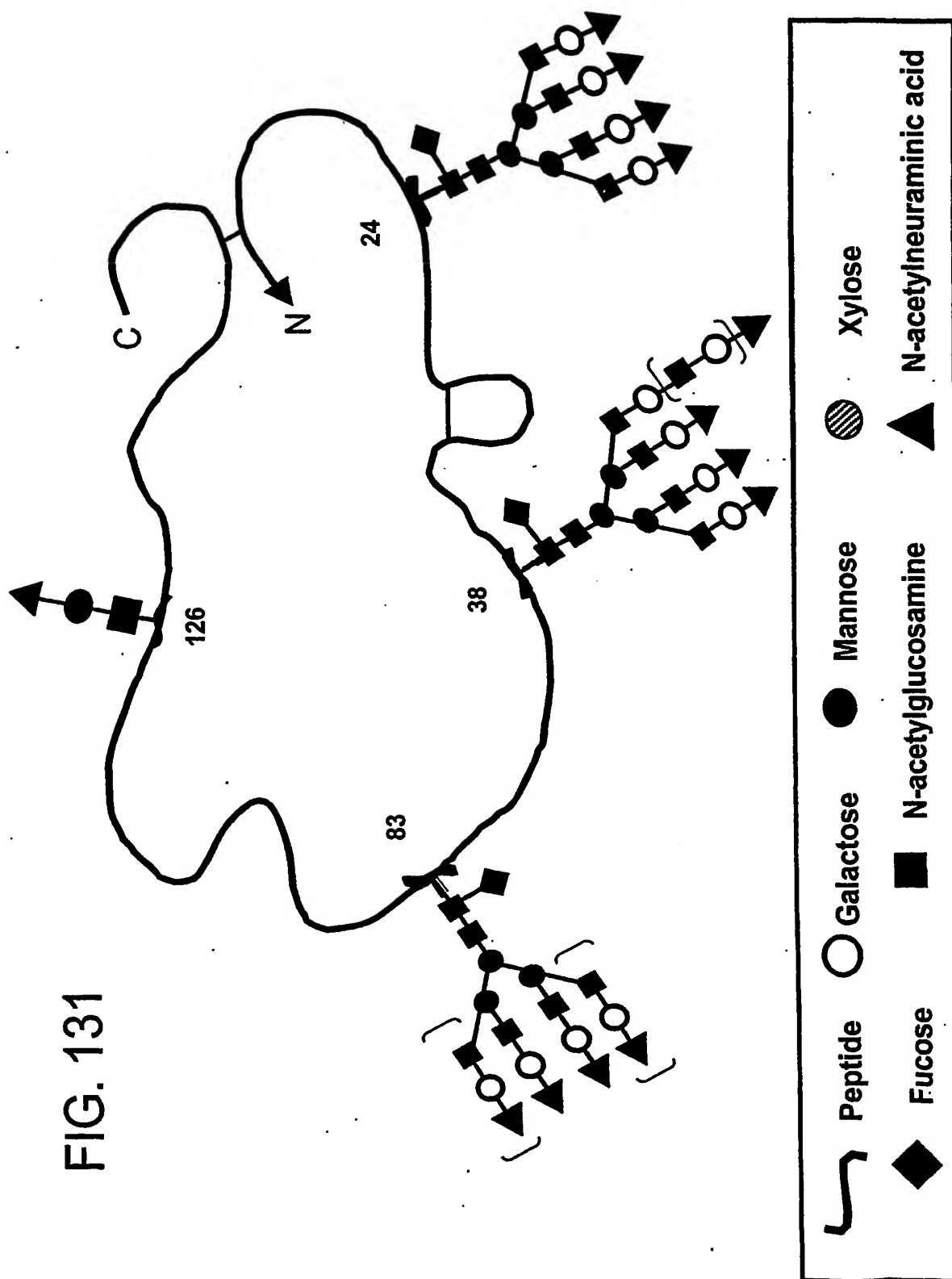


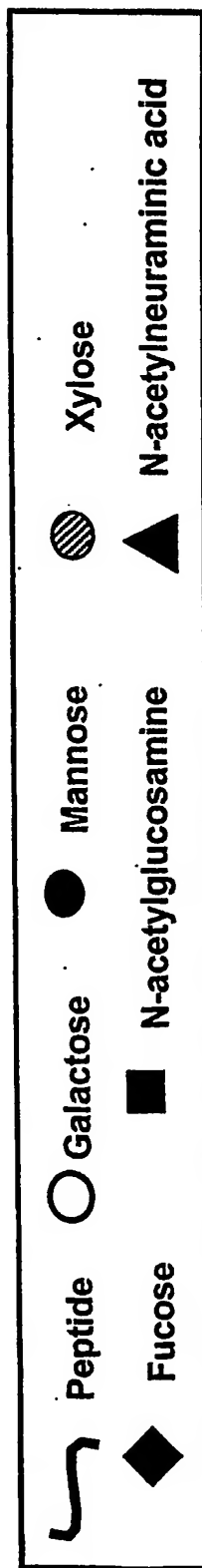
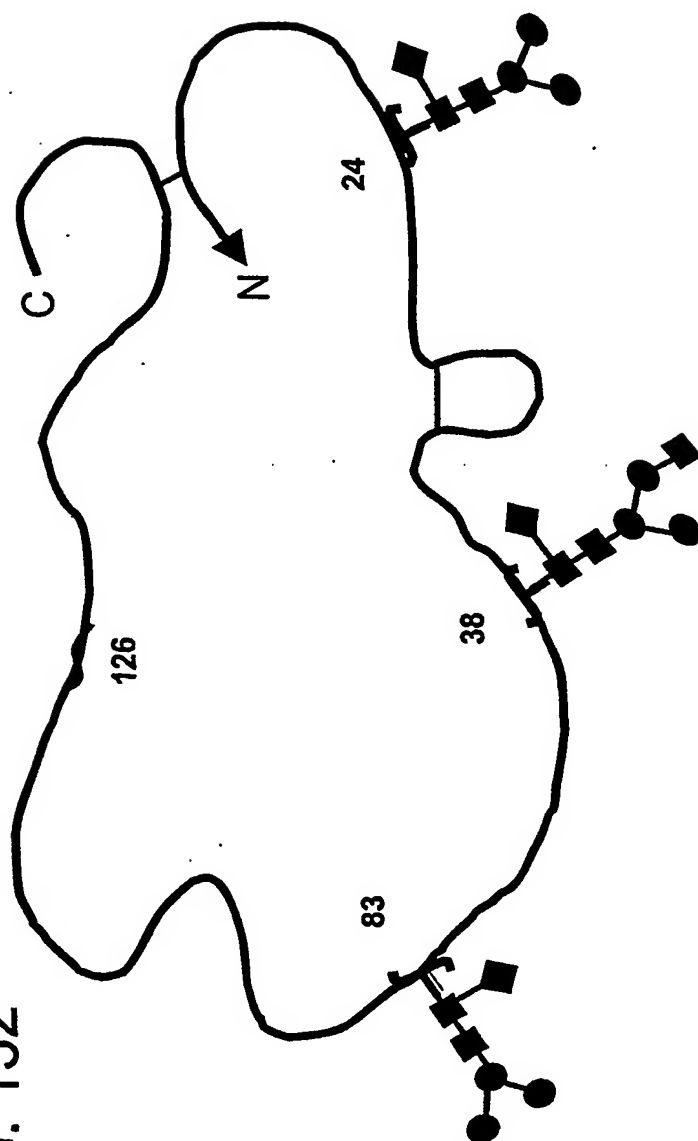
FIG. 130

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FIG. 132



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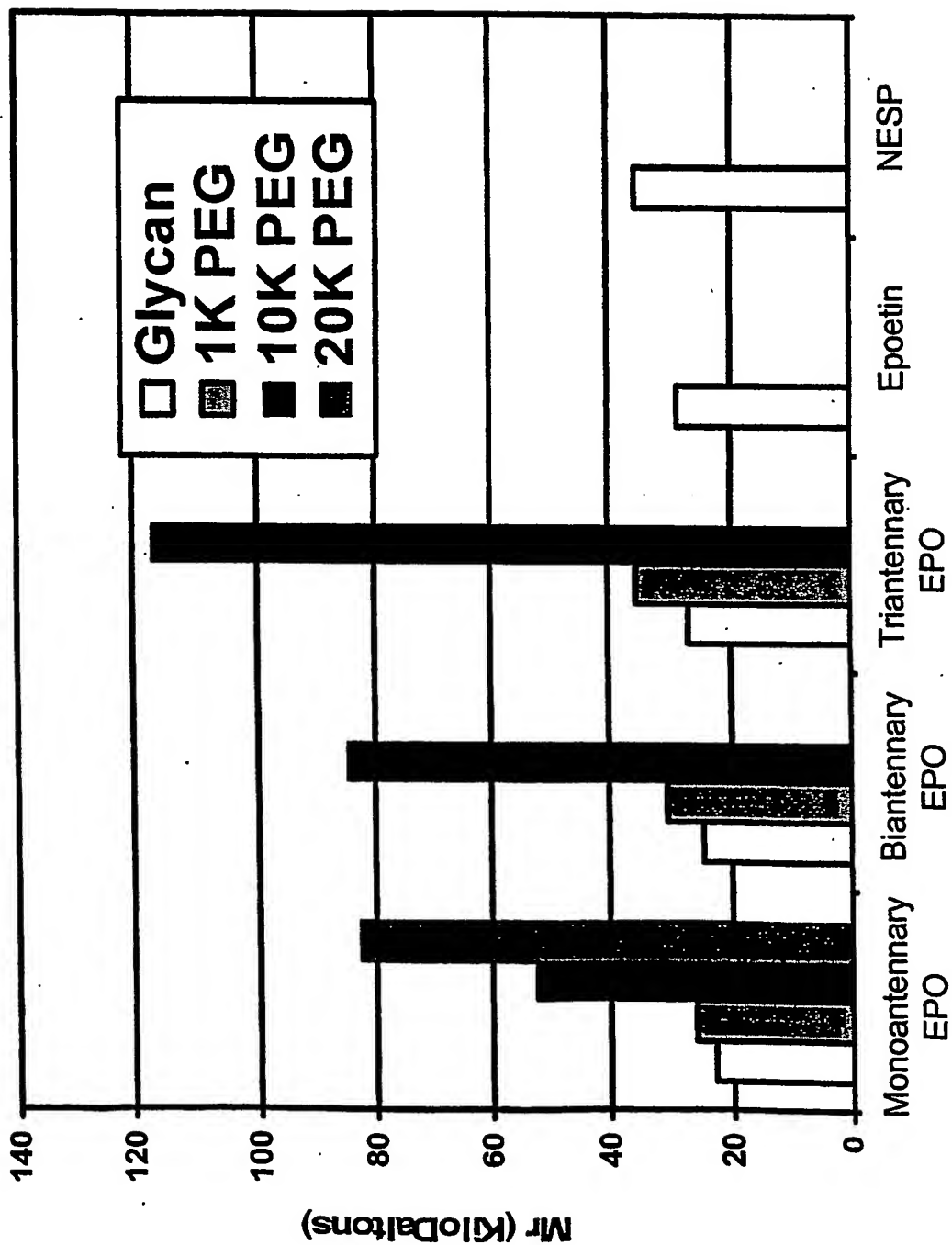
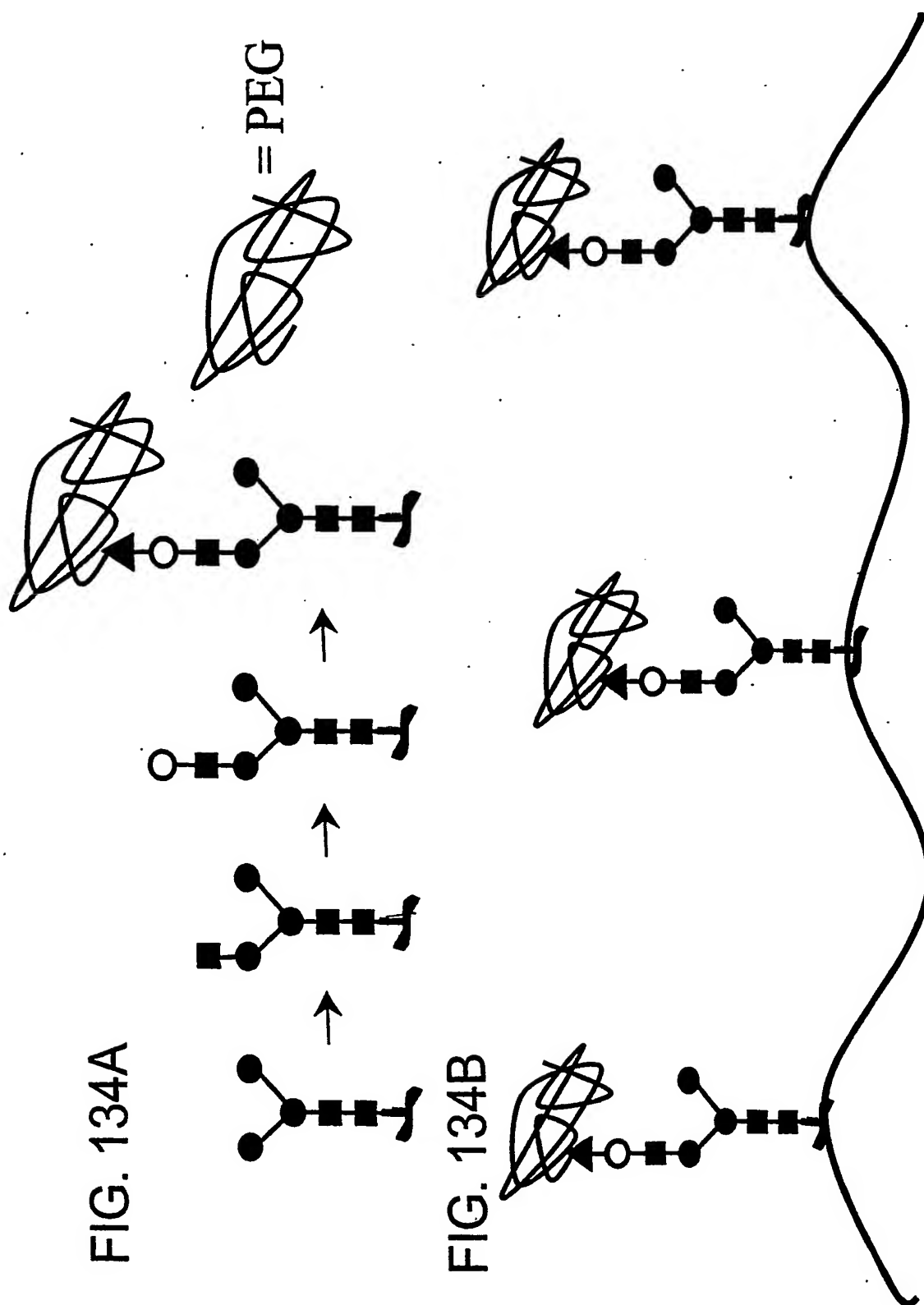


FIG. 133

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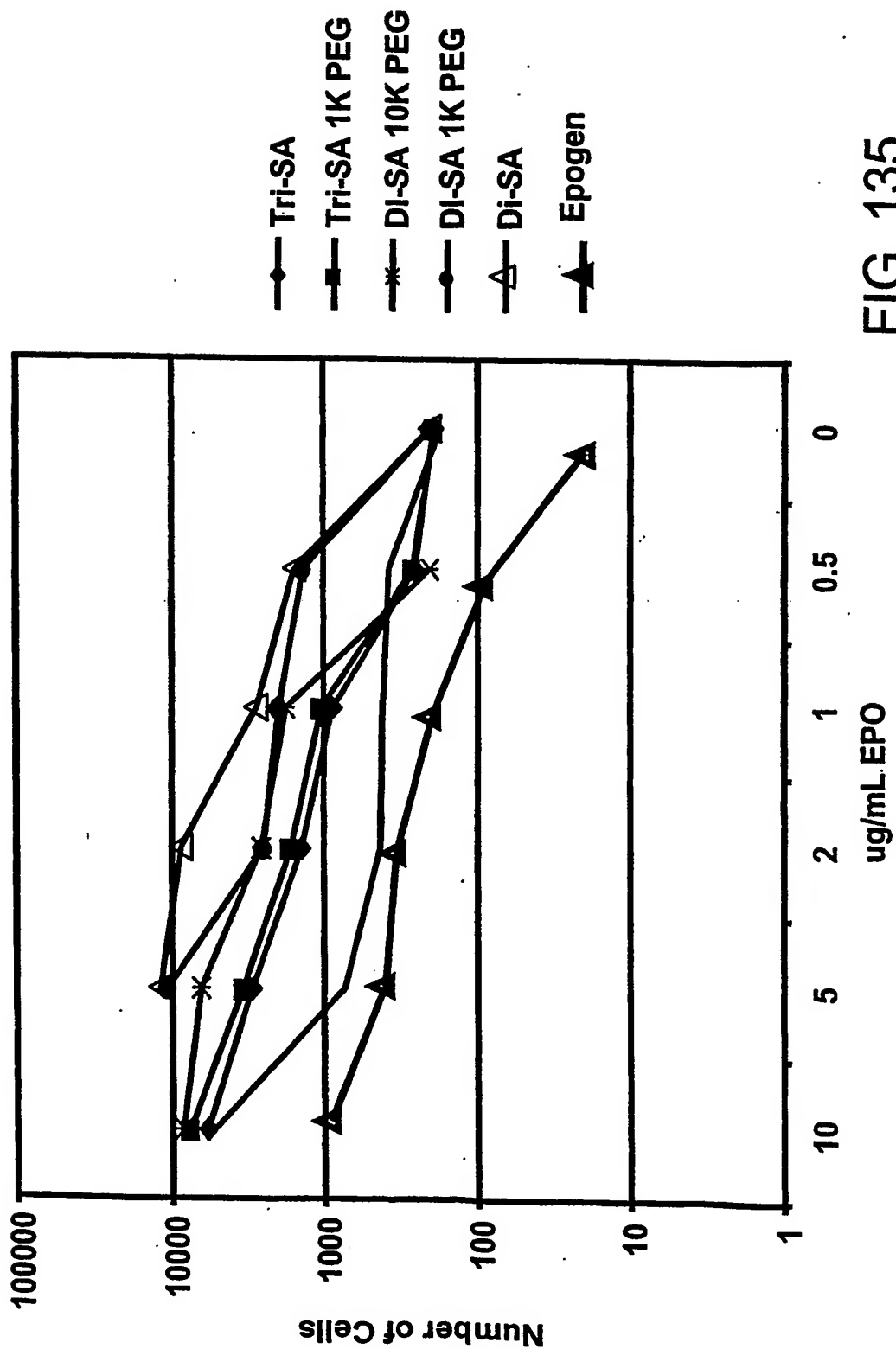


FIG. 135

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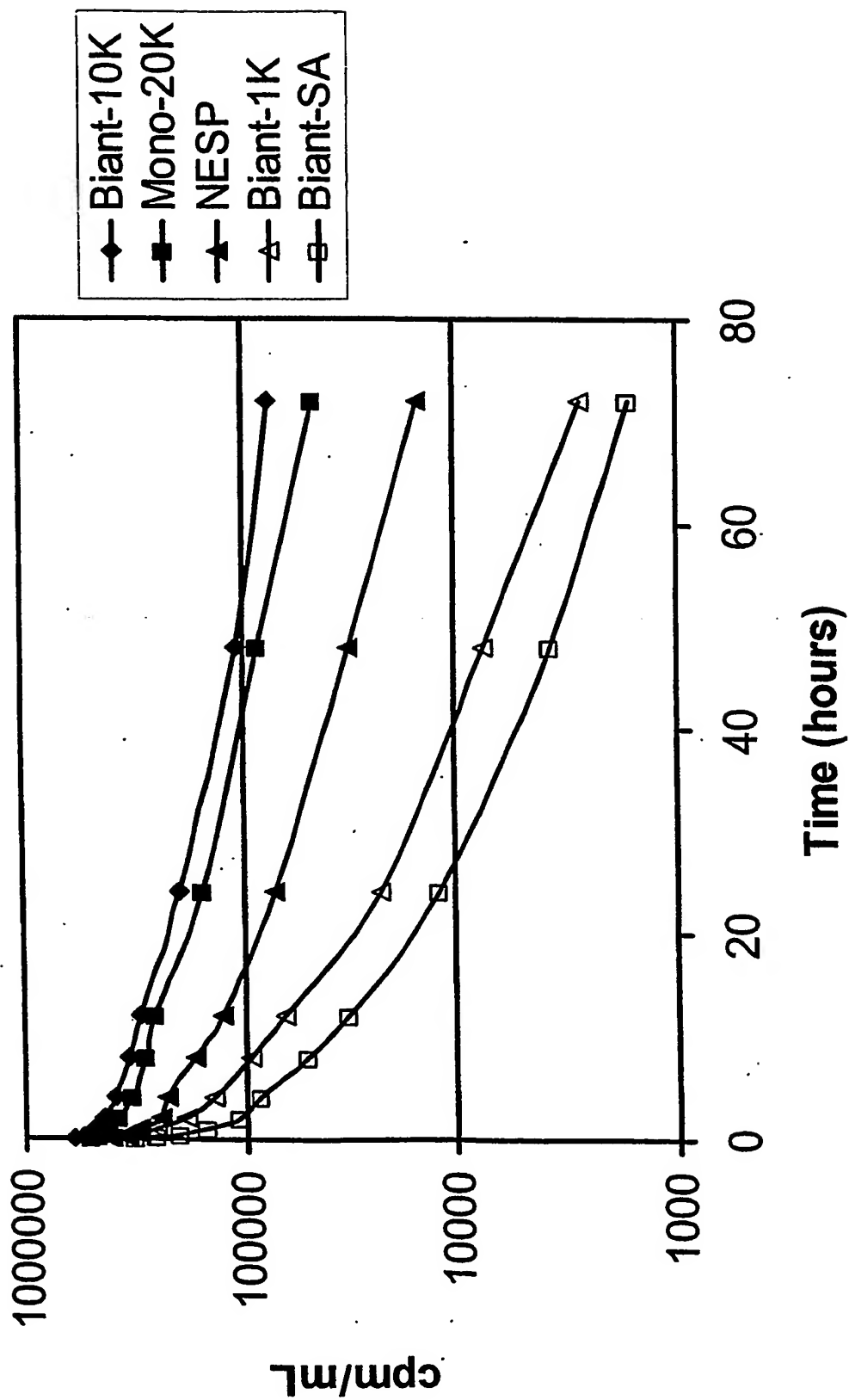


FIG. 136



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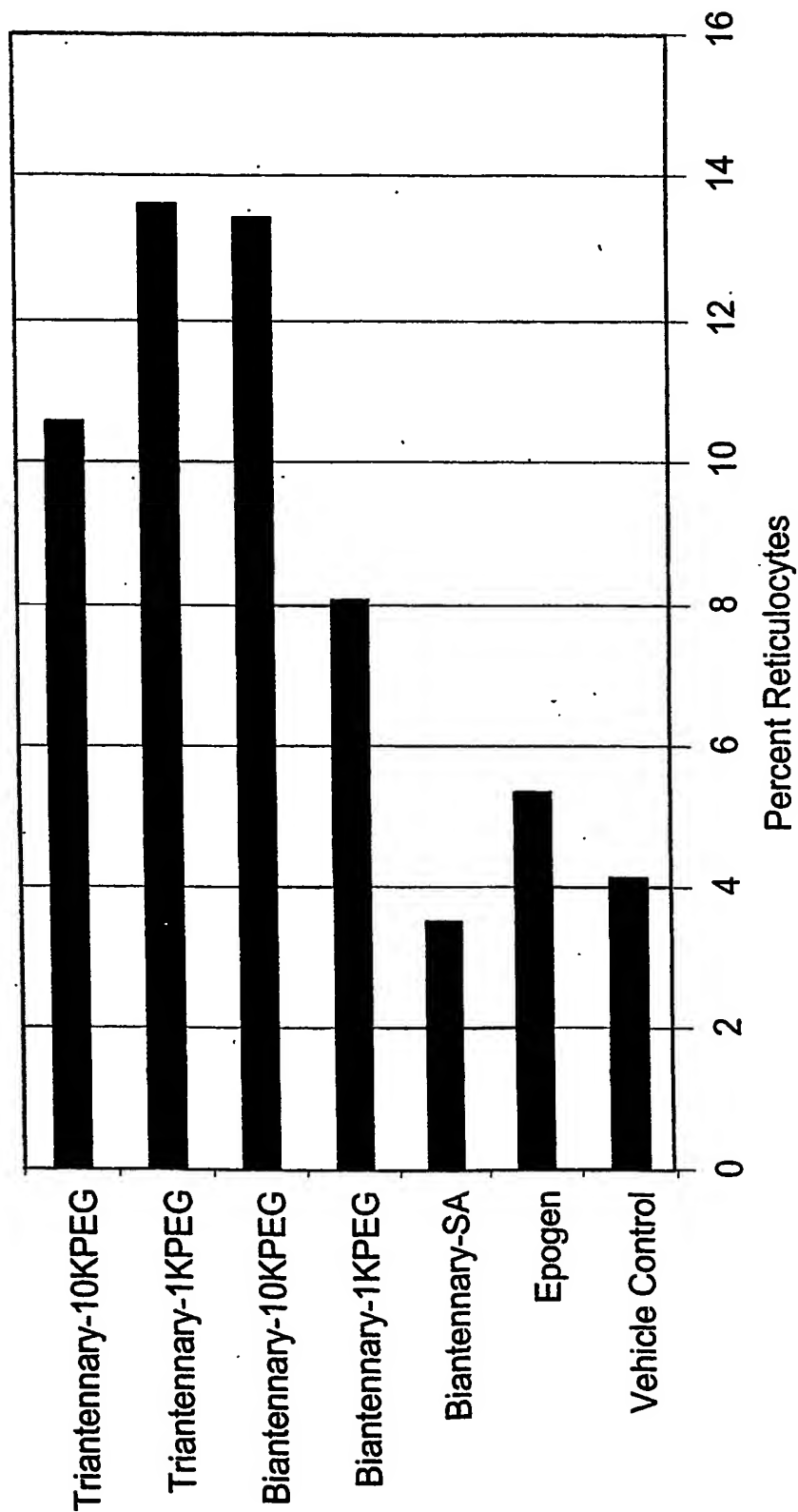


FIG. 137

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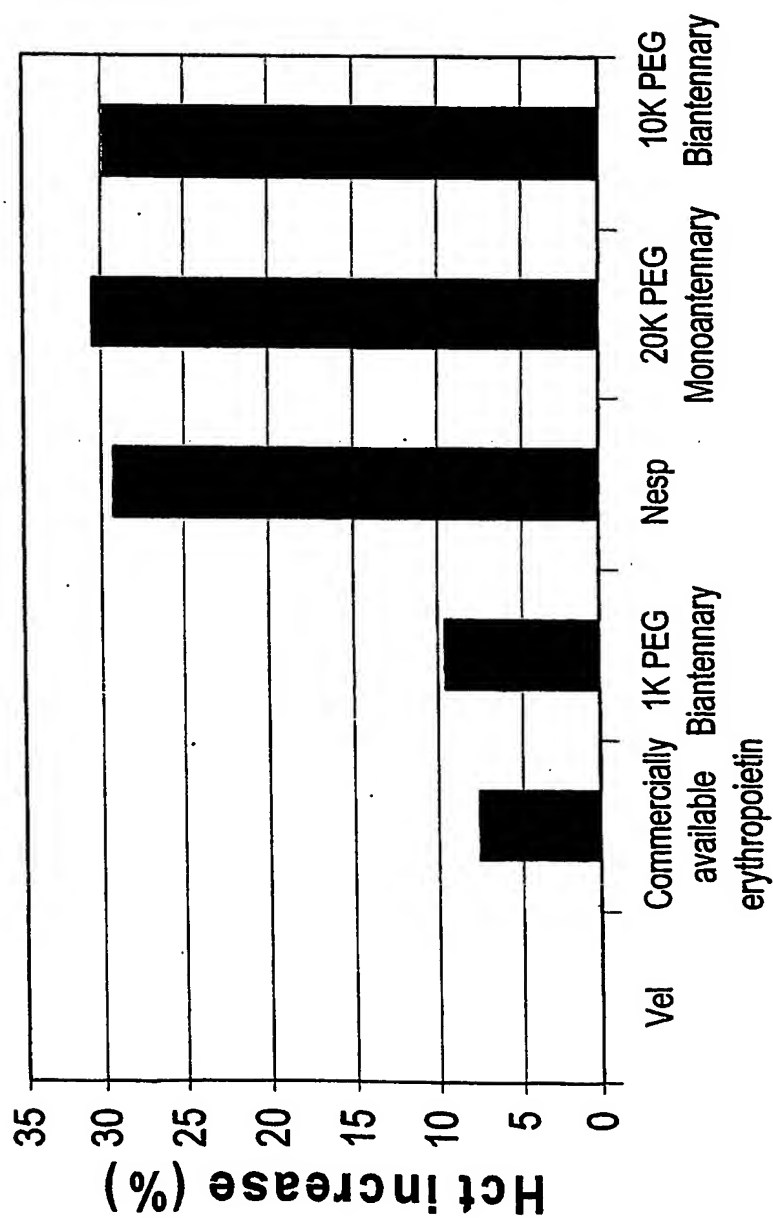


FIG. 138

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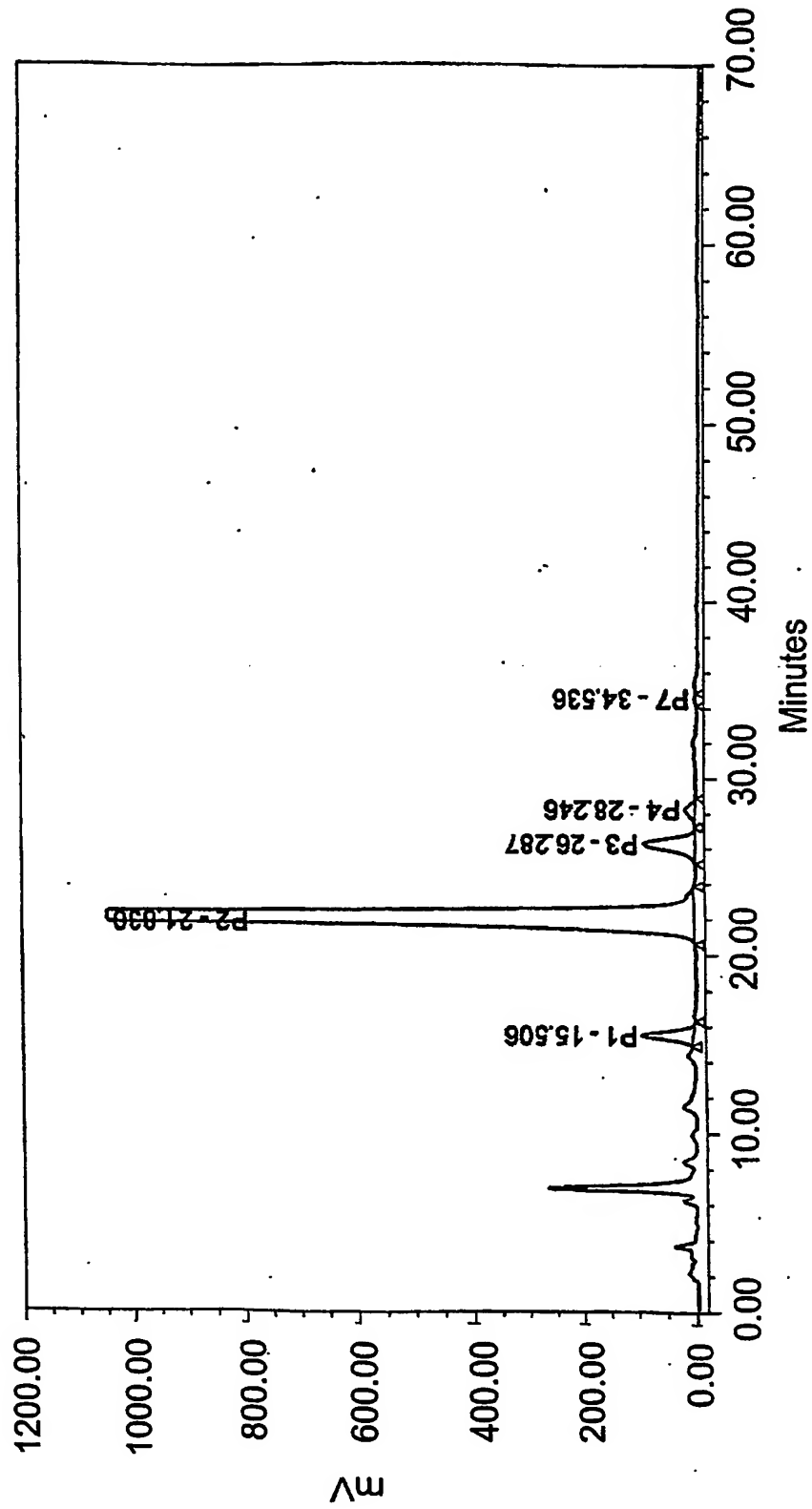


FIG. 139A

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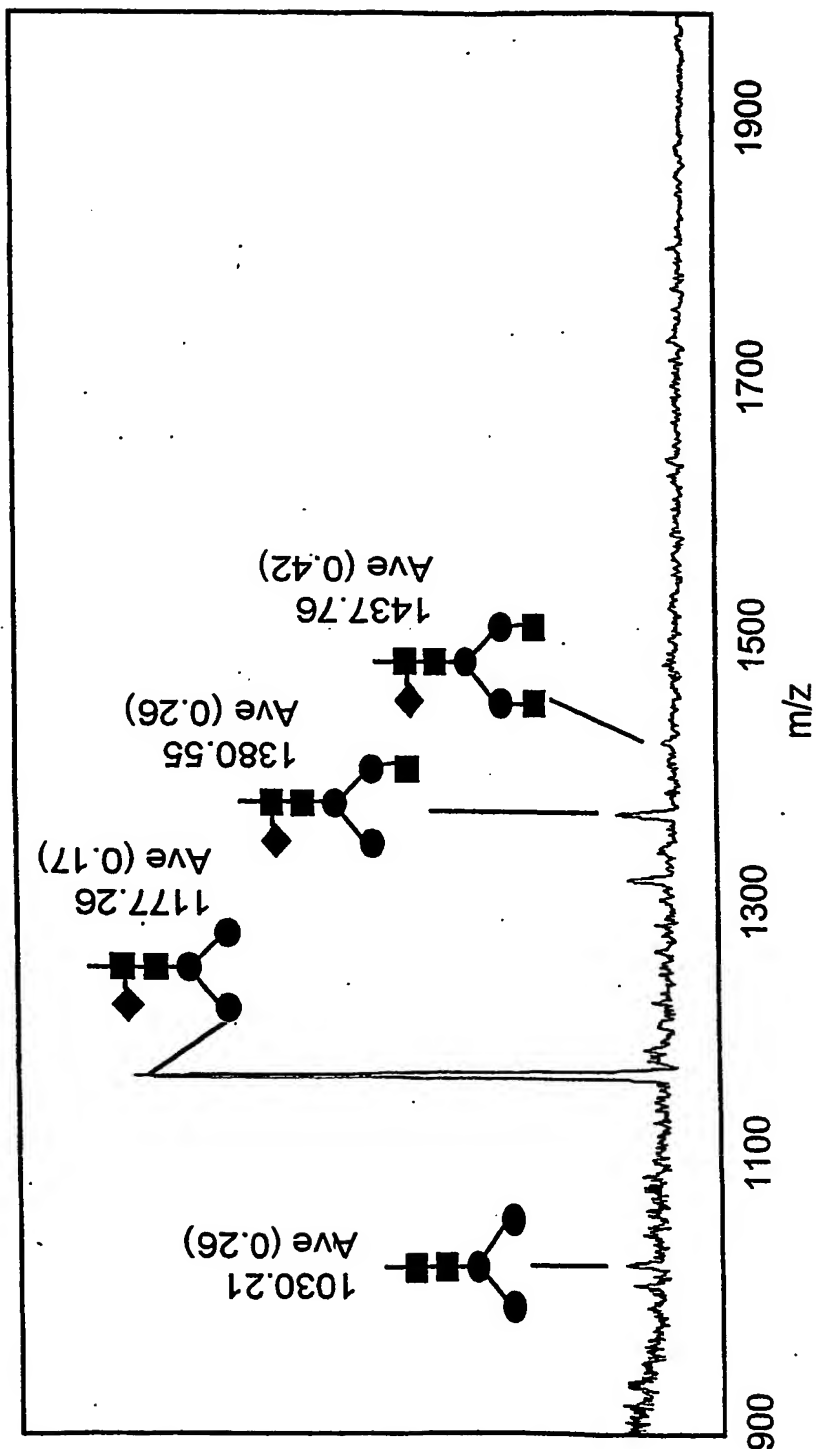


FIG. 139B

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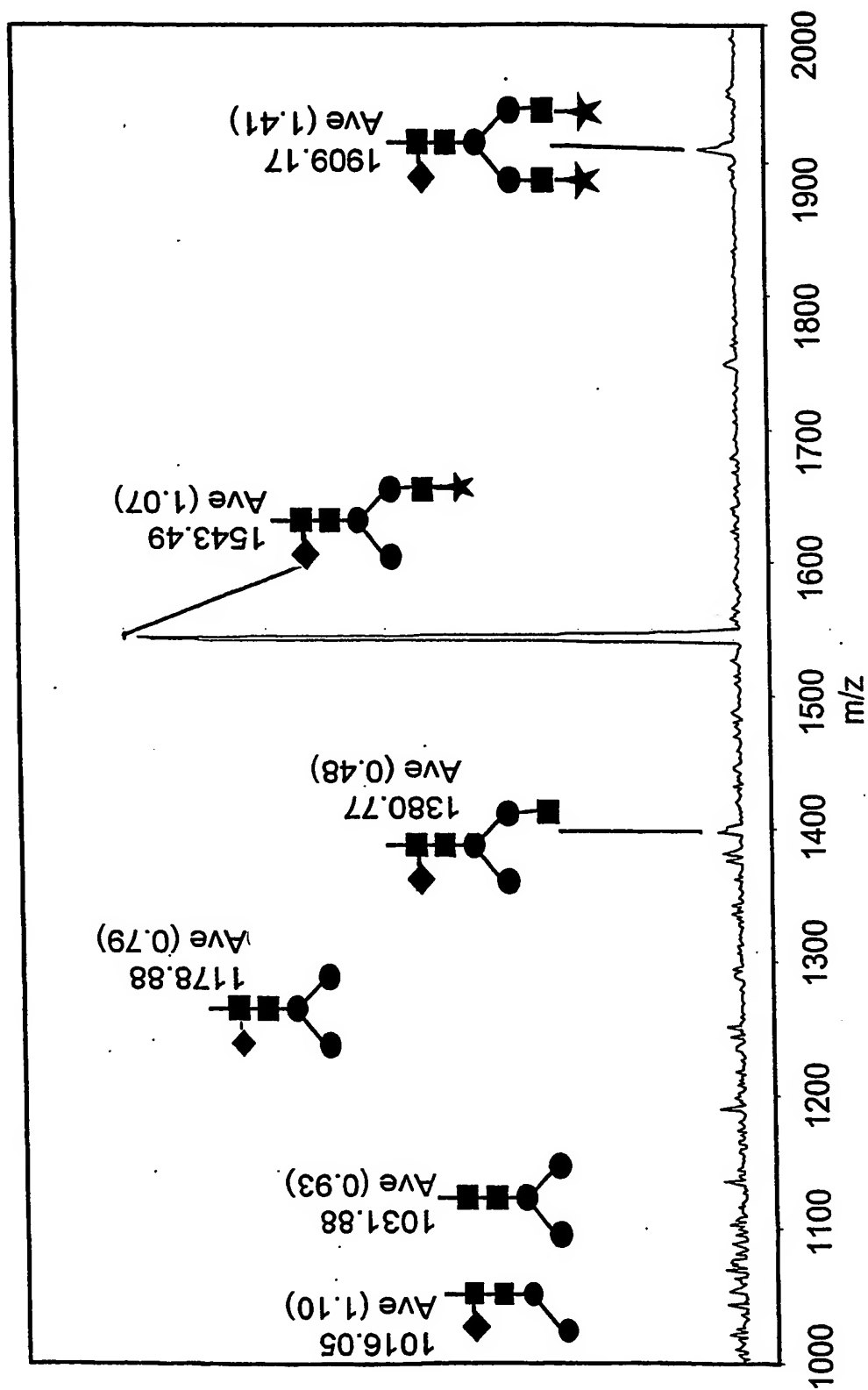


FIG. 140

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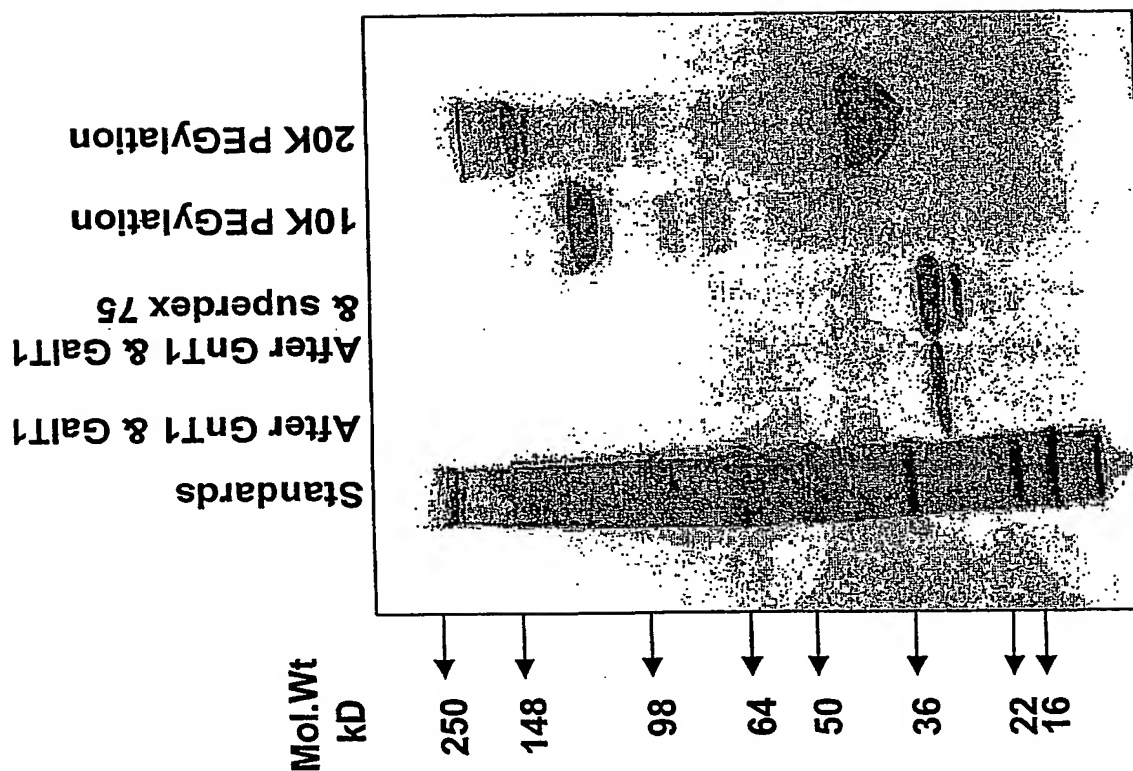


FIG. 141

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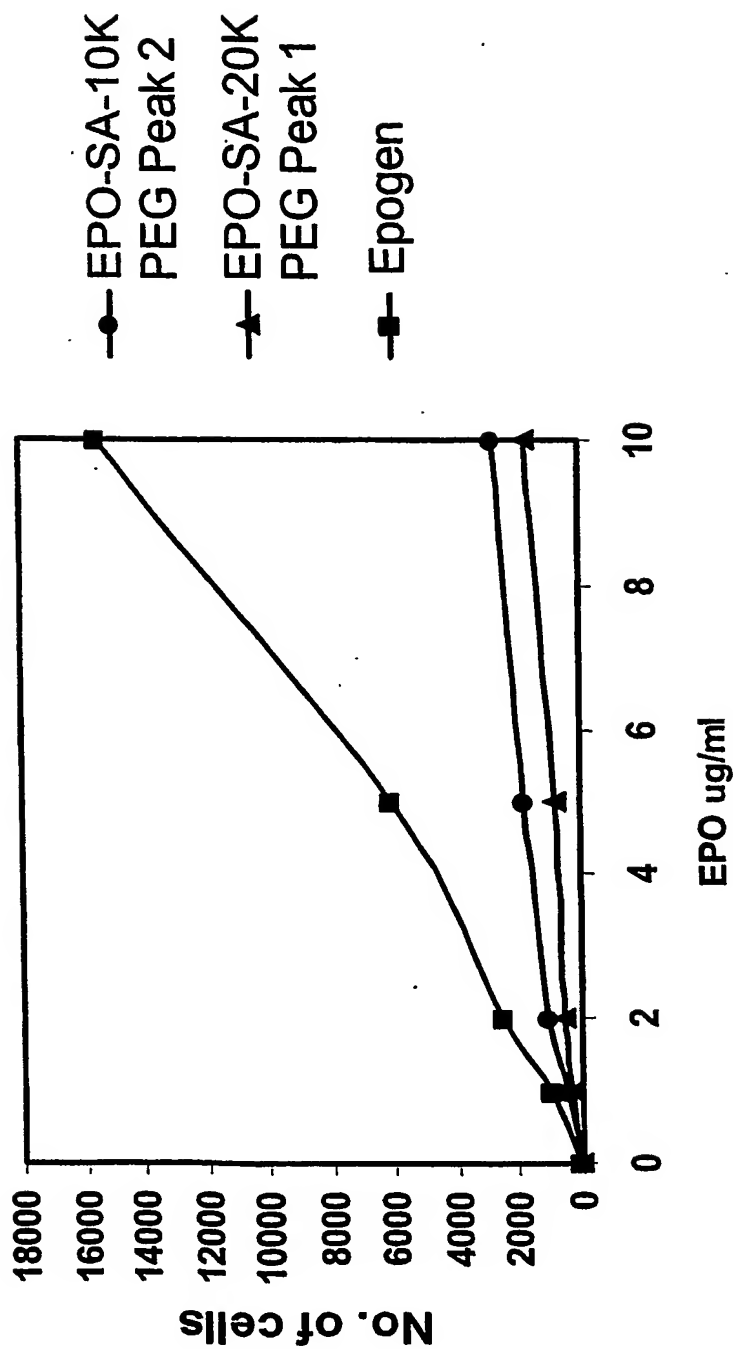


FIG. 142

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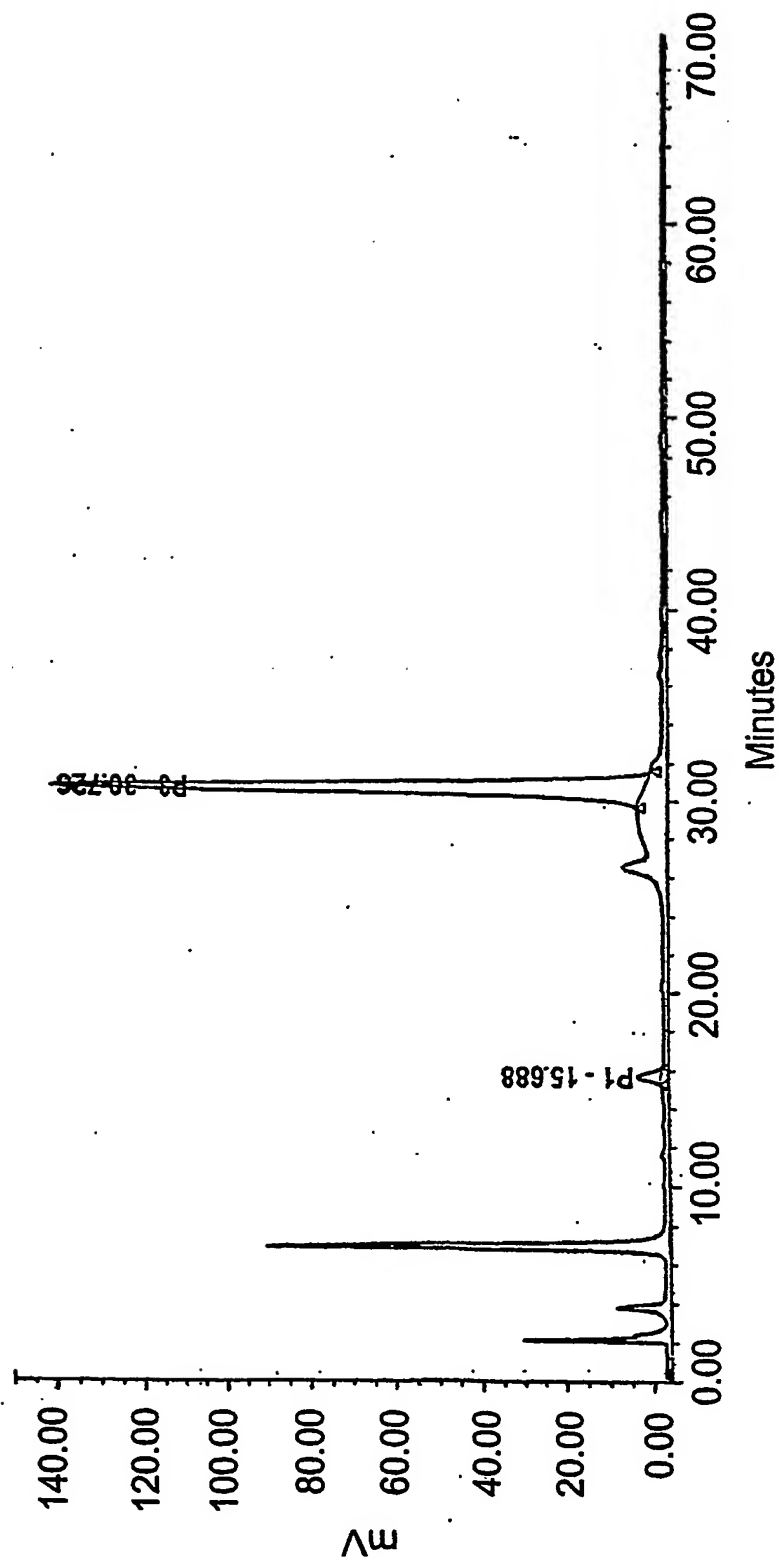


FIG. 143A



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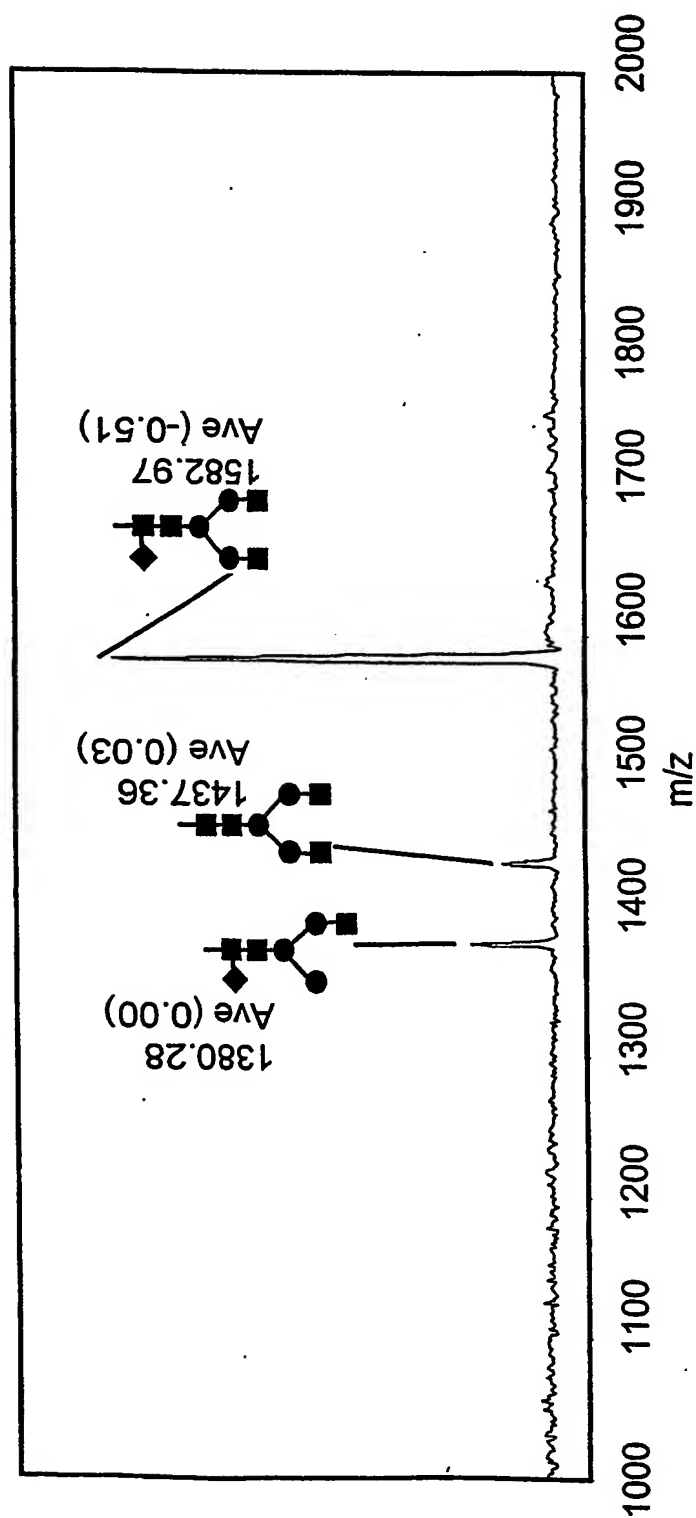


FIG. 143B

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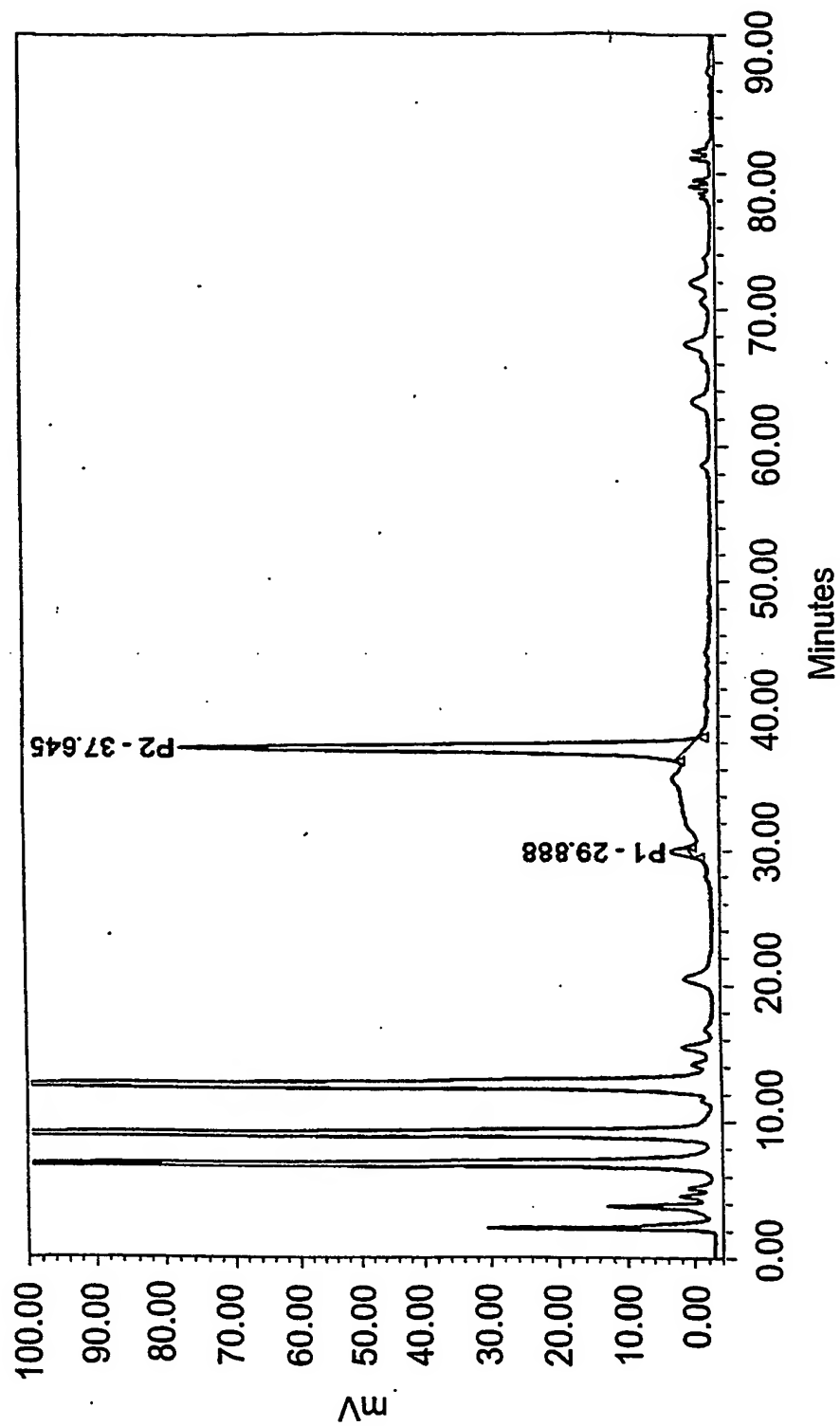


FIG. 144A

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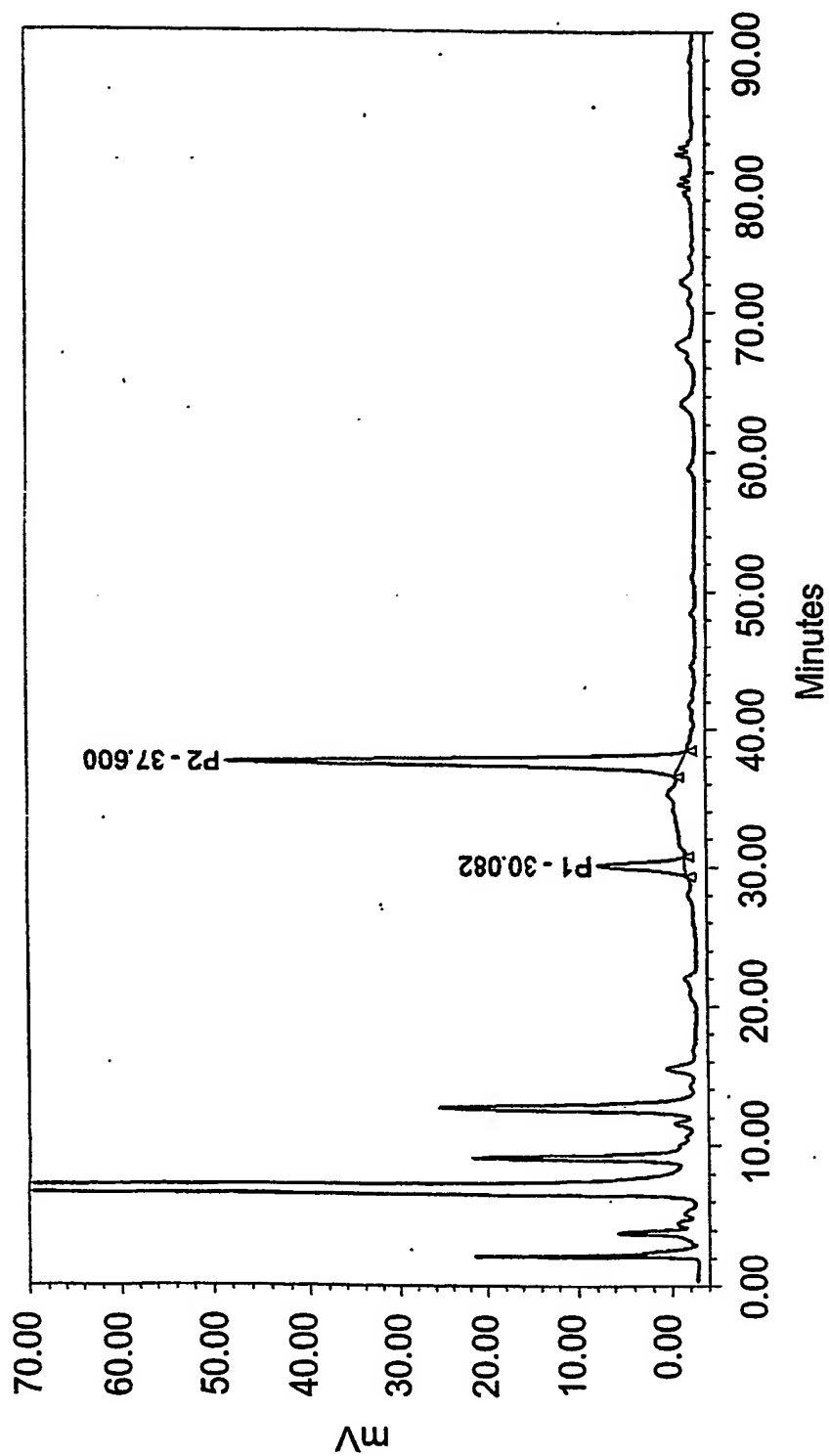


FIG. 144B

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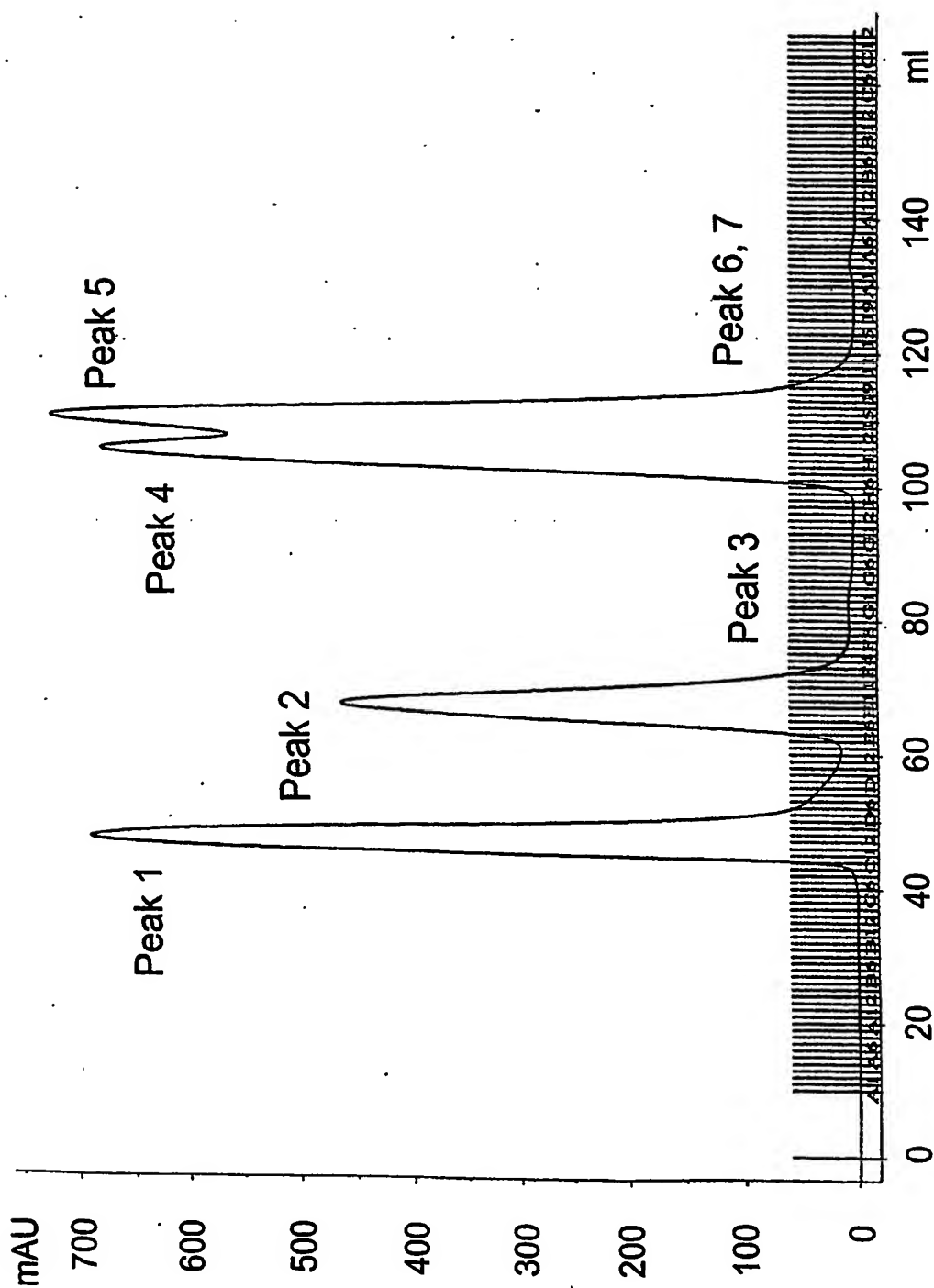


FIG. 145

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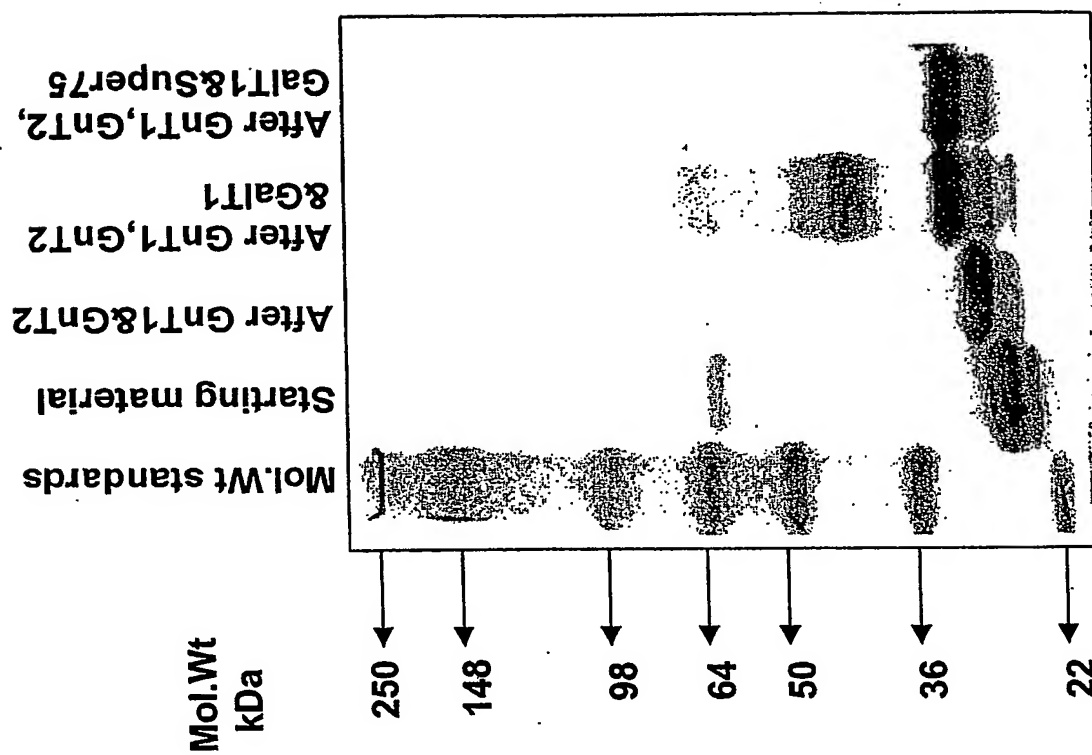


FIG. 146

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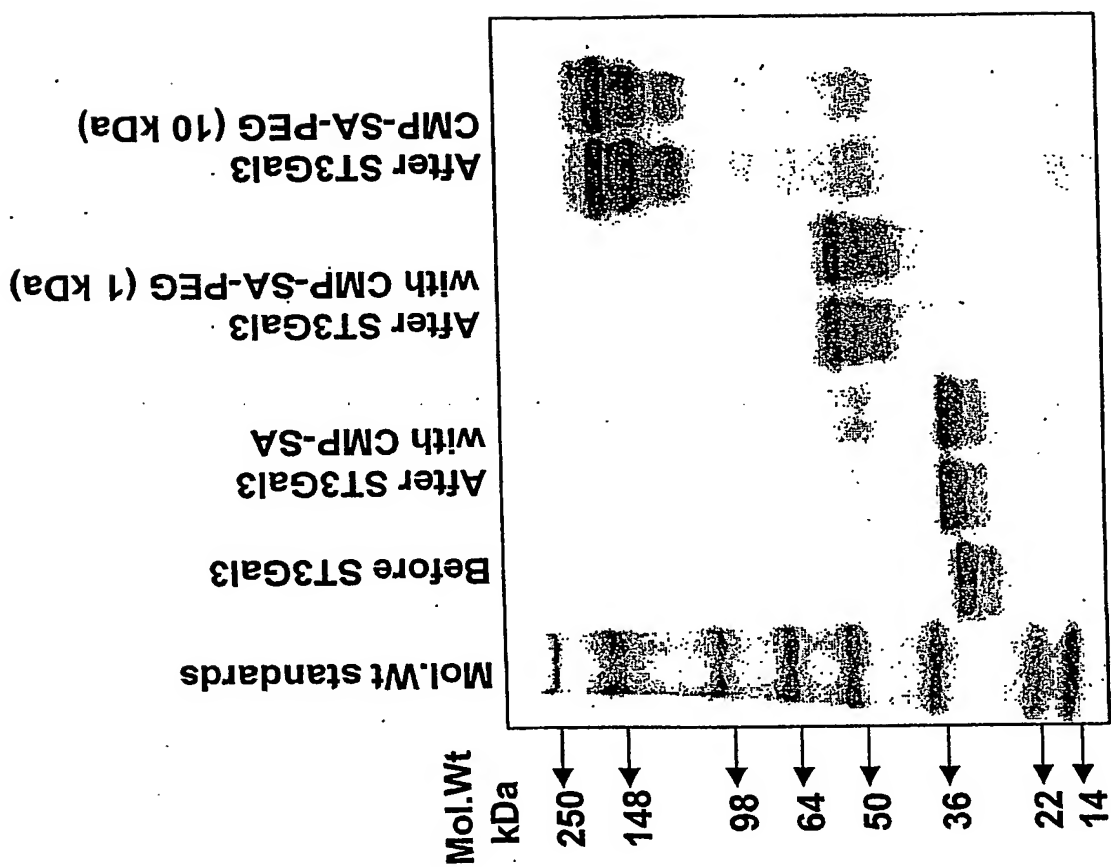


FIG. 147

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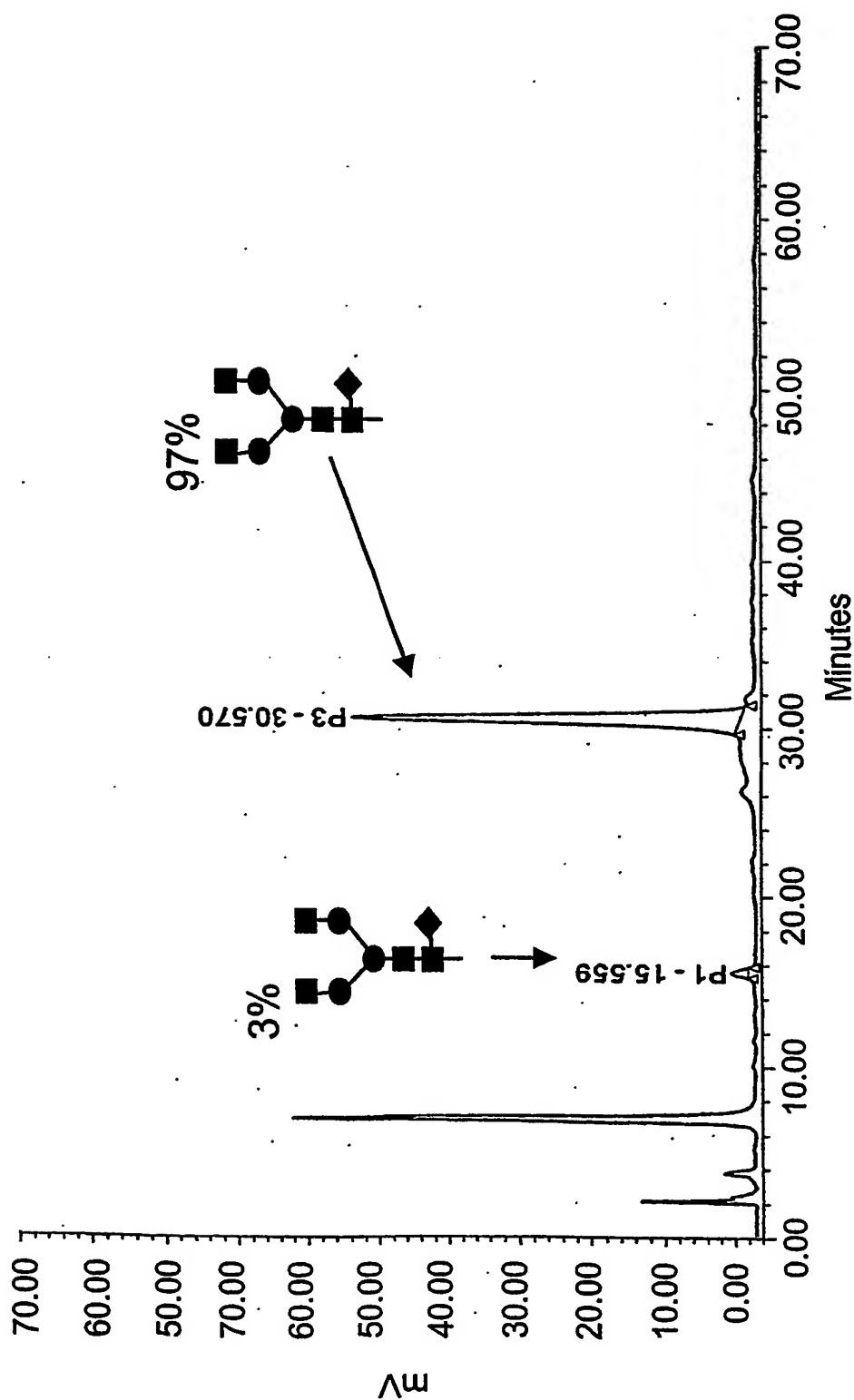


FIG. 148

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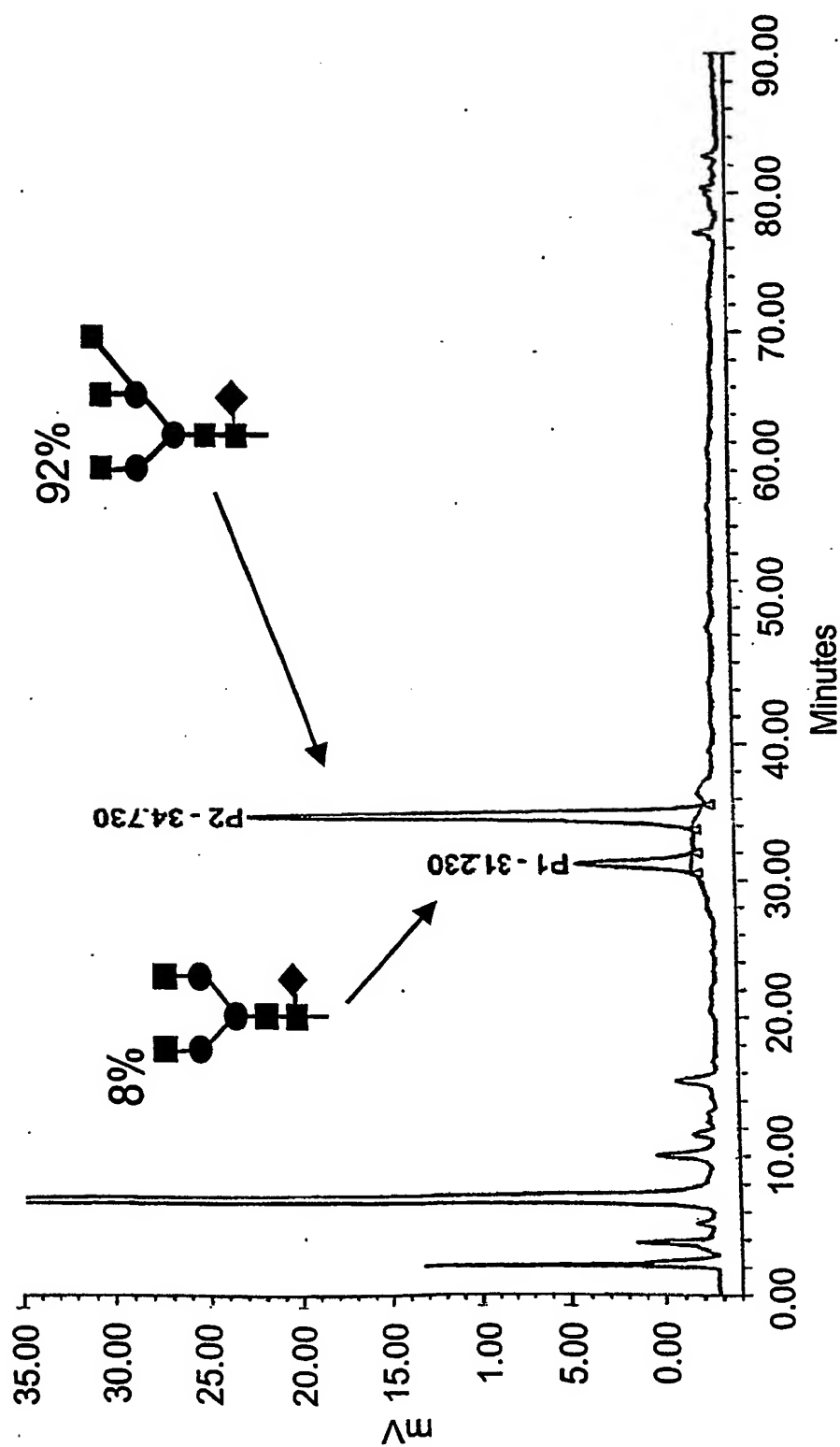


FIG. 149



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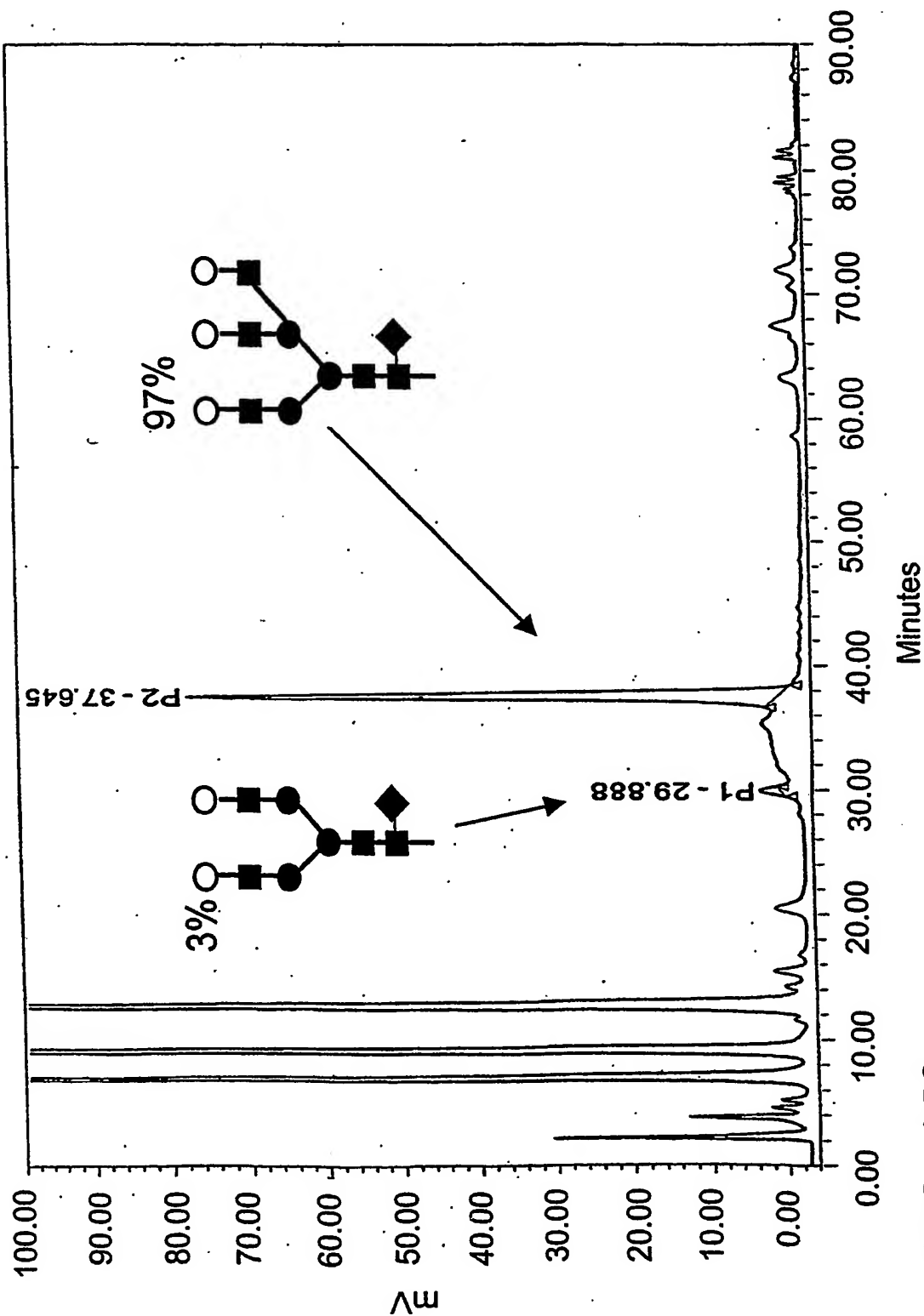


FIG. 150

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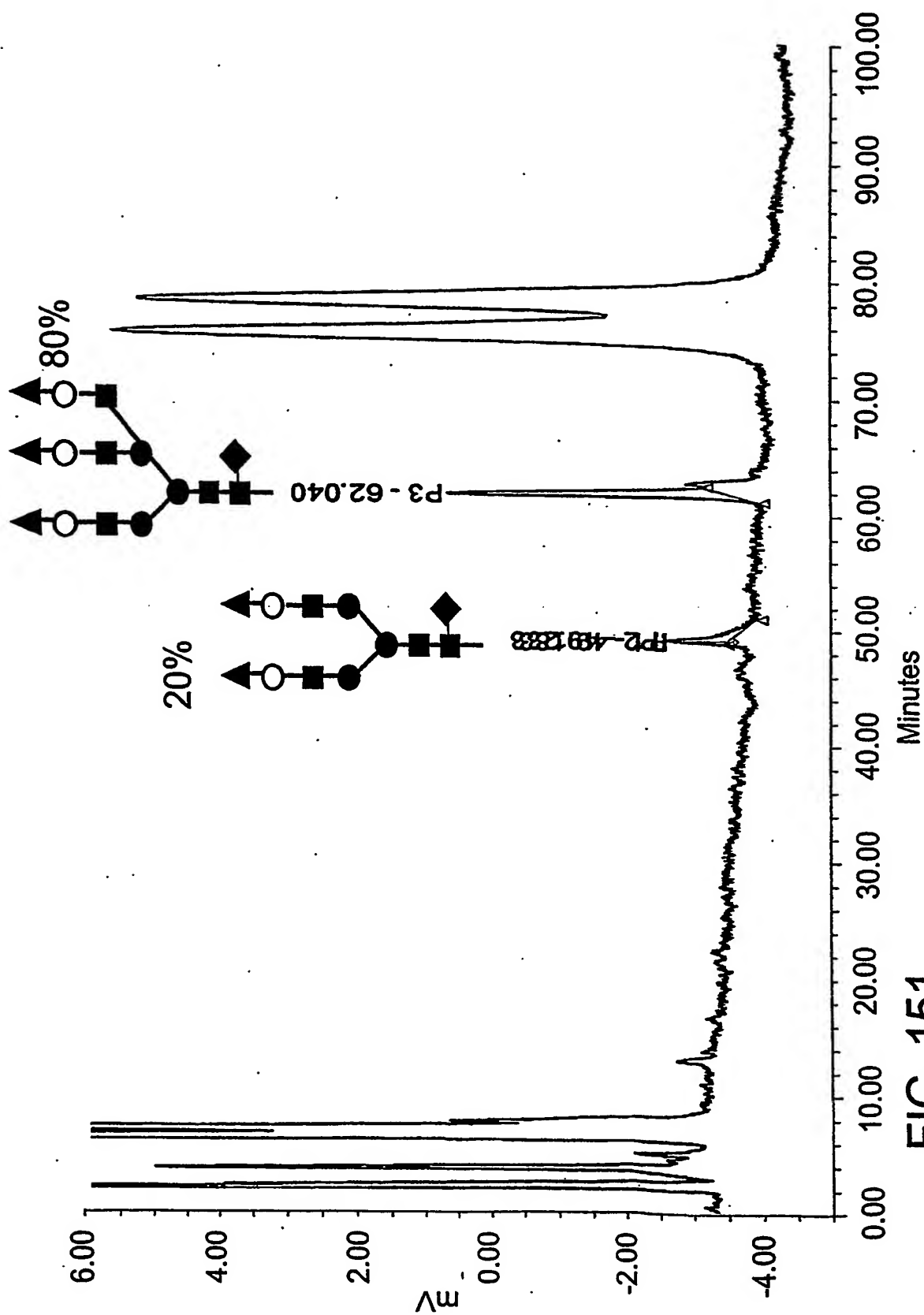


FIG. 151

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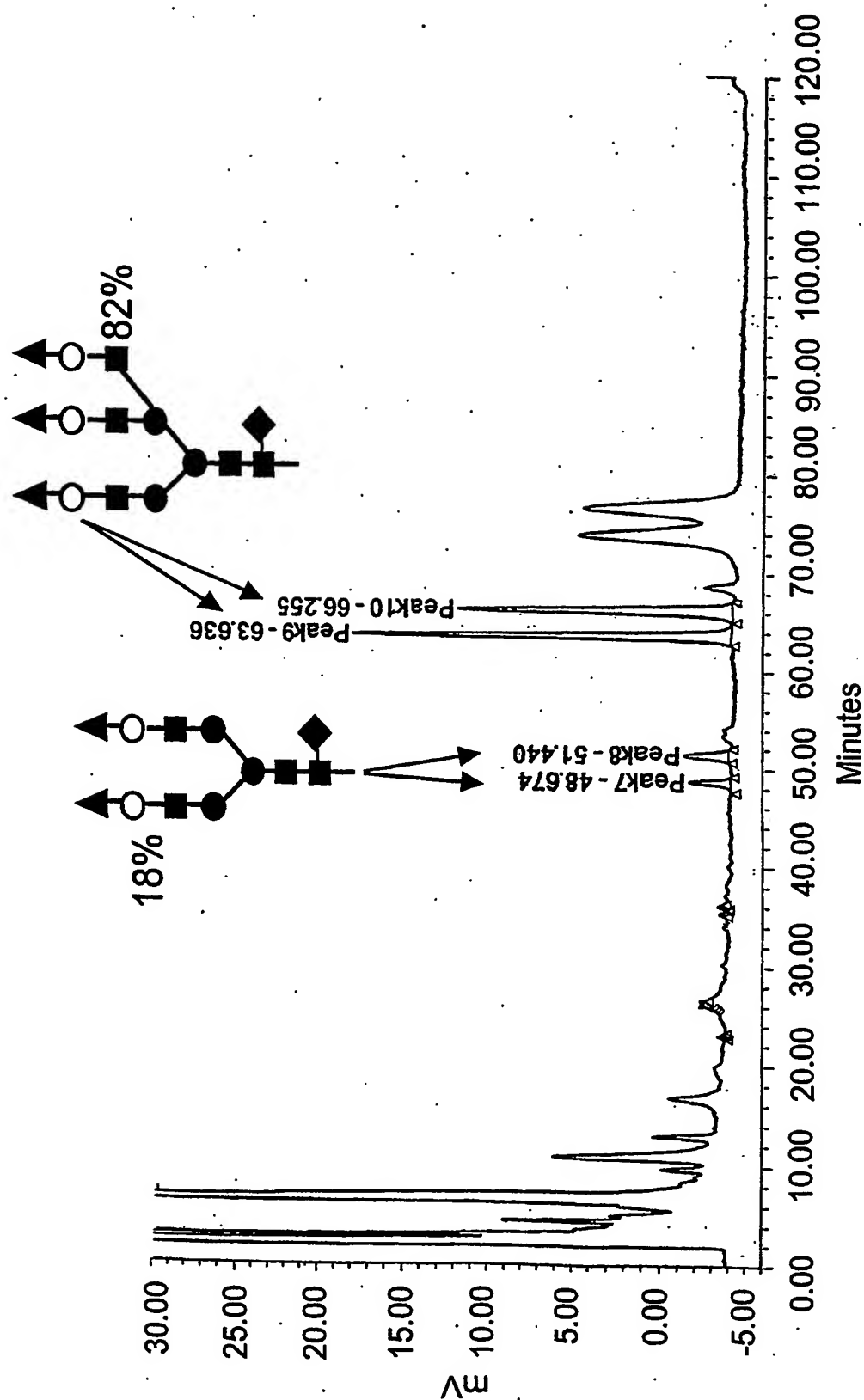
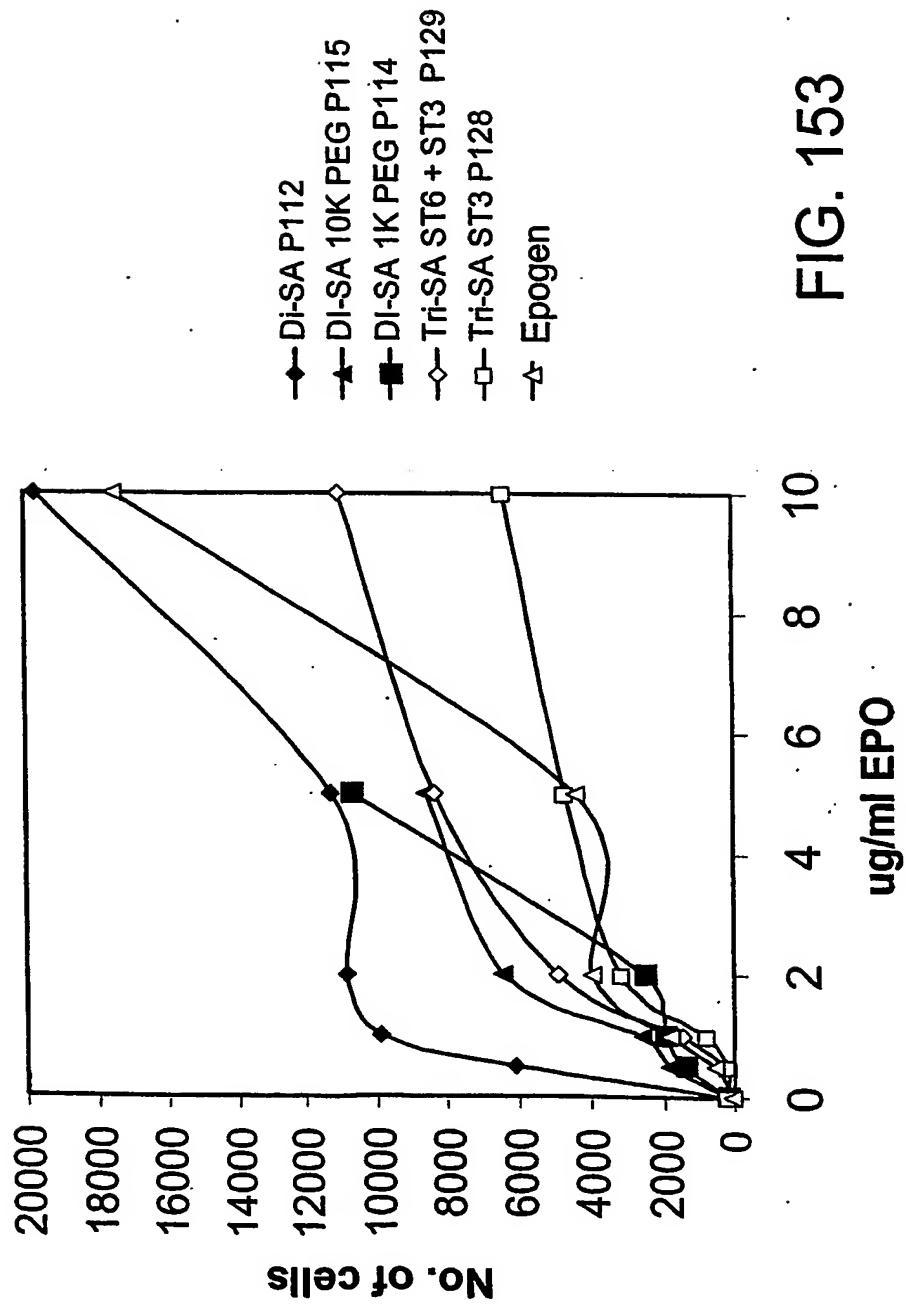


FIG. 152

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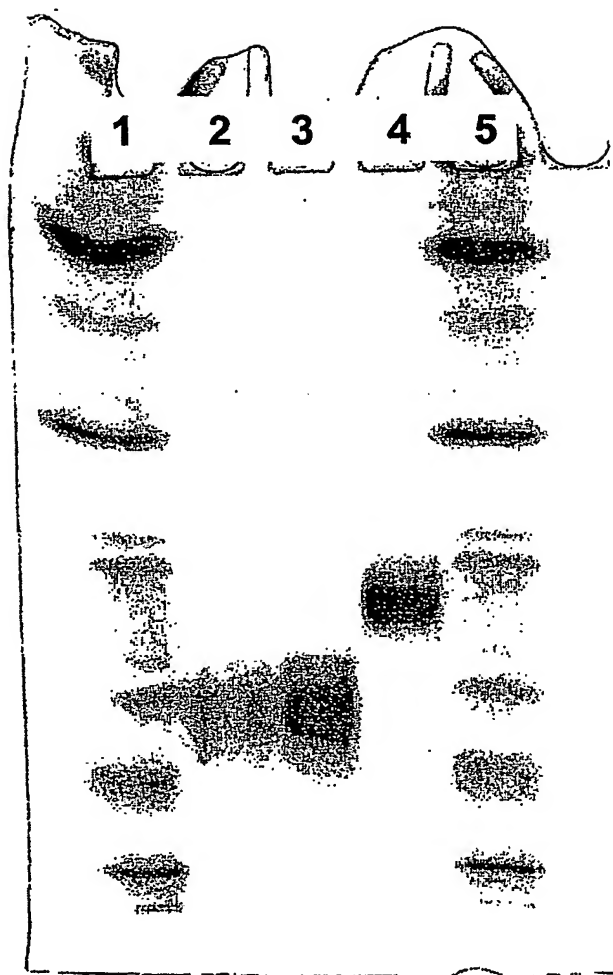


FIG. 154

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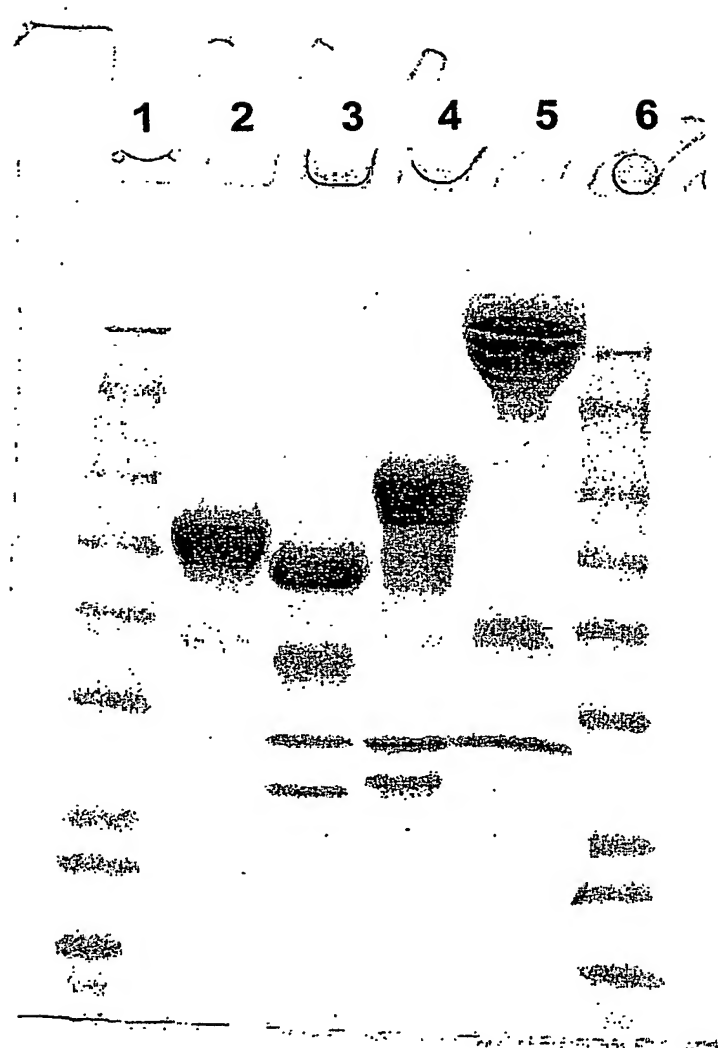


FIG. 155

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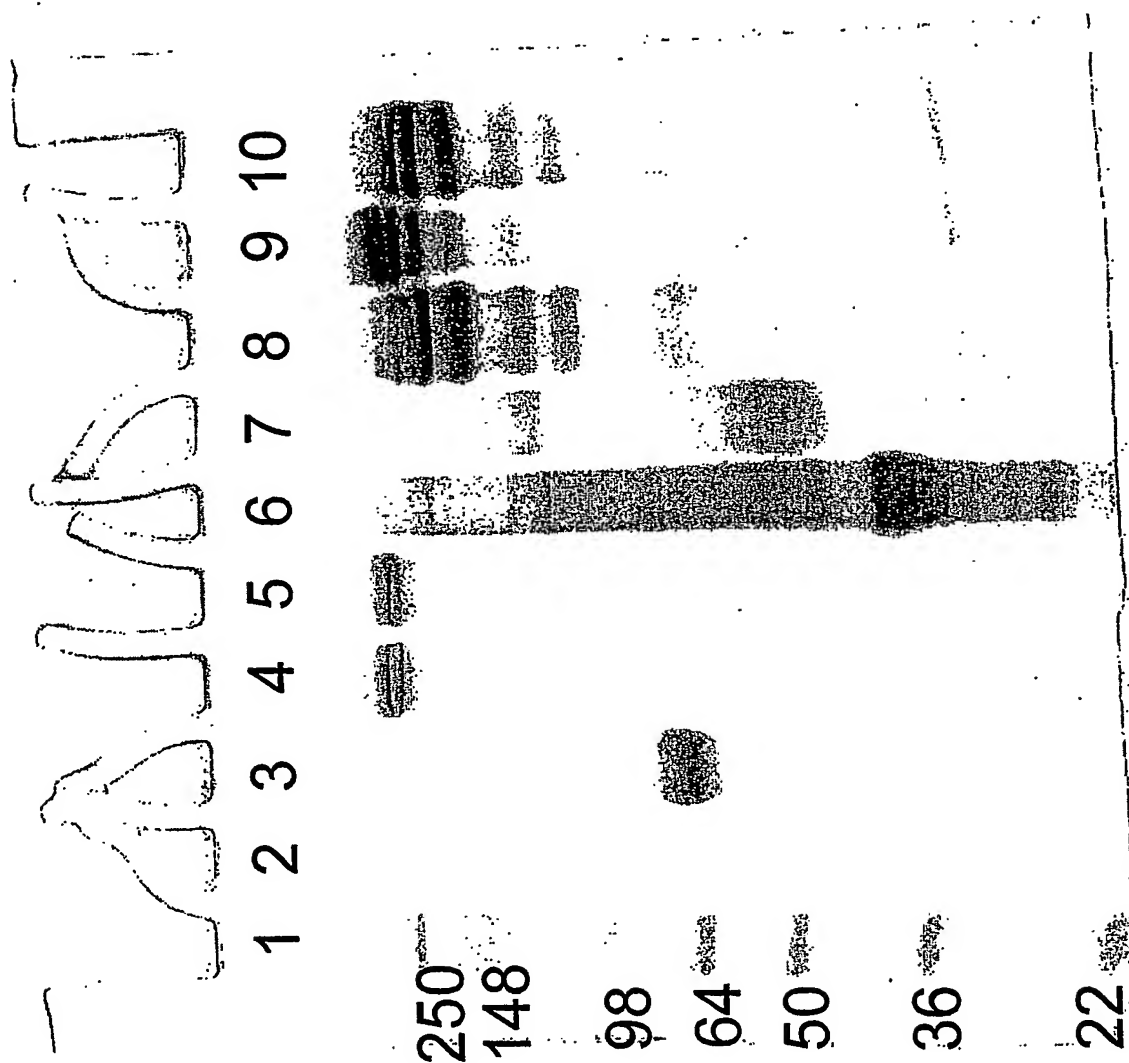


FIG. 156

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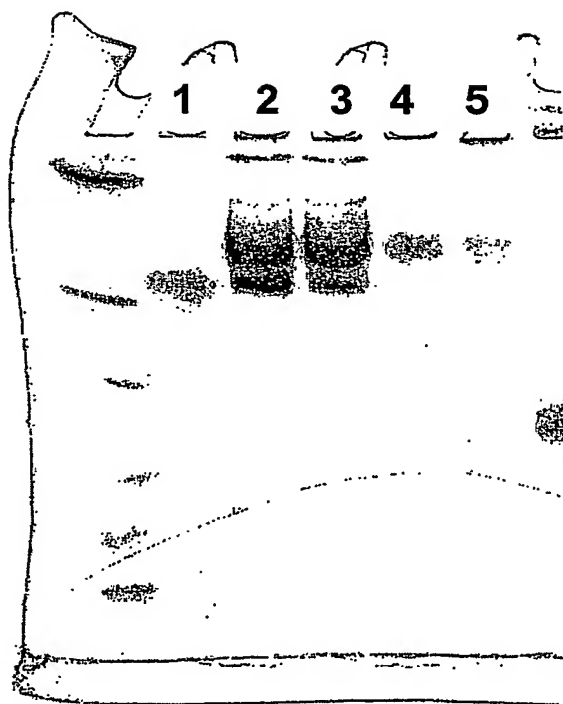


FIG. 157



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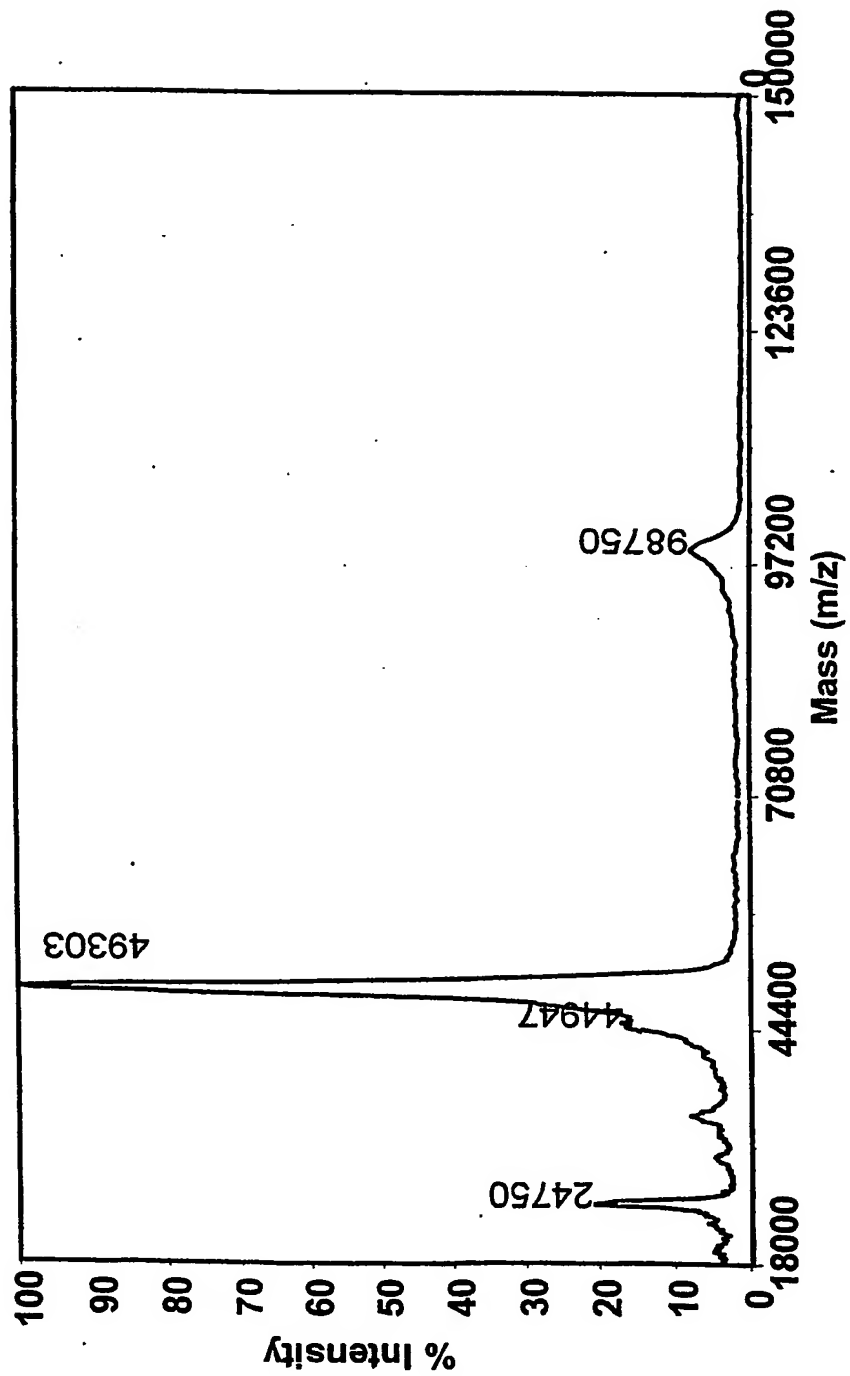


FIG. 158

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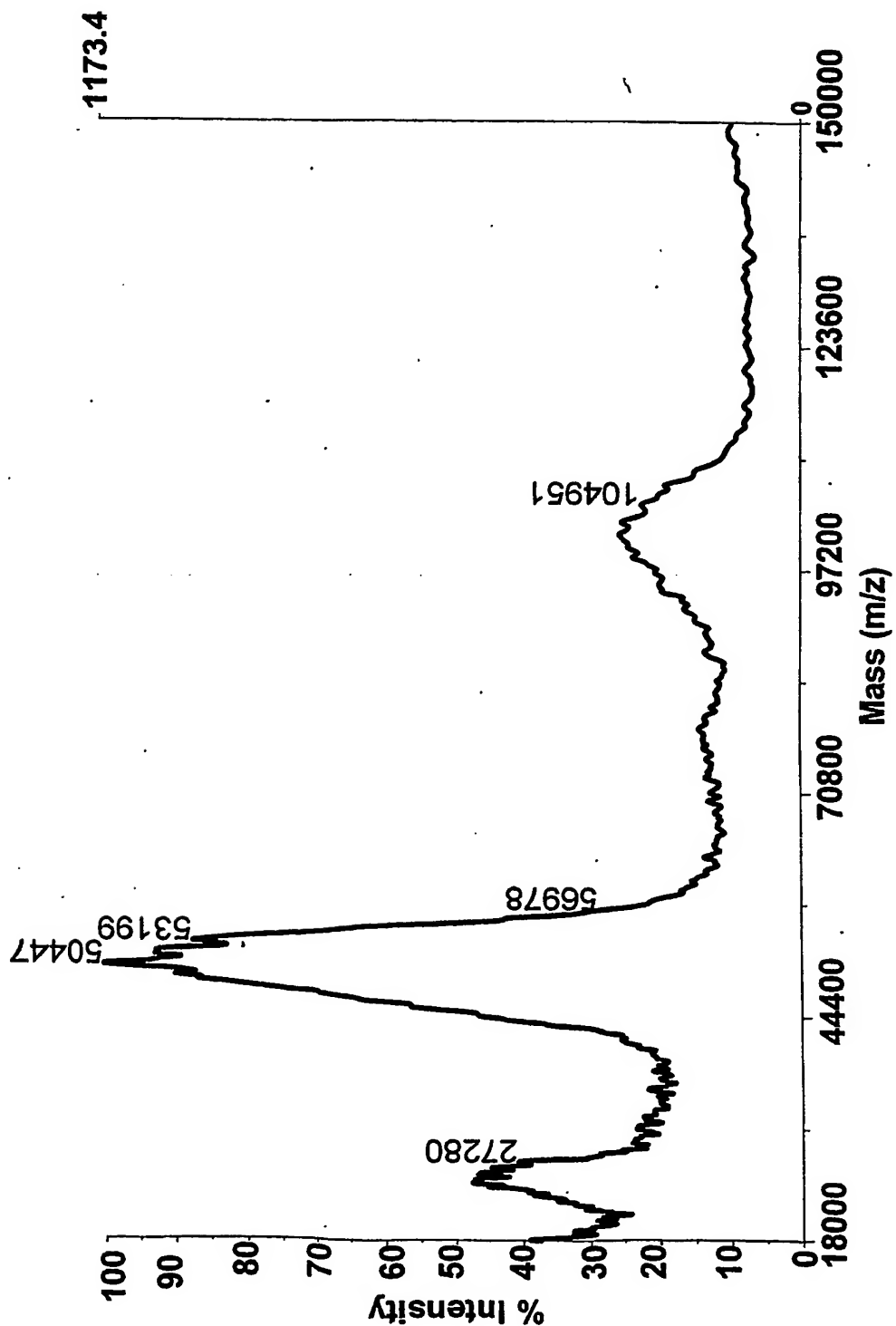


FIG. 159

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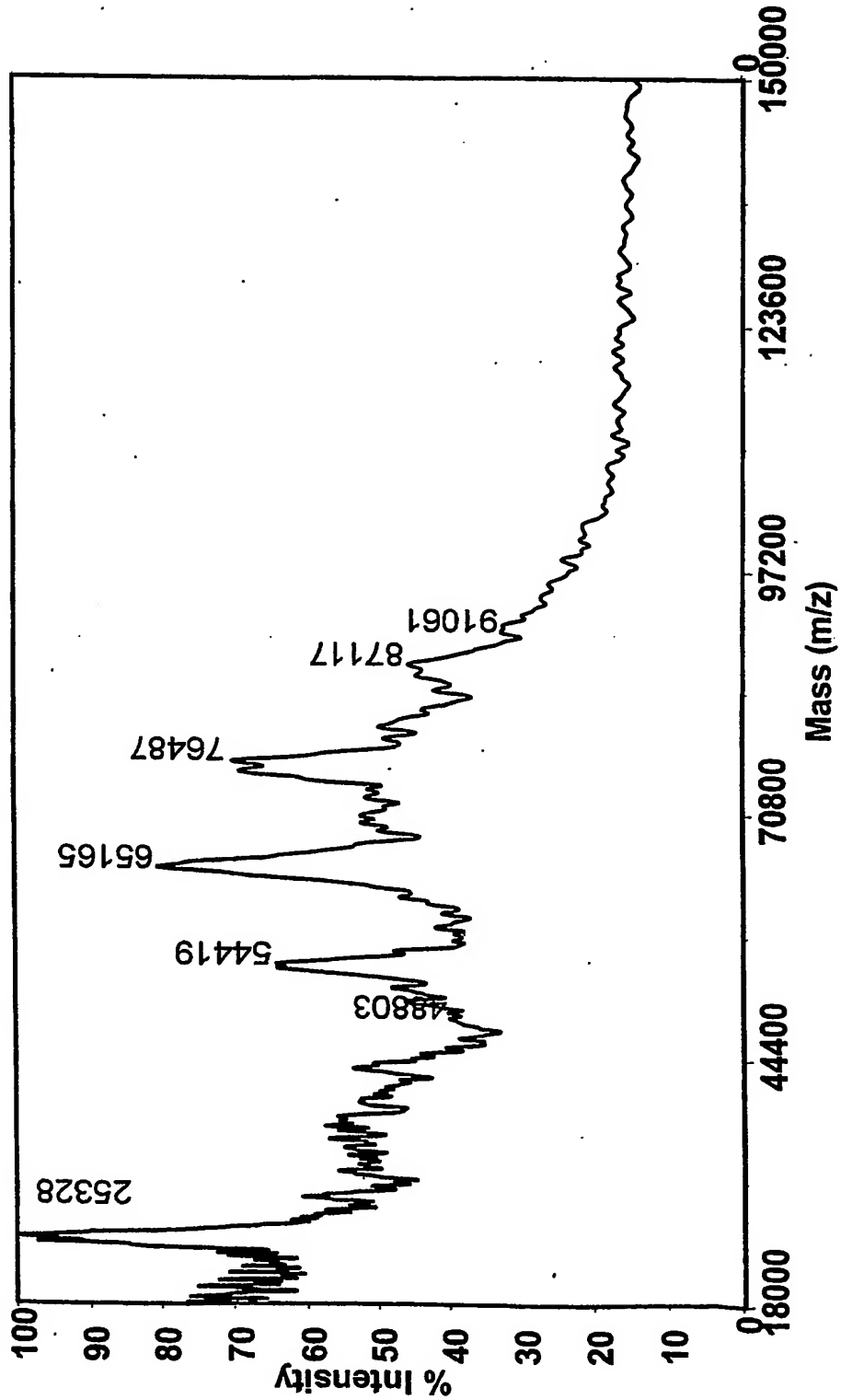


FIG. 160

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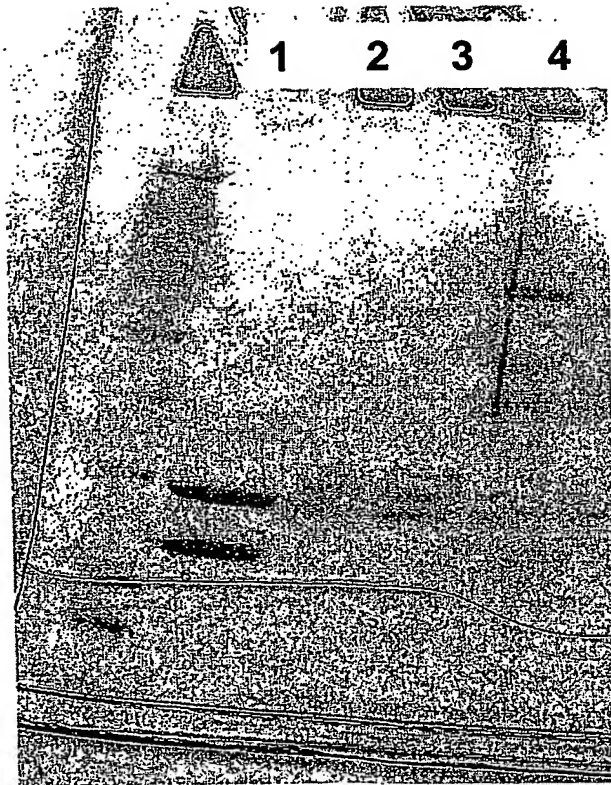


FIG. 161

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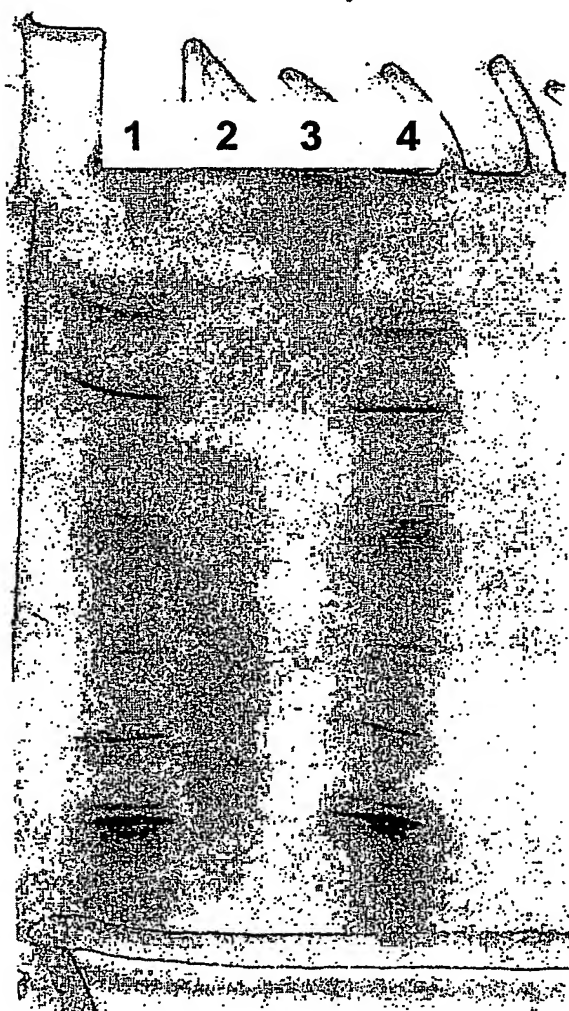


FIG. 162

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FIG. 163

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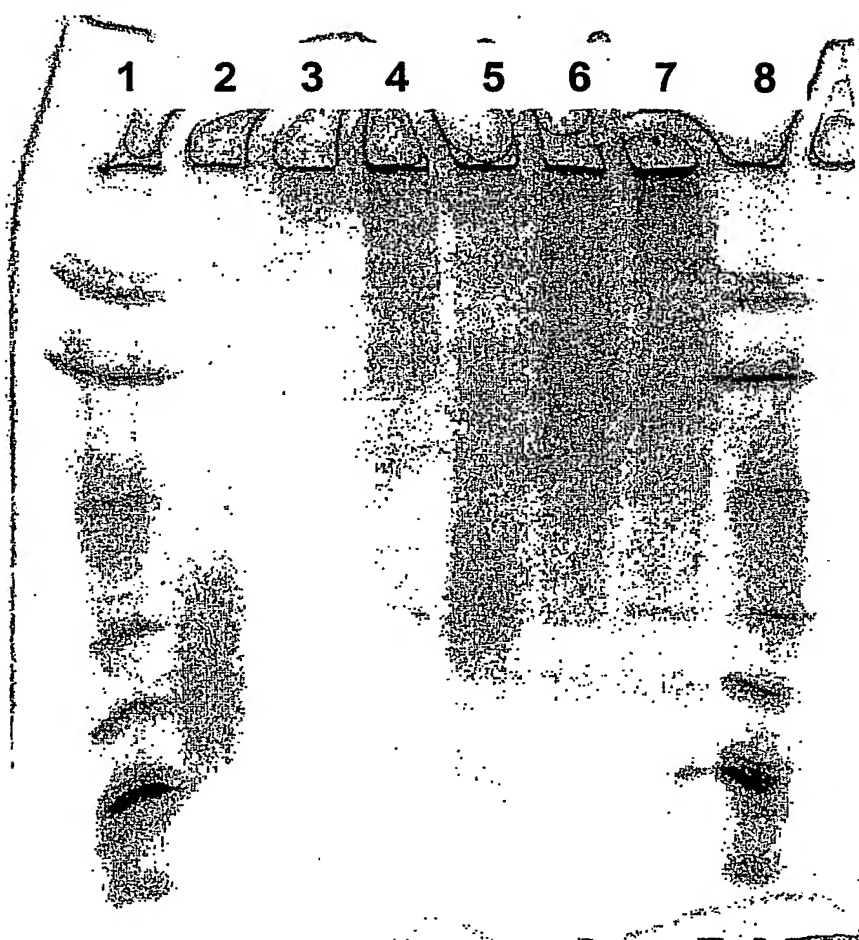


FIG. 164

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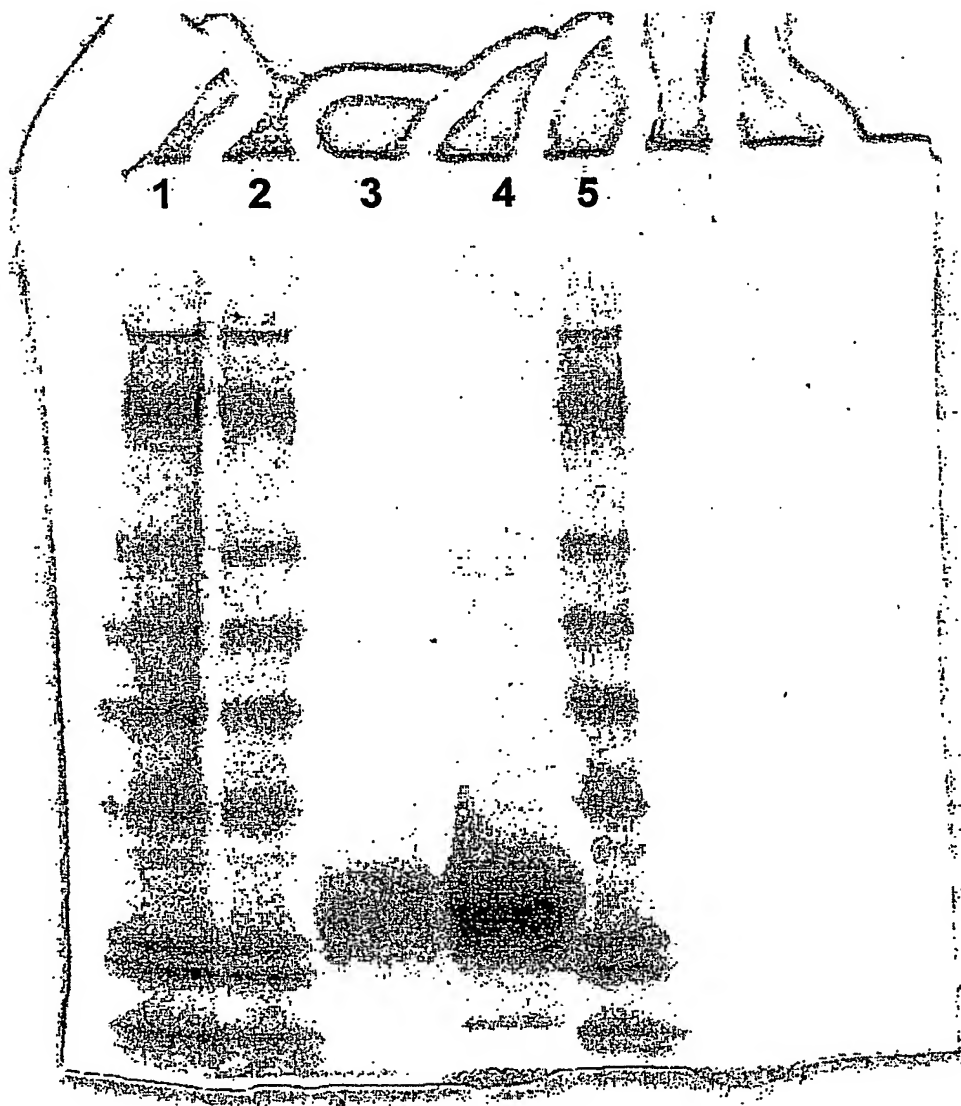


FIG. 165



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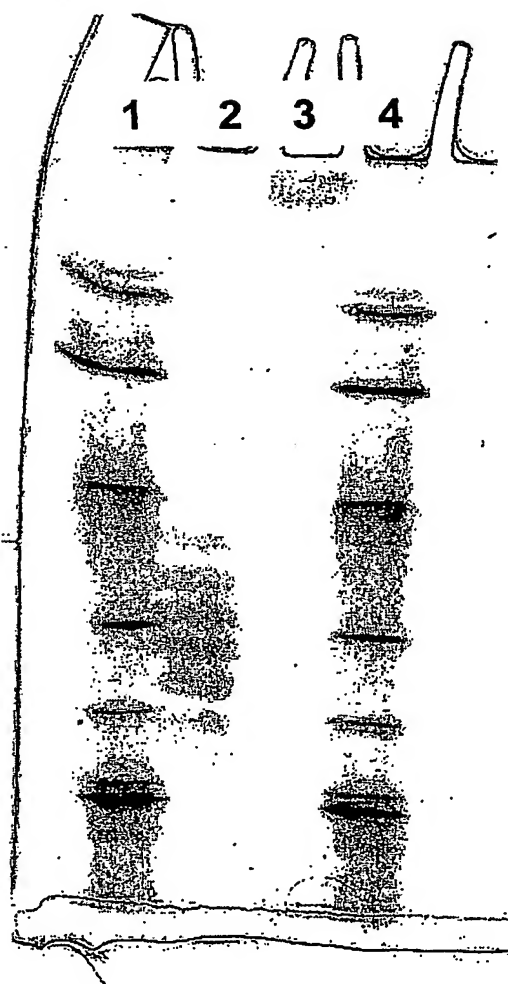


FIG. 166

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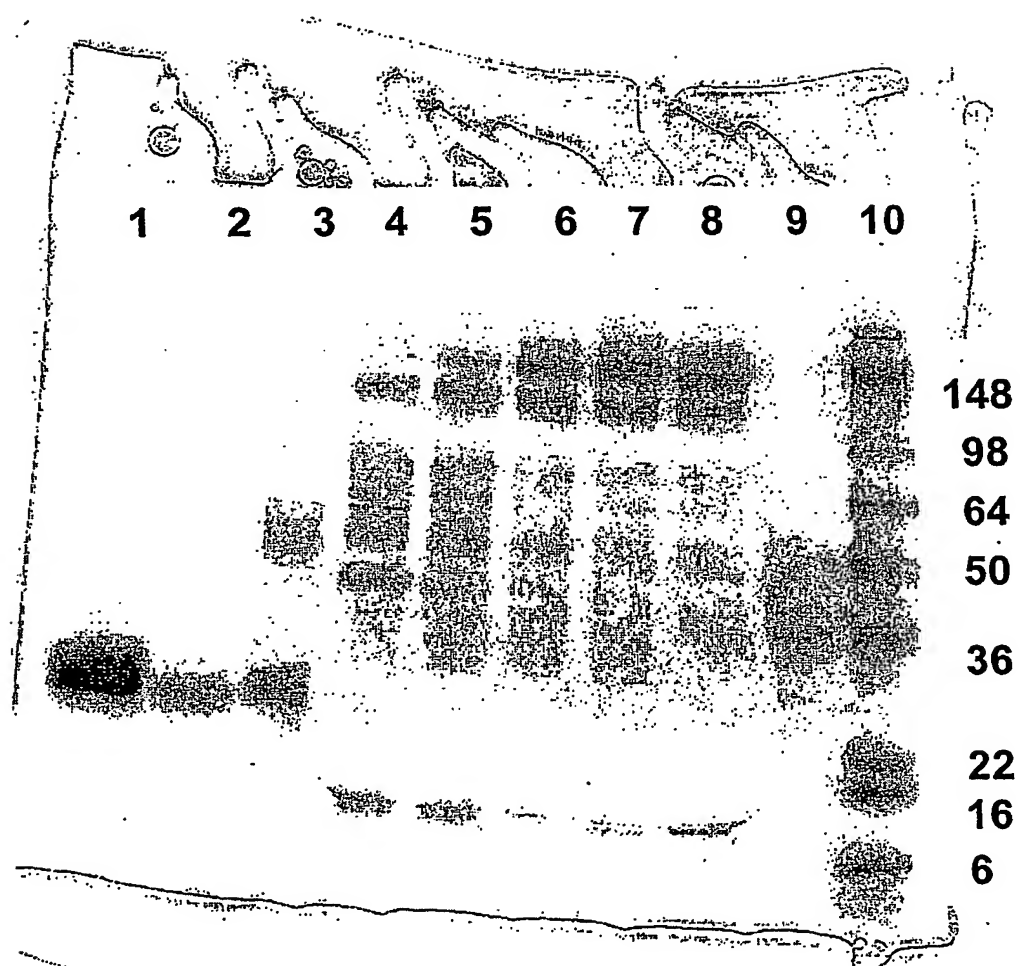


FIG. 167

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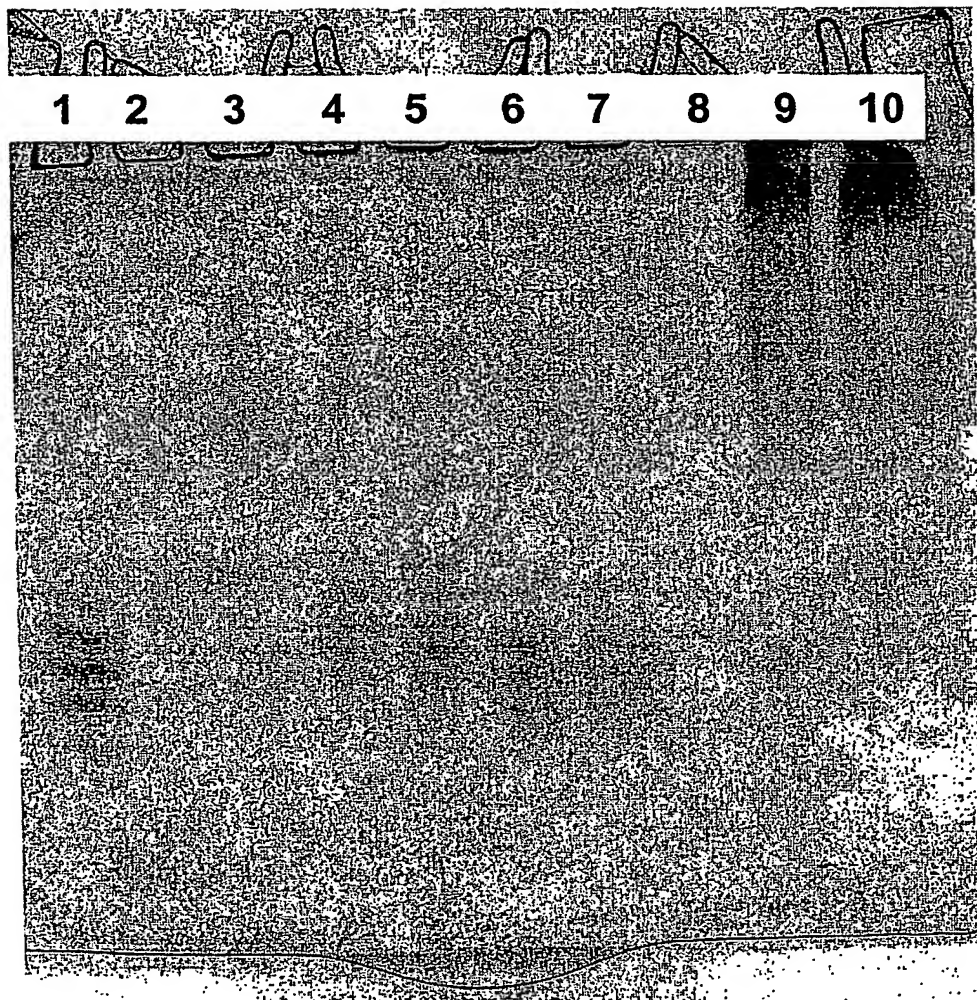


FIG. 168

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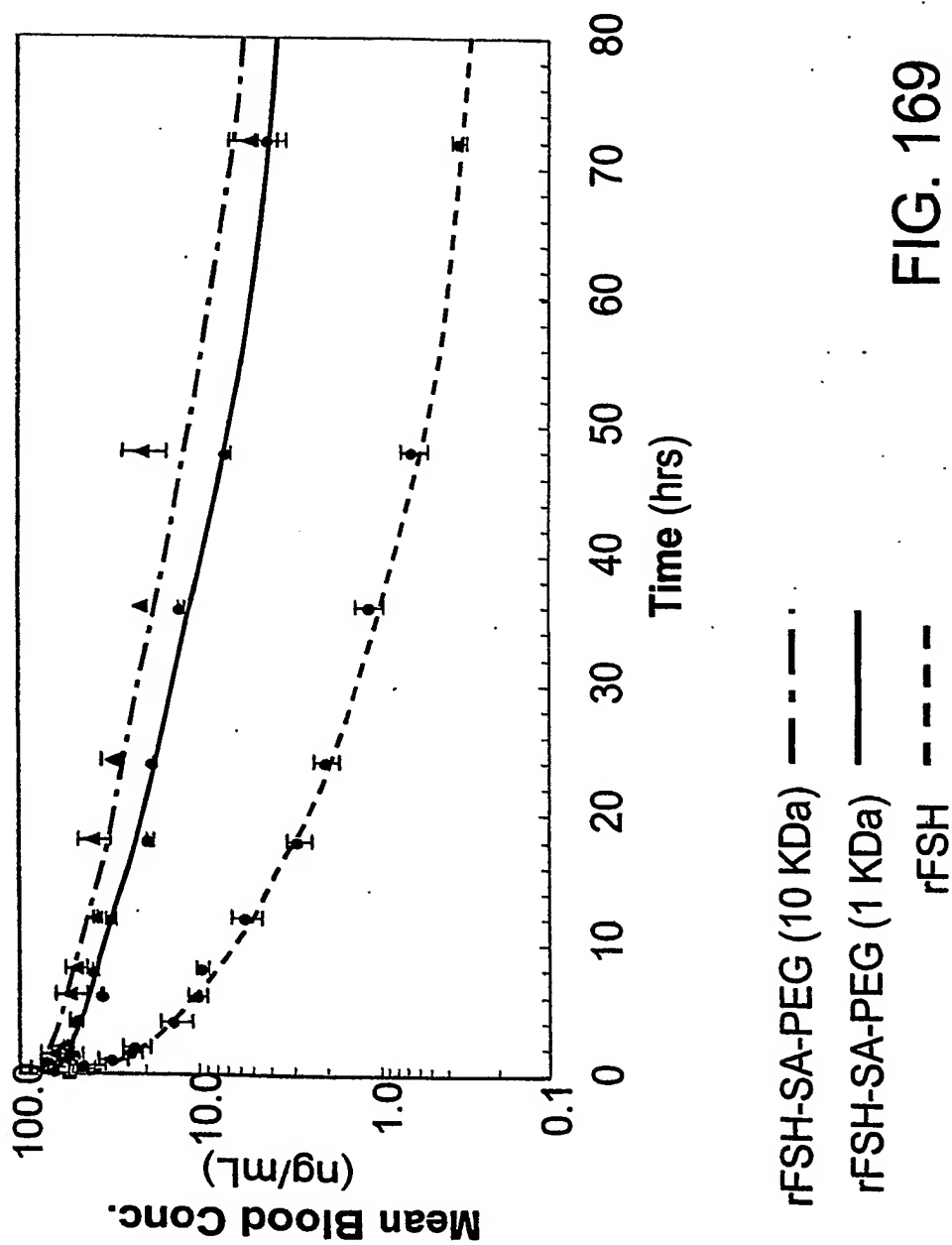


FIG. 169

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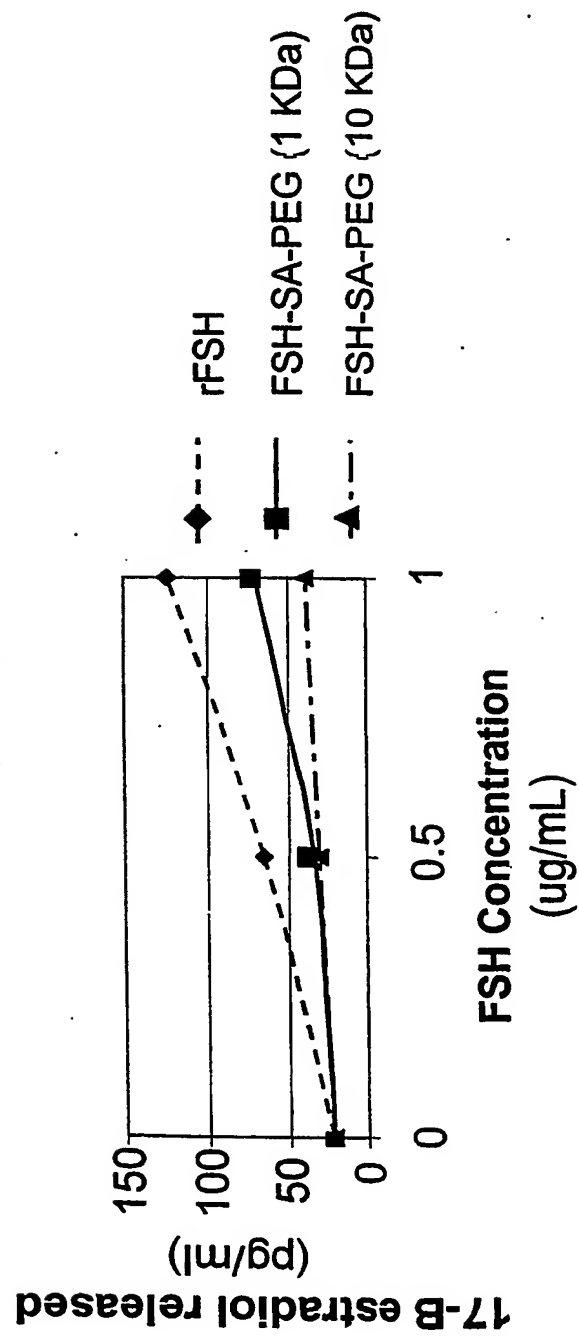


FIG. 170

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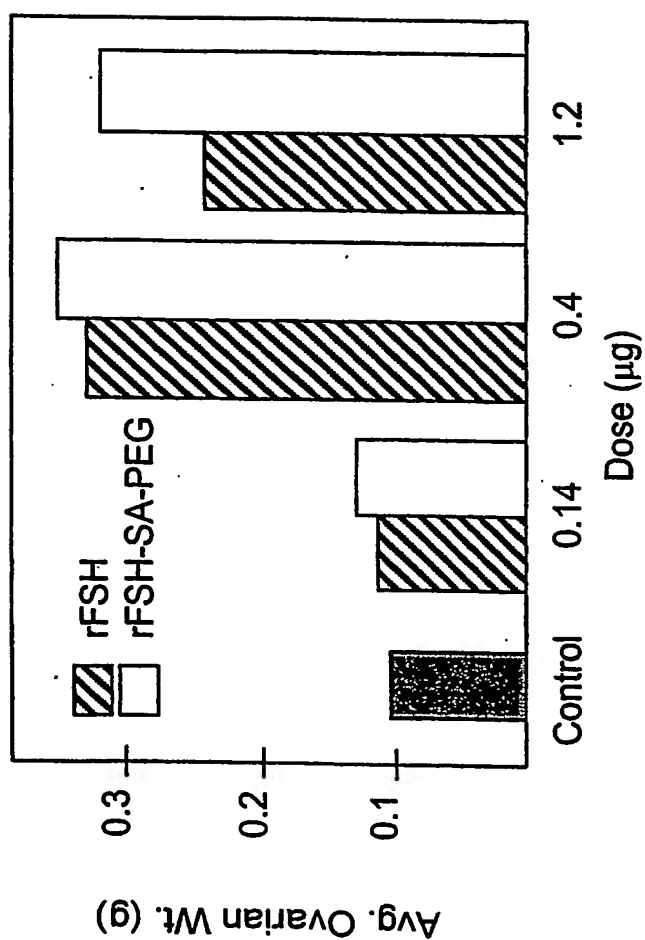


FIG. 171

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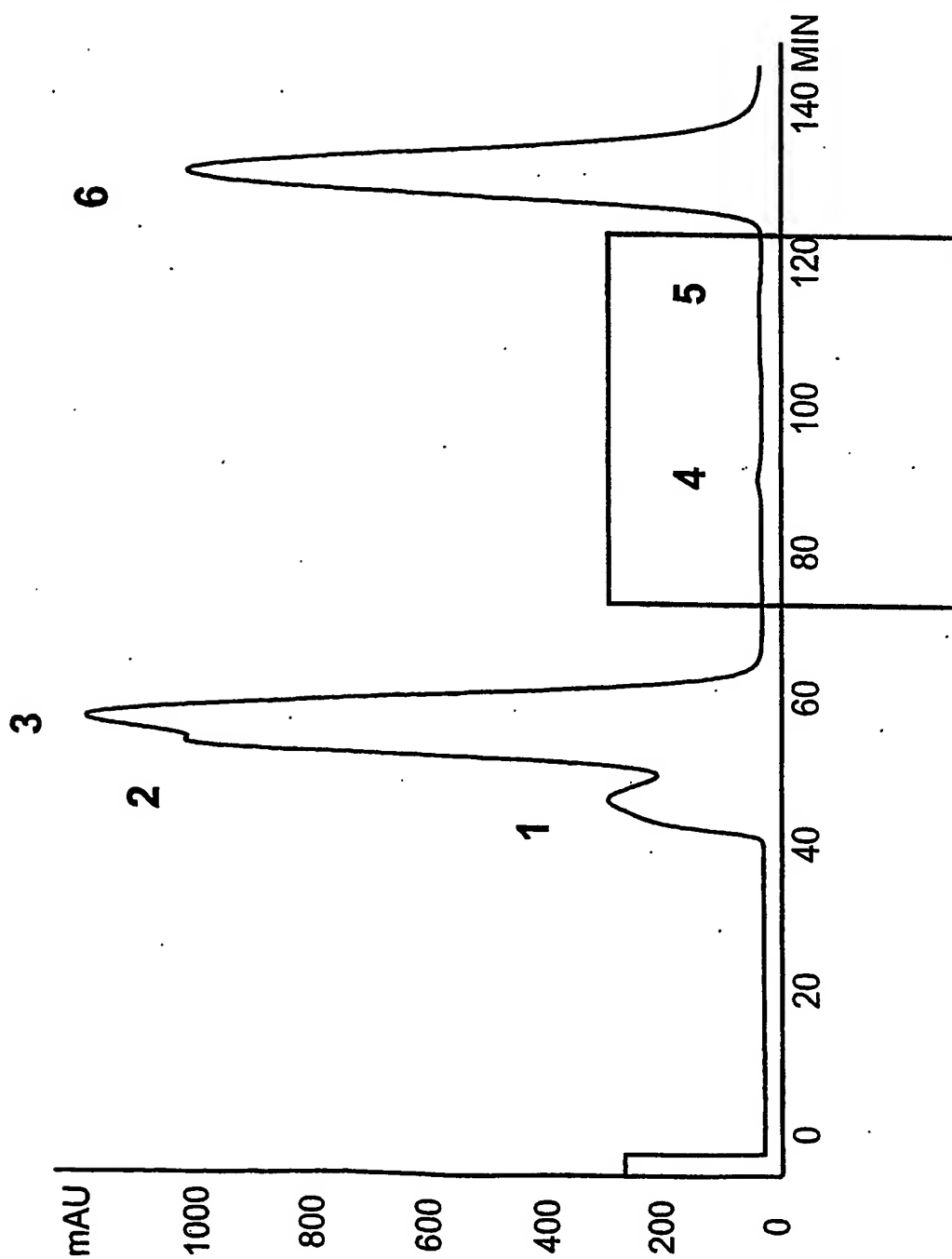


FIG. 172A

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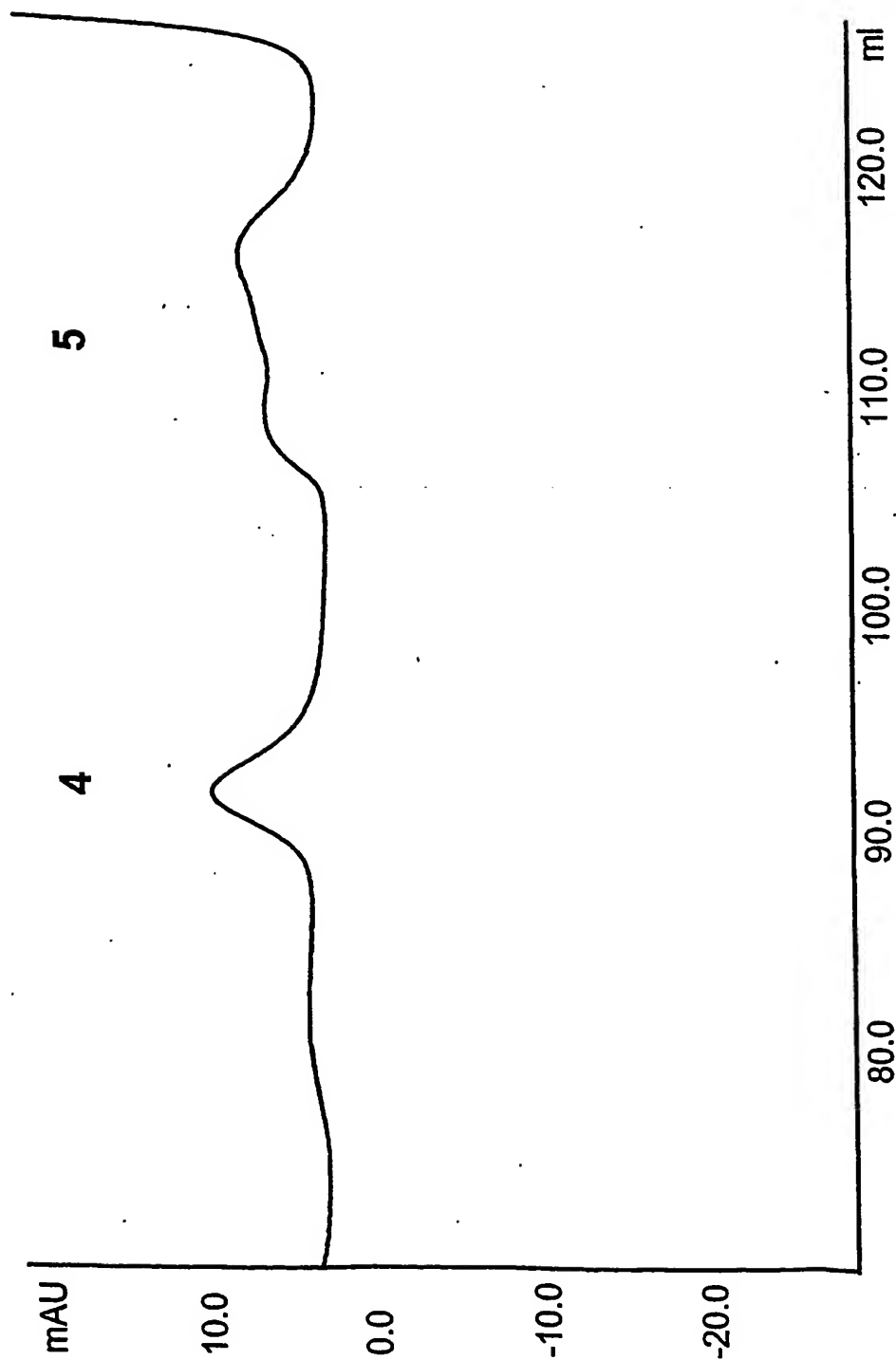


FIG. 172B



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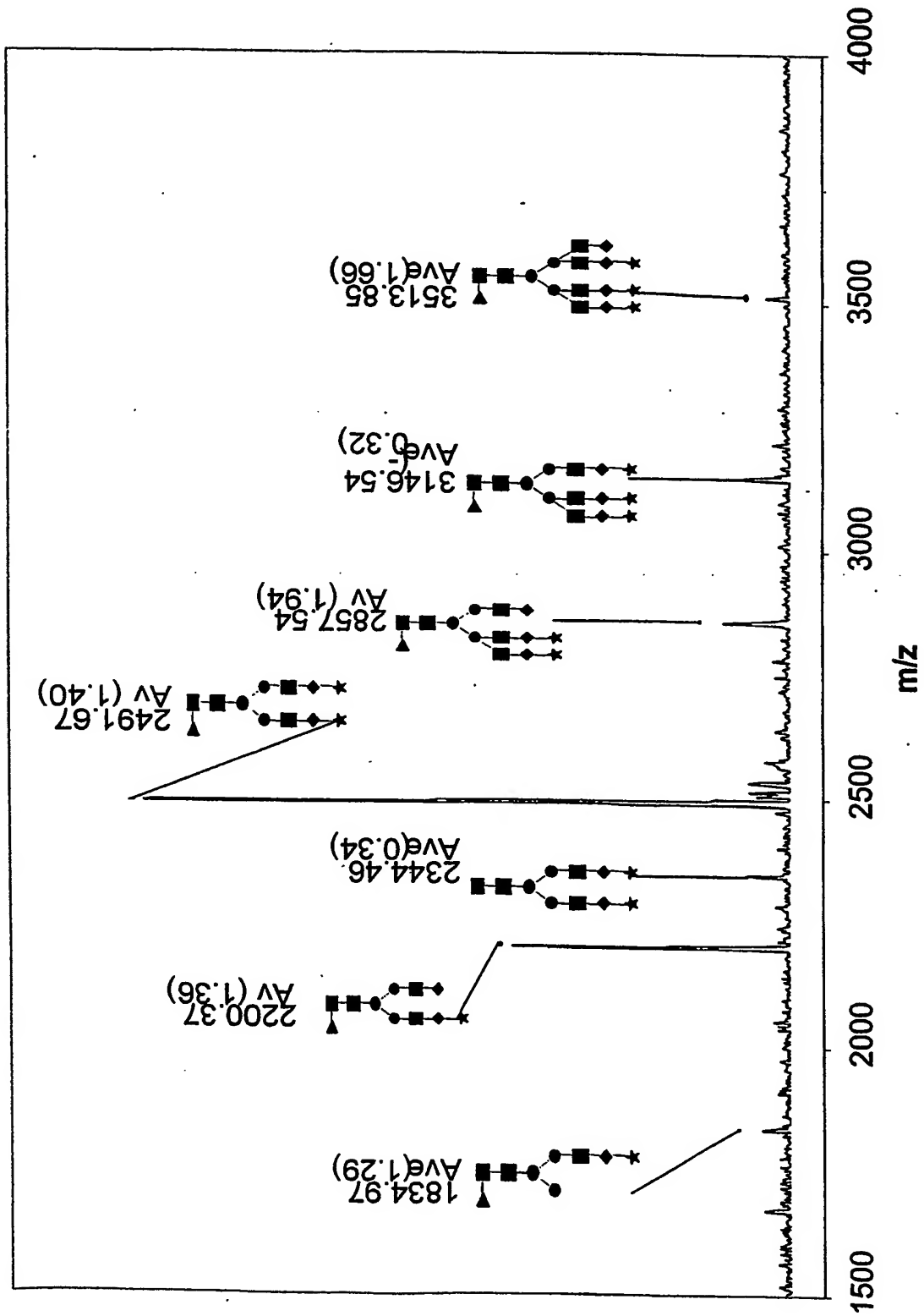


FIG. 173A

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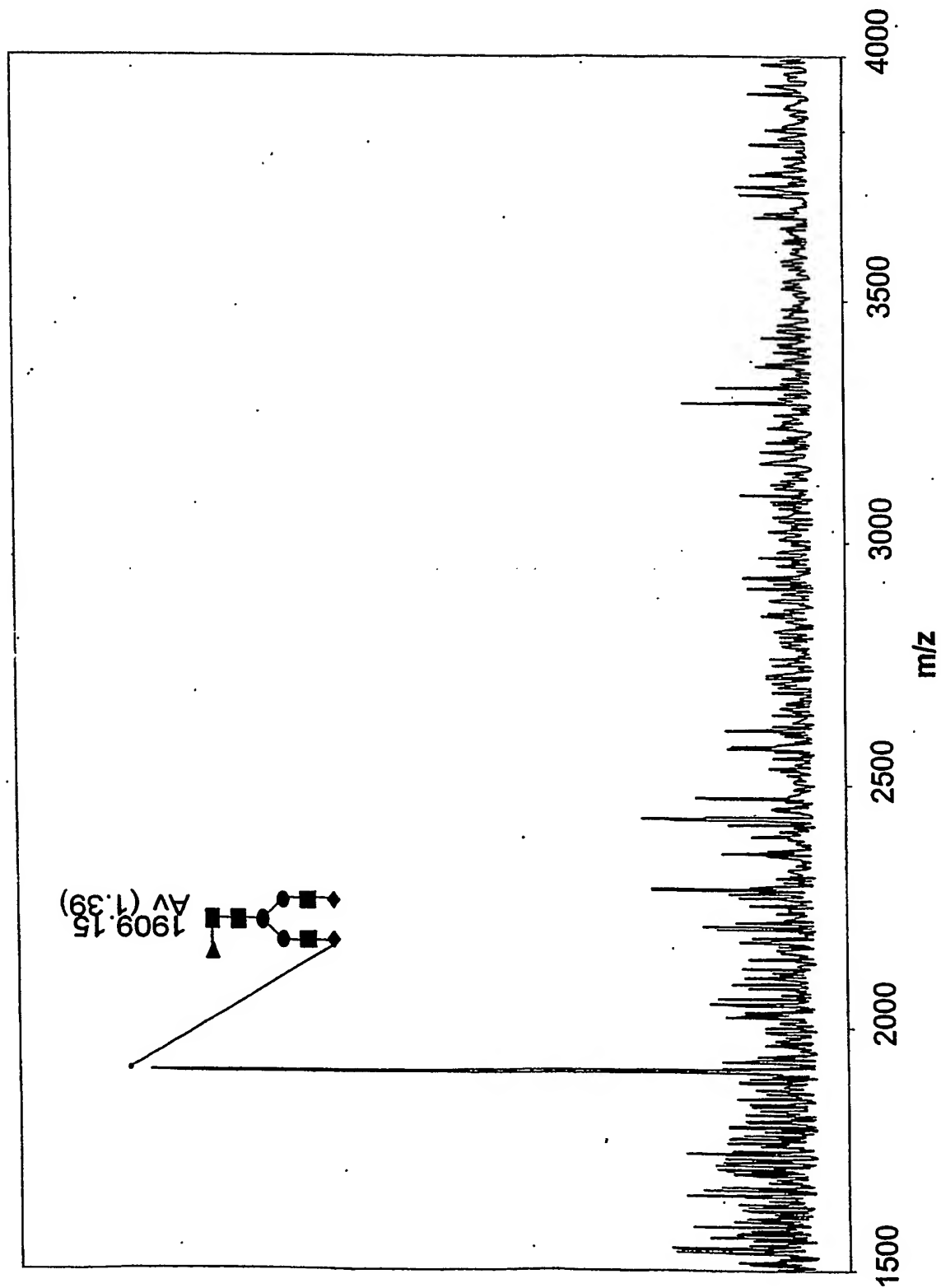


FIG. 173B

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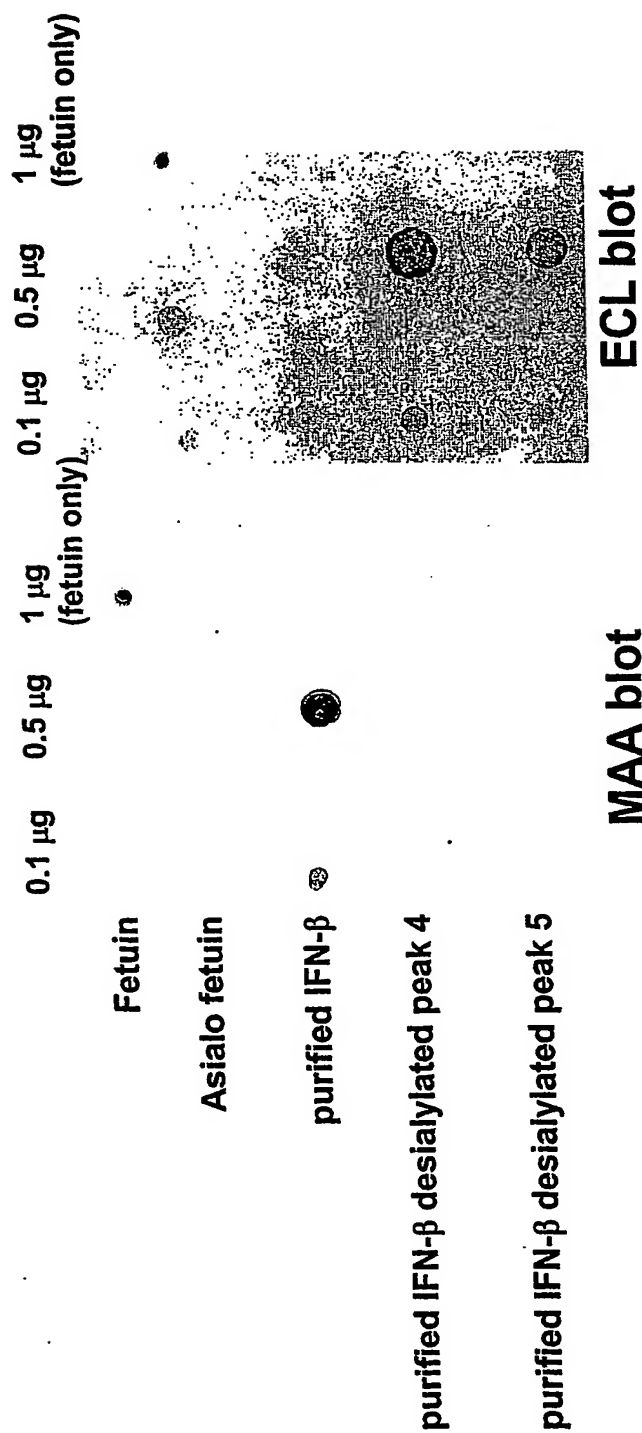


FIG. 174

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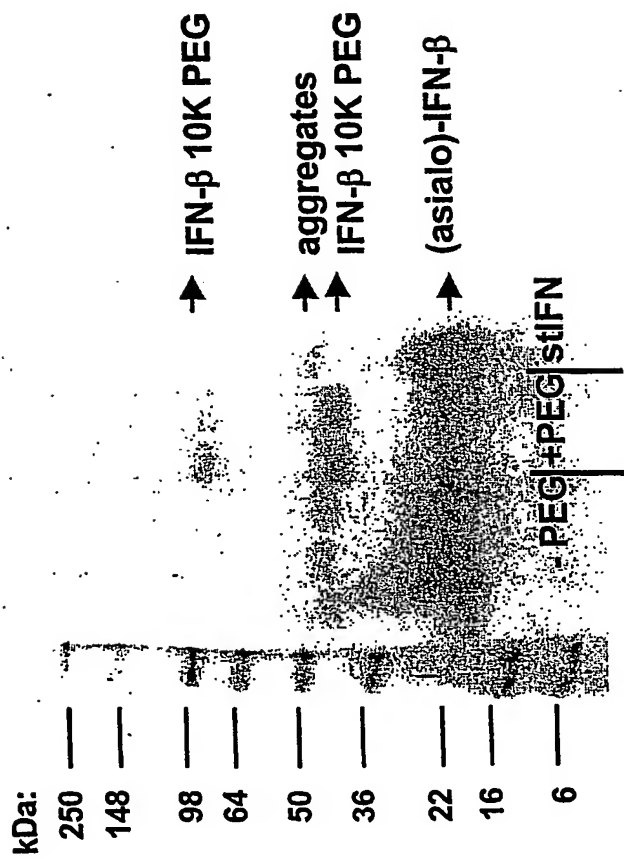
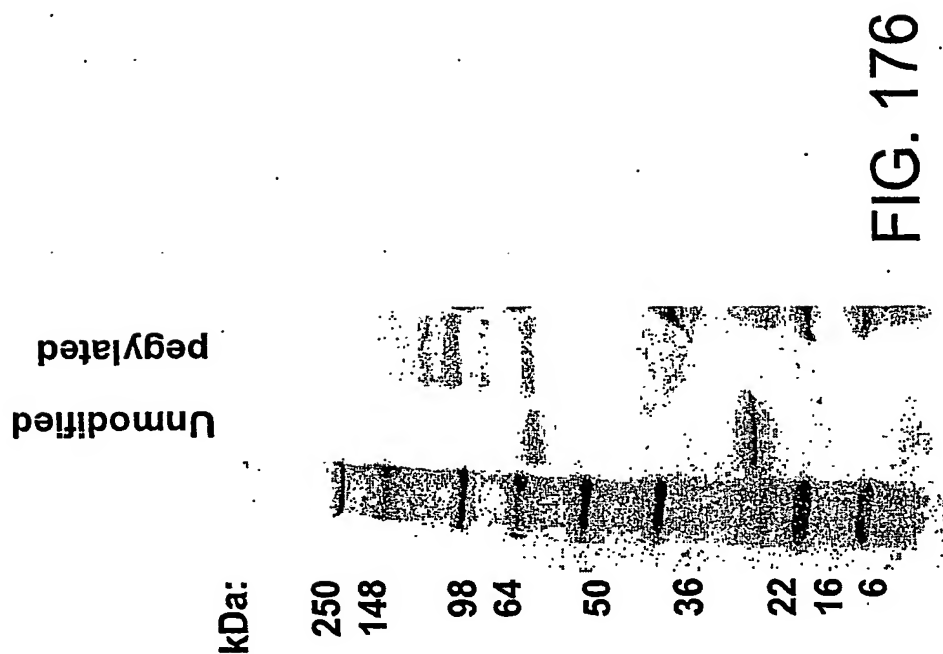


FIG. 175

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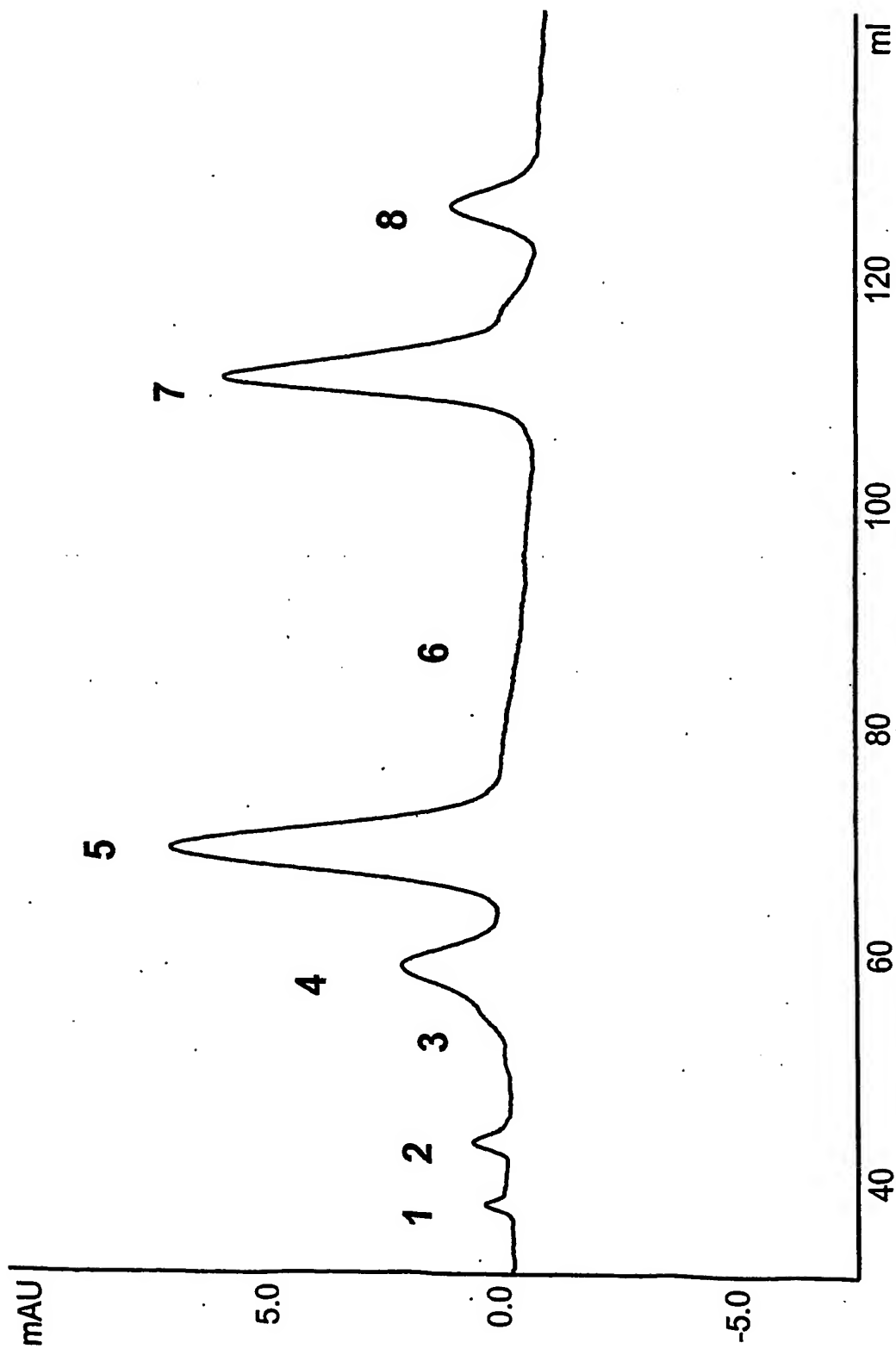


FIG. 177

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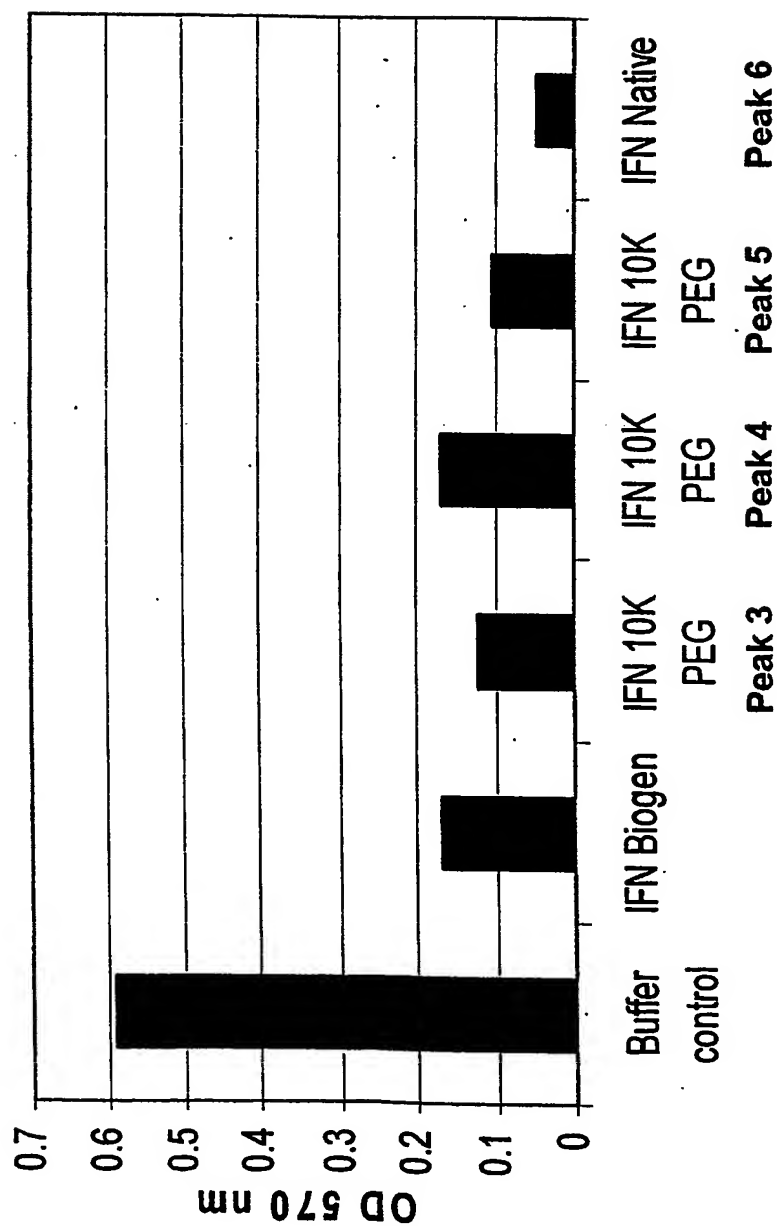


FIG. 178

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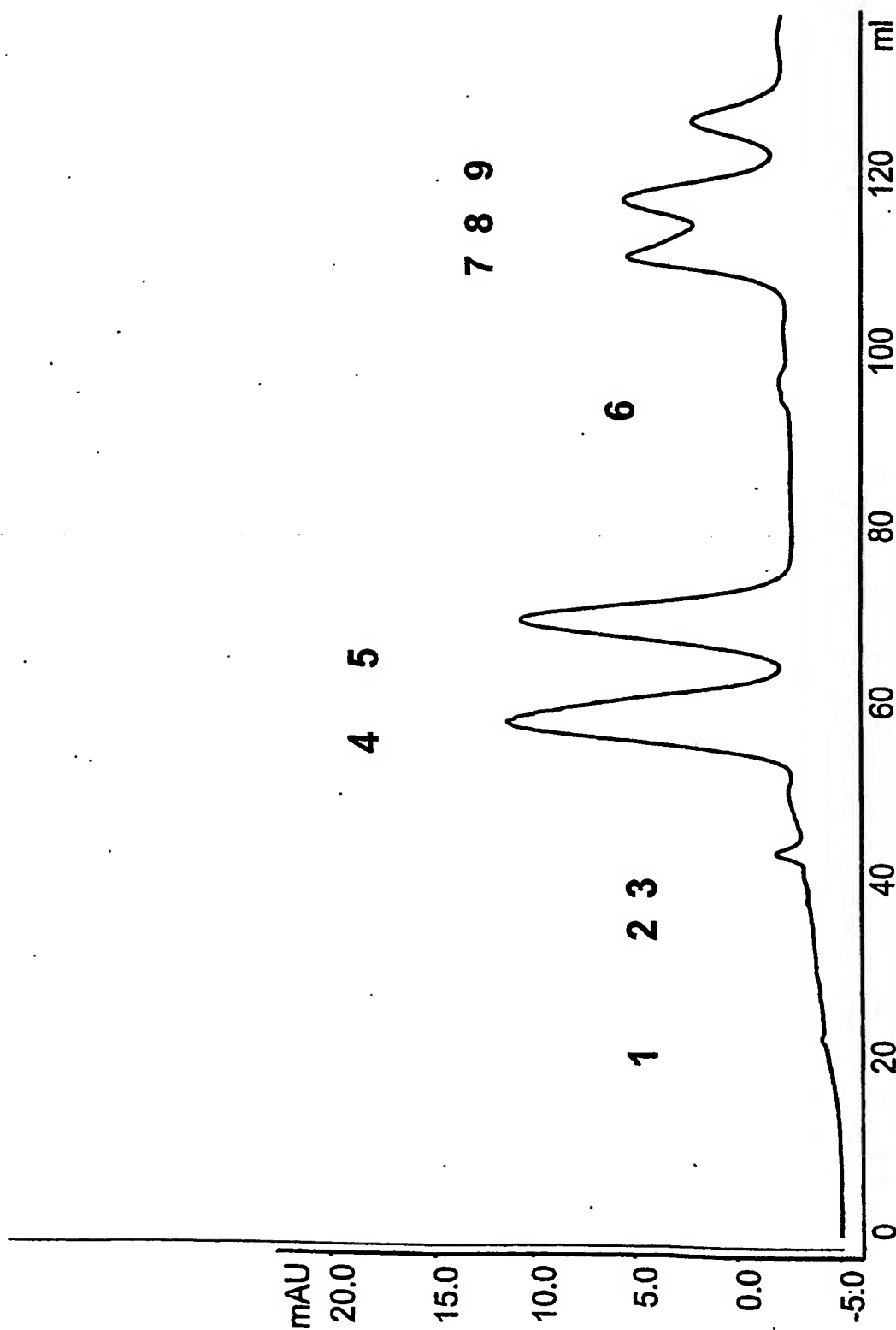


FIG. 179



Mass spectrum showing relative intensity (%) versus mass-to-charge ratio ( $m/z$ ). The x-axis ranges from 11998.0 to 18002.0  $m/z$ . The y-axis represents % Intensity from 0 to 100.

Key peaks are labeled with their  $m/z$  values:

- Man<sub>5</sub>-R: 14898.3
- Man<sub>6</sub>-R: 15062.14
- Protein: 13682.38
- Man<sub>7</sub>-R: 15226.41
- Man<sub>8</sub>-R: 15387.06
- Man<sub>9</sub>-R: 15549.62

Other labeled peaks include: 14898.37, 15002.14, 15067.04, 15222.41, 15415.30, 15410.02, 15481.00, 15530.02, 13682.30, 13681.48, and 14794.81.

**FIG. 180A**

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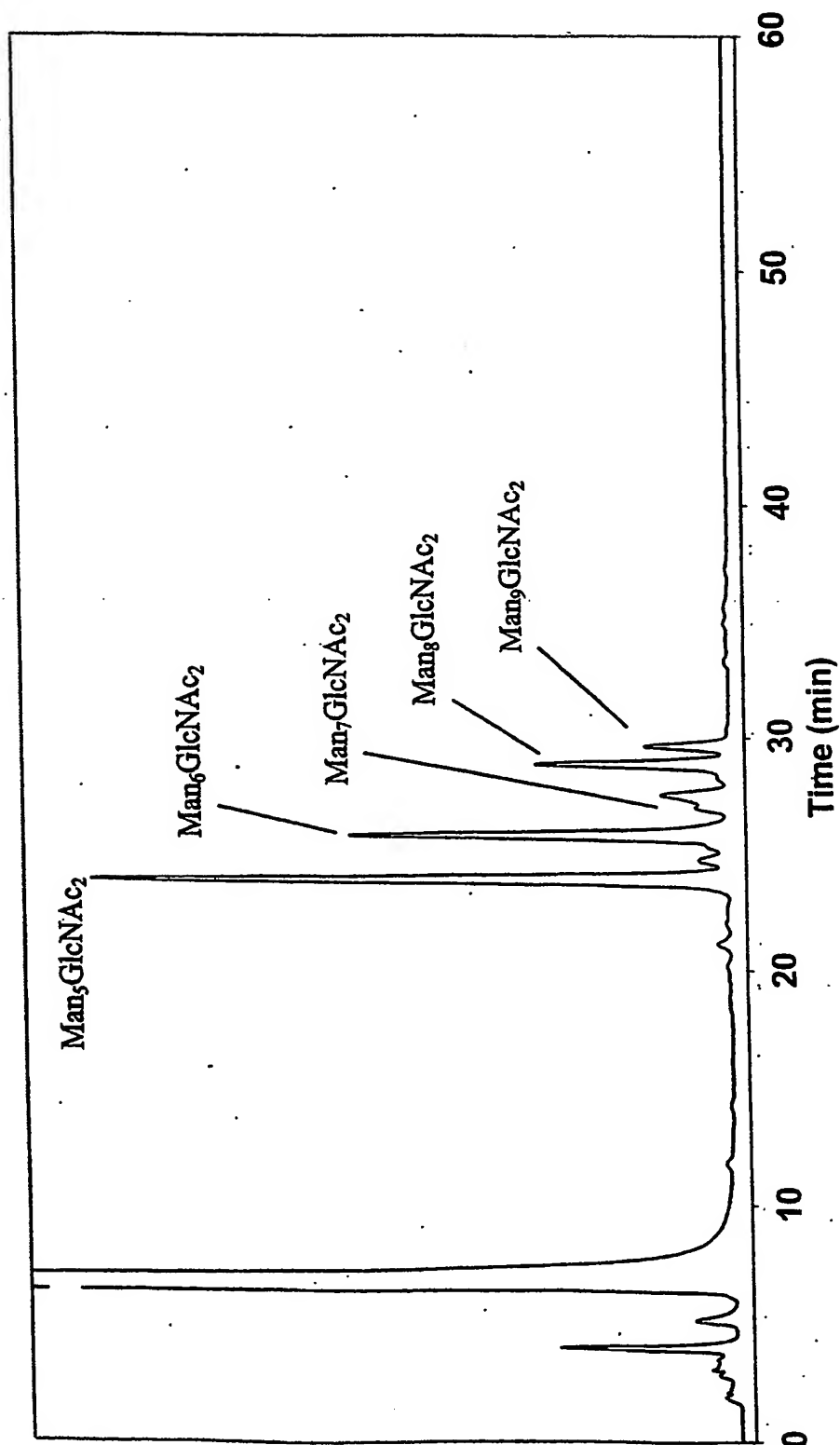


FIG. 180B

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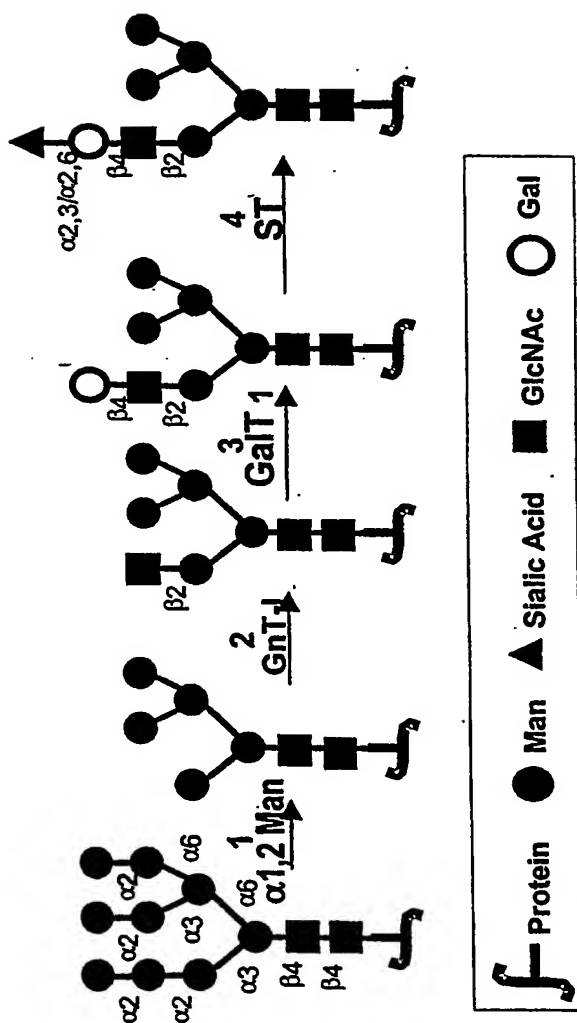


FIG. 181

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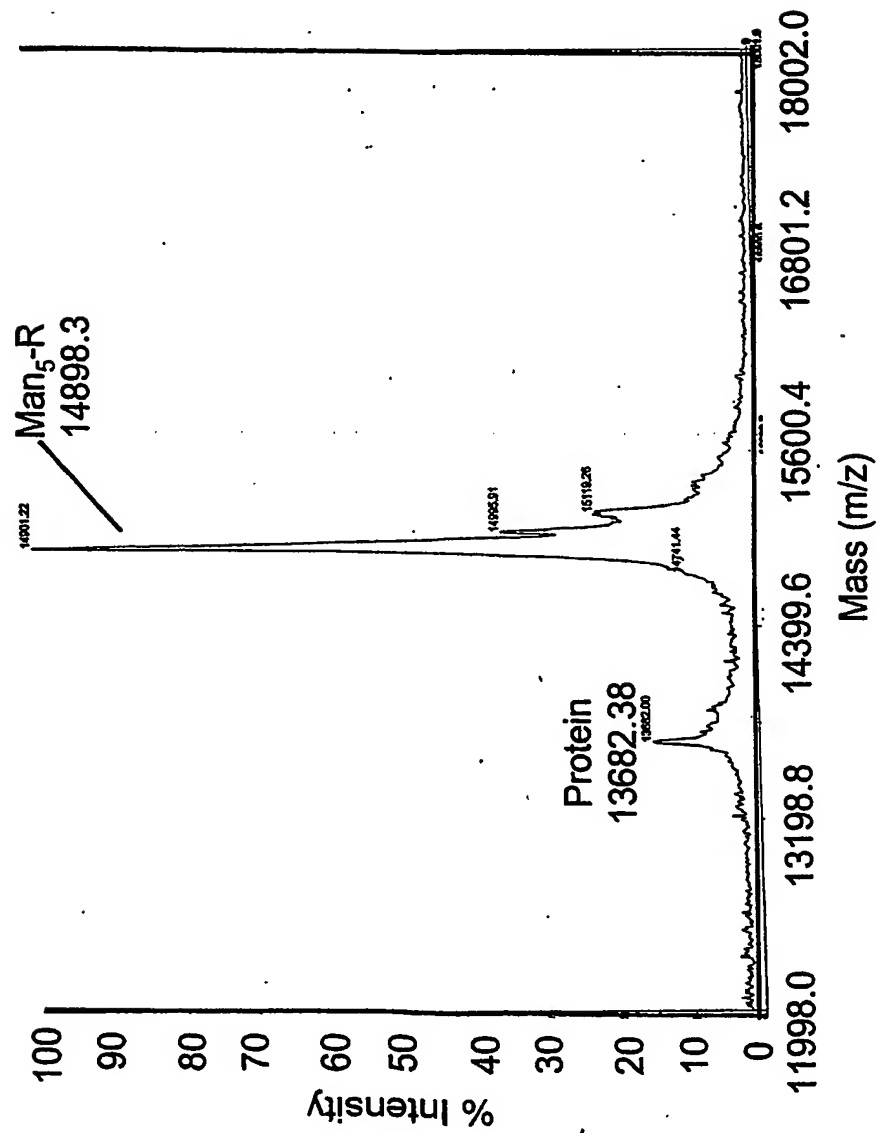


FIG. 182A

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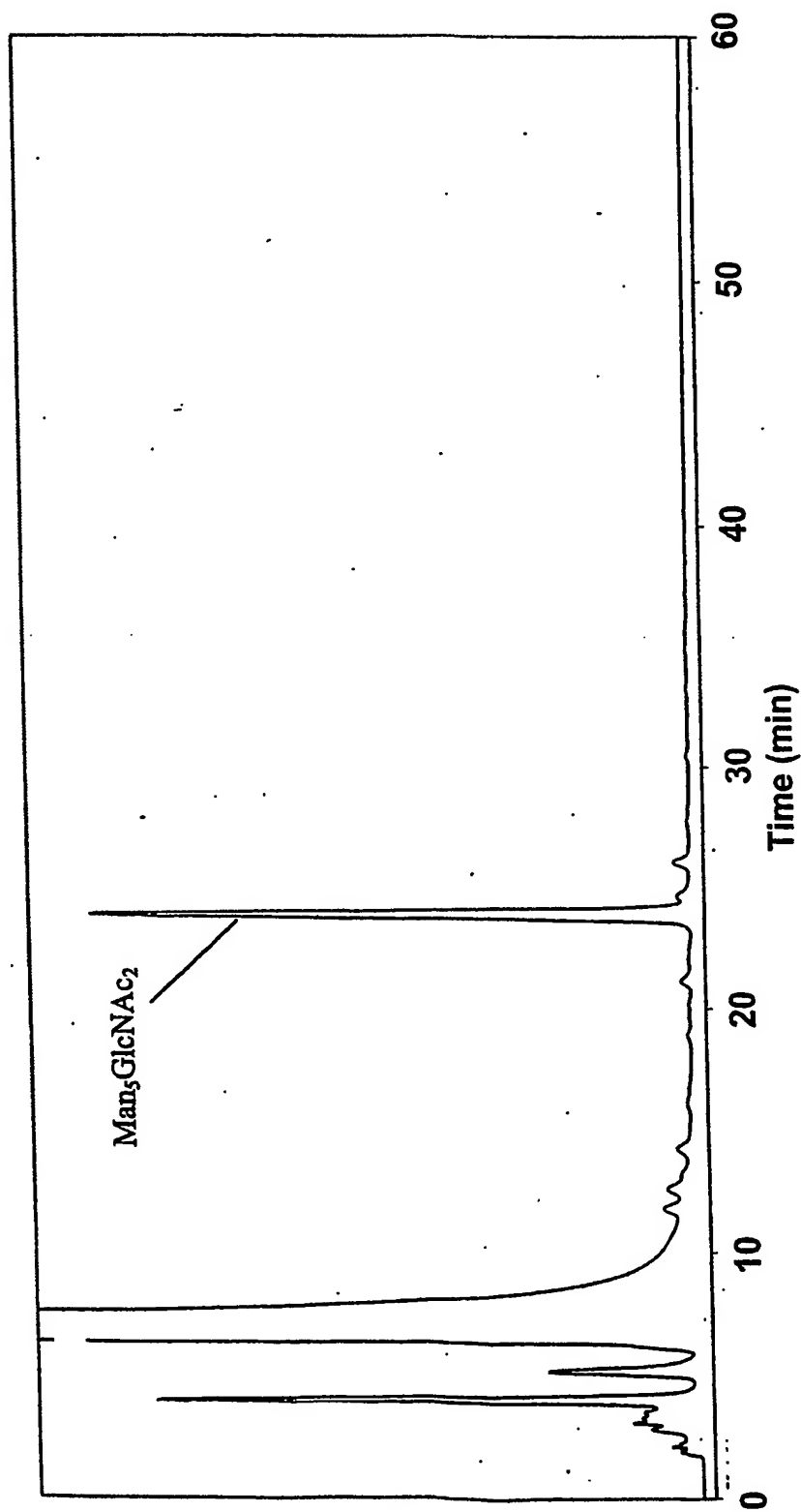


FIG. 182B

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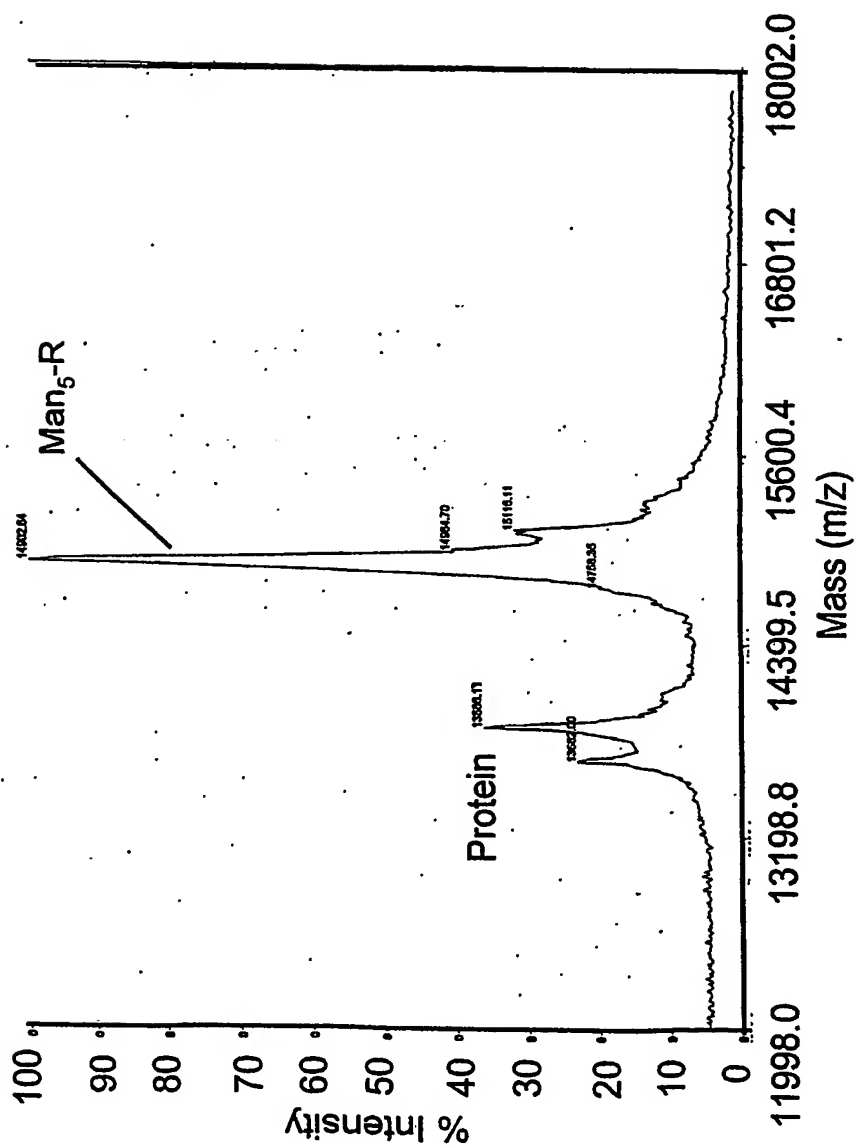


FIG. 183

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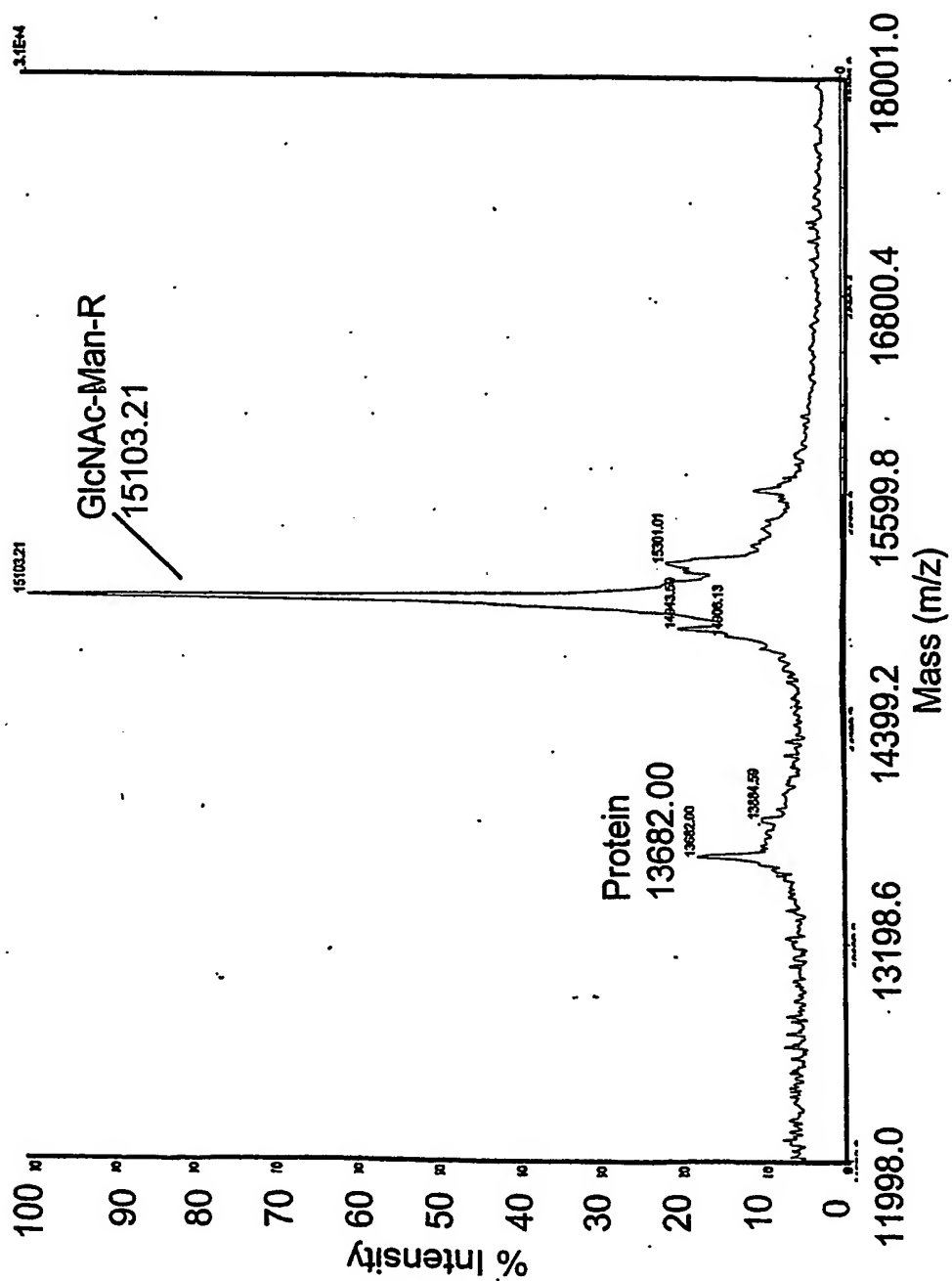


FIG. 184

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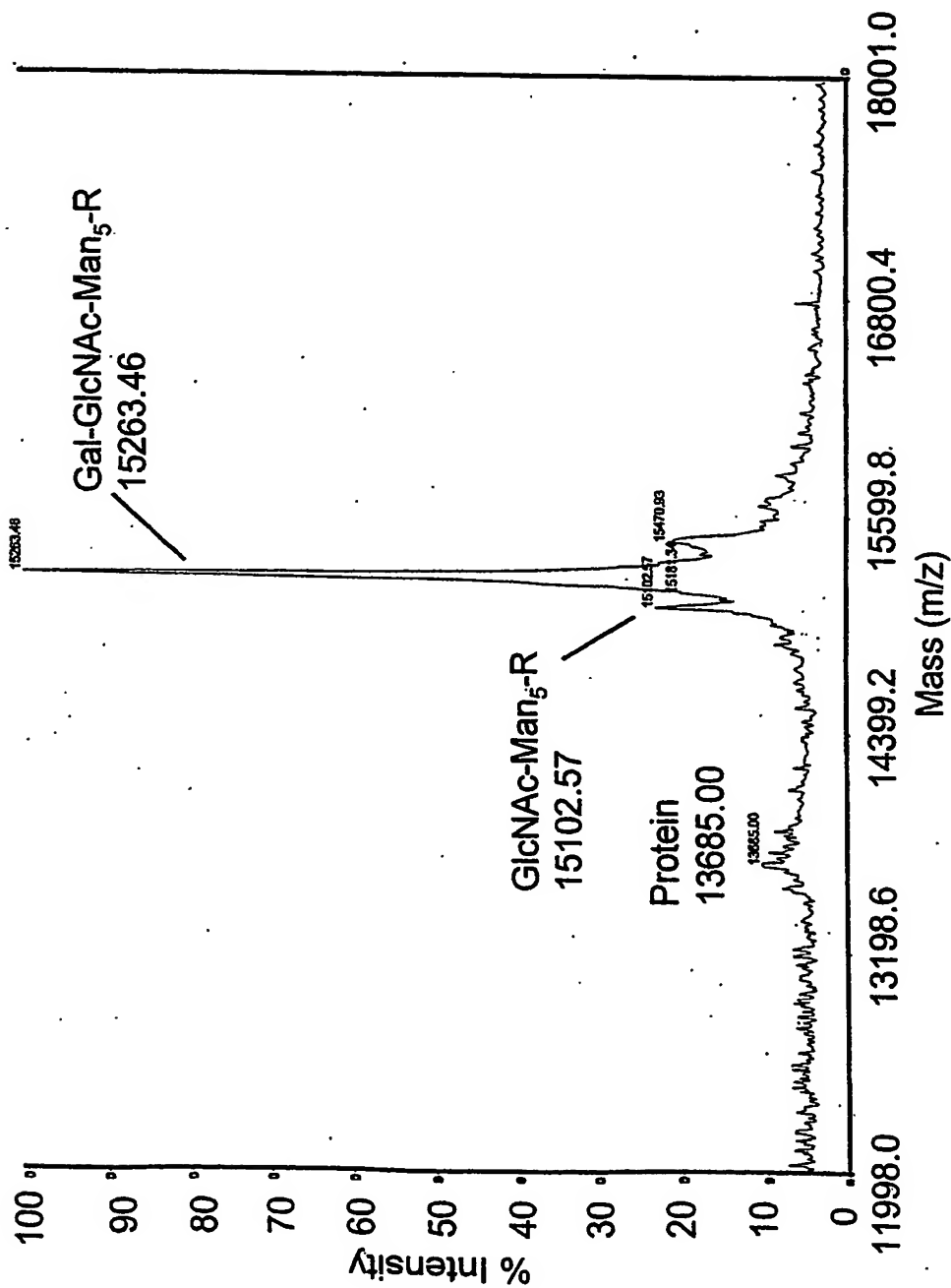


FIG. 185



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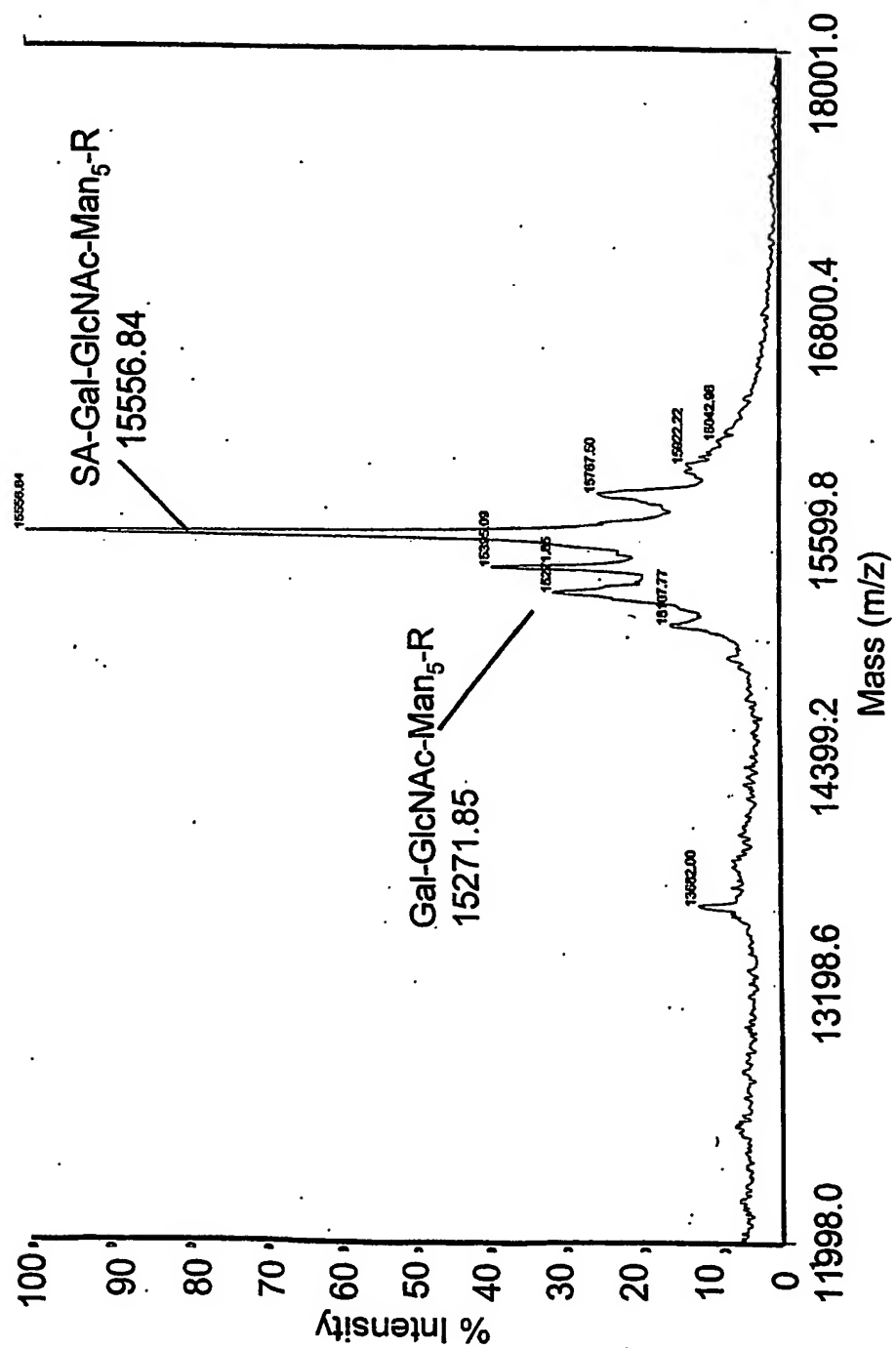


FIG. 186

[illegible]

FIG. 187A

Mass spectrum of CMP-SA-PEG. The x-axis represents Mass (m/z) from 5999.0 to 30001.0, and the y-axis represents % Intensity from 0 to 100. The base peak is at m/z 10546.44. Other significant peaks are labeled with their m/z values.

m/z	Approx. % Intensity
6018.41	95
6074.82	85
6106.88	82
6264.37	80
6471.81	75
6728.08	72
6818.80	70
6932.01	68
7055.08	65
7480.81	62
7615.38	60
7648.78	58
76428.80	58
7719.80	55
7819.01	52
7919.01	50
8019.01	48
8119.01	45
8219.01	42
8319.01	40
8419.01	38
8519.01	35
8619.01	32
8719.01	30
8819.01	28
8919.01	25
9019.01	22
9119.01	20
9219.01	18
9319.01	15
9419.01	12
9519.01	10
9619.01	8
9719.01	5
9819.01	3
9919.01	2
10019.01	1
10119.01	1
10219.01	1
10319.01	1
10419.01	1
10546.44	100
10646.44	95
10746.44	90
10846.44	85
10946.44	80
11046.44	75
11146.44	70
11246.44	65
11346.44	60
11446.44	55
11546.44	50
11646.44	45
11746.44	40
11846.44	35
11946.44	30
12046.44	25
12146.44	20
12246.44	15
12346.44	10
12446.44	8
12546.44	5
12646.44	3
12746.44	2
12846.44	1
12946.44	1
13046.44	1
13146.44	1
13246.44	1
13346.44	1
13446.44	1
13546.44	1
13646.44	1
13746.44	1
13846.44	1
13946.44	1
14046.44	1
14146.44	1
14246.44	1
14346.44	1
14446.44	1
14546.44	1
14646.44	1
14746.44	1
14846.44	1
14946.44	1
15046.44	1
15146.44	1
15246.44	1
15346.44	1
15446.44	1
15546.44	1
15646.44	1
15746.44	1
15846.44	1
15946.44	1
16046.44	1
16146.44	1
16246.44	1
16346.44	1
16446.44	1
16546.44	1
16646.44	1
16746.44	1
16846.44	1
16946.44	1
17046.44	1
17146.44	1
17246.44	1
17346.44	1
17446.44	1
17546.44	1
17646.44	1
17746.44	1
17846.44	1
17946.44	1
18046.44	1
18146.44	1
18246.44	1
18346.44	1
18446.44	1
18546.44	1
18646.44	1
18746.44	1
18846.44	1
18946.44	1
19046.44	1
19146.44	1
19246.44	1
19346.44	1
19446.44	1
19546.44	1
19646.44	1
19746.44	1
19846.44	1
19946.44	1
20046.44	1
20146.44	1
20246.44	1
20346.44	1
20446.44	1
20546.44	1
20646.44	1
20746.44	1
20846.44	1
20946.44	1
21046.44	1
21146.44	1
21246.44	1
21346.44	1
21446.44	1
21546.44	1
21646.44	1
21746.44	1
21846.44	1
21946.44	1
22046.44	1
22146.44	1
22246.44	1
22346.44	1
22446.44	1
22546.44	1
22646.44	1
22746.44	1
22846.44	1
22946.44	1
23046.44	1
23146.44	1
23246.44	1

**FIG. 187B**

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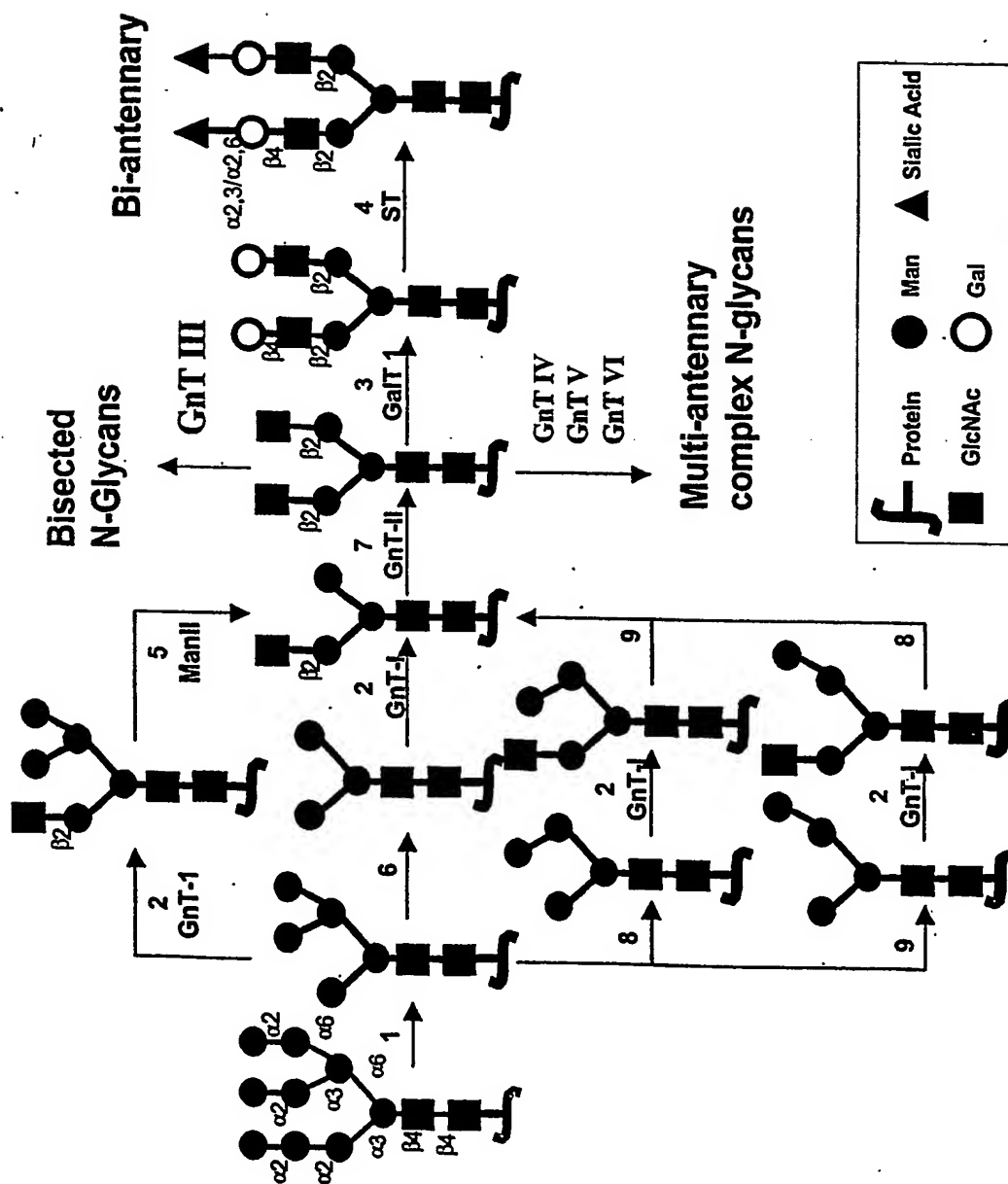


FIG. 188

Diagram illustrating the structures of the six glycoproteins (GnT V, VI, II, III, I, IV) and their common core structure (Man $\beta$ 1-4-R).

```

graph TD
    GnTV[GnT V] --- GlcNAc1-6[GlcNAc $\beta$ 1-6]
    GnTVI[GnT VI] --- GlcNAc1-4[GlcNAc $\beta$ 1-4]
    GnTII[GnT II] --- GlcNAc1-2[GlcNAc $\beta$ 1-2]
    GnTII --- Man1-6[Man $\alpha$ 1-6]
    GnTIII[GnT III] --- GlcNAc1-4[GlcNAc $\beta$ 1-4]
    GnTIII --- Man1-4-R[Man $\beta$ 1-4-R]
    GnTI[GnT I] --- GlcNAc1-2[GlcNAc $\beta$ 1-2]
    GnTI --- Man1-3[Man $\alpha$ 1-3]
    GnTIV[GnT IV] --- GlcNAc1-4[GlcNAc $\beta$ 1-4]
    GnTIV --- Man1-3[Man $\alpha$ 1-3]
    Man1-6 --- Man1-4-R
    Man1-3 --- Man1-4-R
  
```

The diagram shows the following structures:

- GnT V: GlcNAc $\beta$ 1-6
- GnT VI: GlcNAc $\beta$ 1-4
- GnT II: GlcNAc $\beta$ 1-2 and Man $\alpha$ 1-6
- GnT III: GlcNAc $\beta$ 1-4 and Man $\beta$ 1-4-R
- GnT I: GlcNAc $\beta$ 1-2 and Man $\alpha$ 1-3
- GnT IV: GlcNAc $\beta$ 1-4 and Man $\alpha$ 1-3

The common core structure is Man $\beta$ 1-4-R, which is connected to the structures of GnT II, GnT III, and GnT IV.

**FIG. 189**

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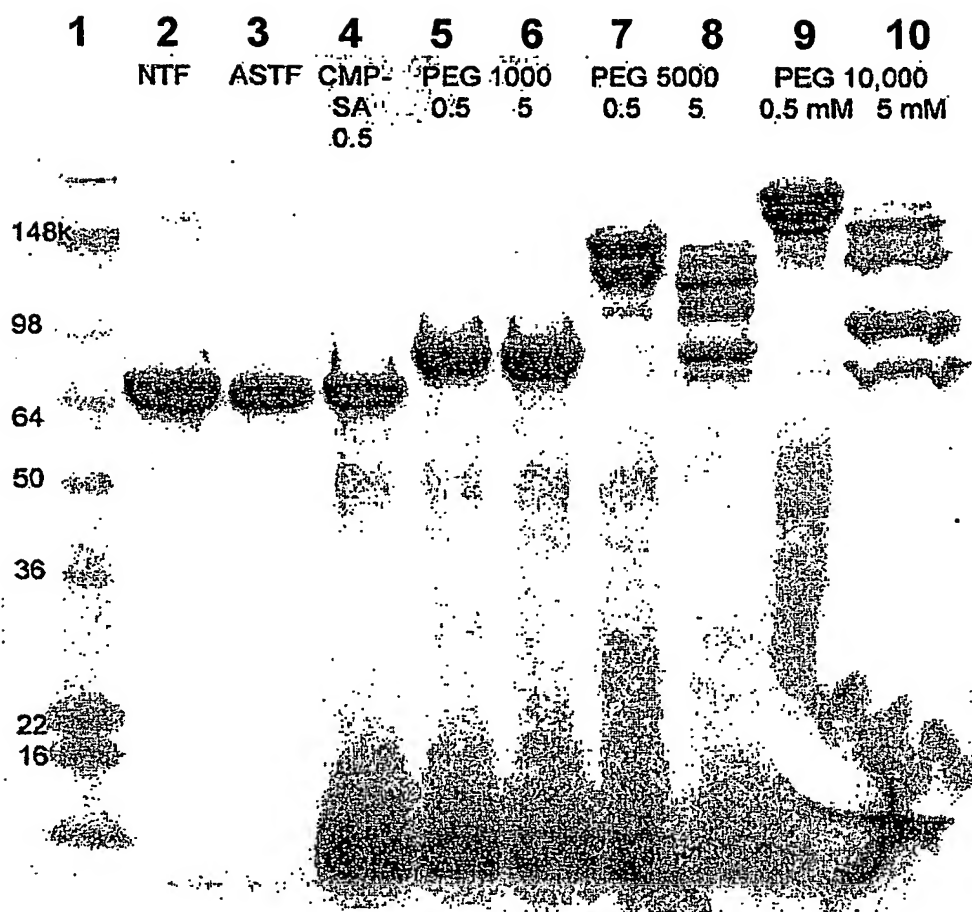


FIG. 190

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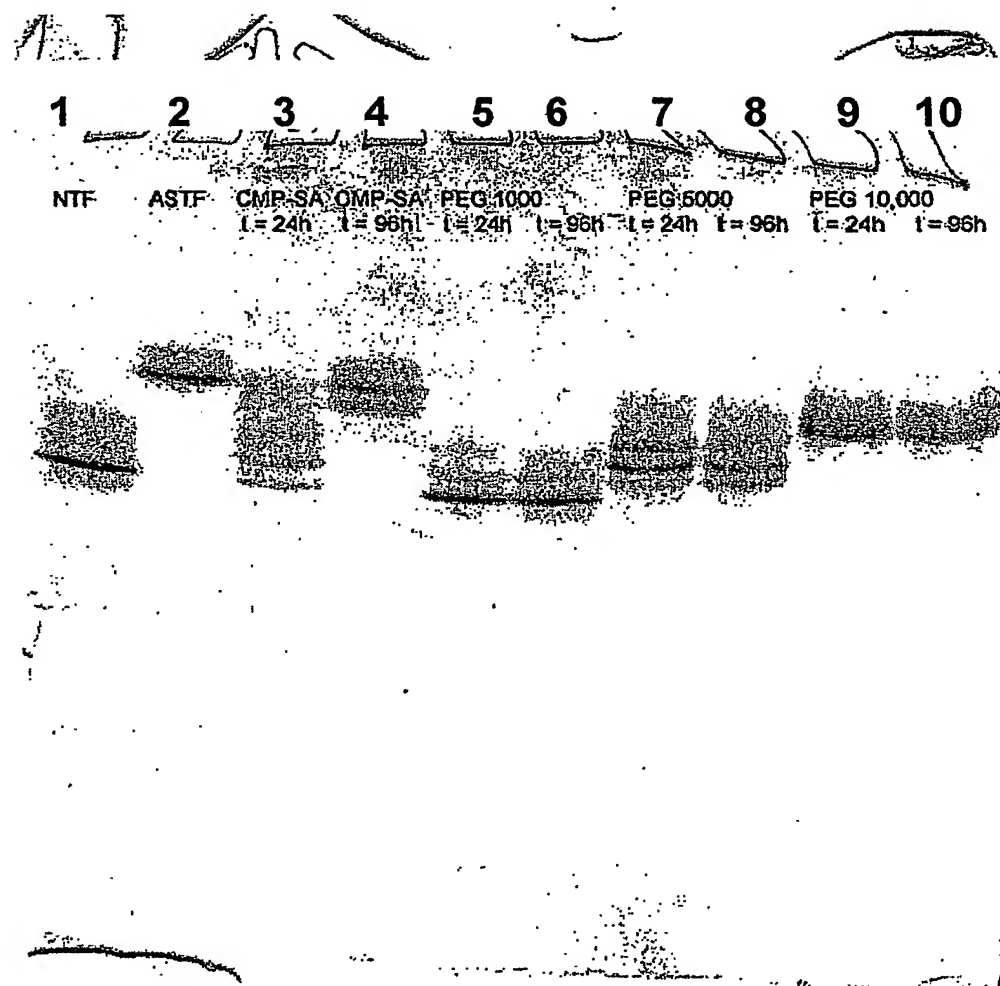
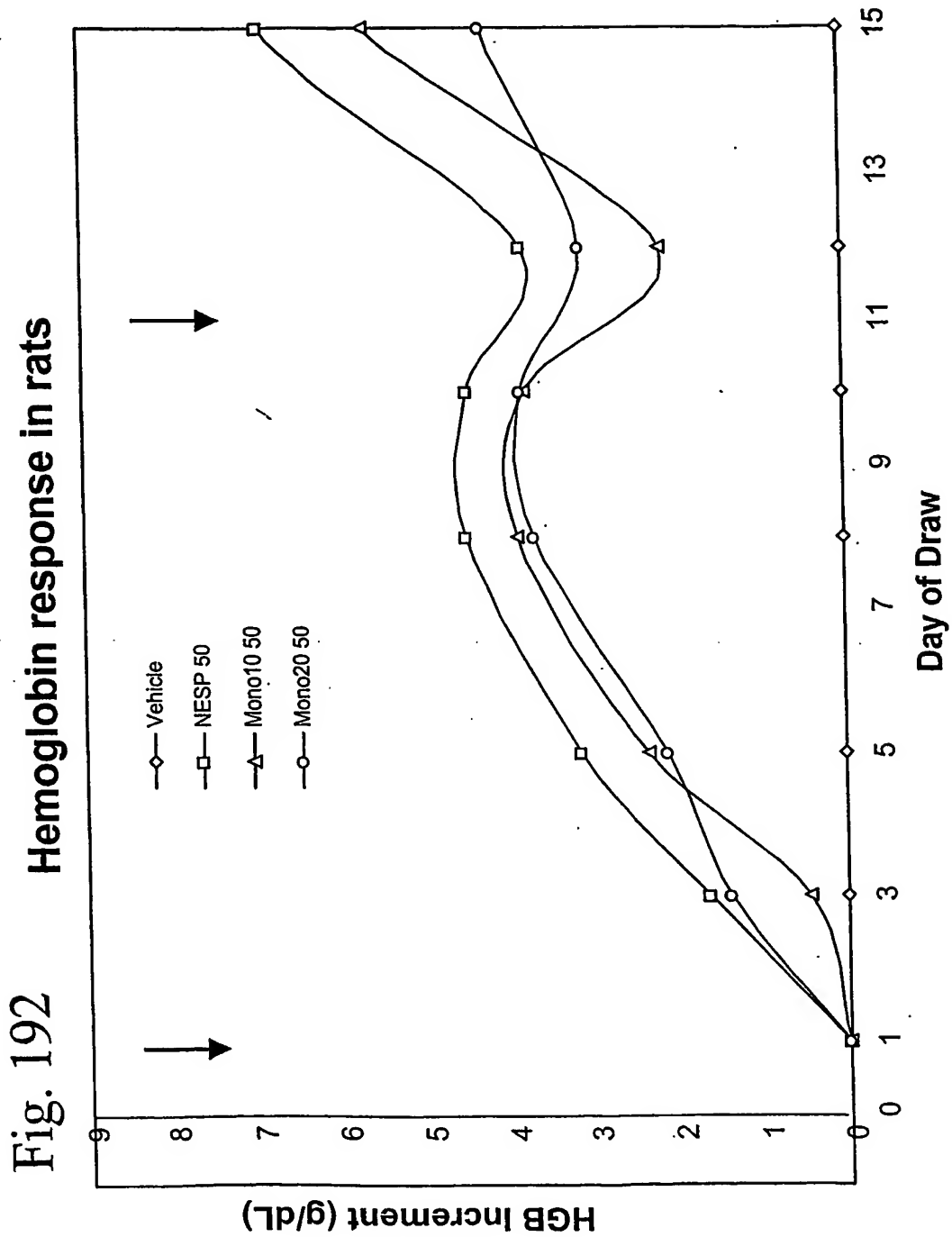


FIG. 191

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